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1. DATA SET IDENTIFICATION

1.1 Title of Catalog document

EMAP-Estuaries Program Level Database
1990 Virginian Province
Benthic Taxon Data Summarized by Station

1.2 Authors of the Catalog entry

Charles Strobel, U.S. EPA NHEERL-AED
Melissa Hughes, OAO Corporation

1.3 Catalog revision date

28 March 1996

1.4 Data set name

BEN_SPEC

1.5 Task Group

    Estuaries

1.6 Data set identification code

    00030

1.7 Version

    001

1.8 Requested Acknowledgment

If you plan to publish these data in any way, EPA requires a standard statement for work it has supported:

"Although the data described in this article have been funded wholly or in part by the U. S. Environmental Protection Agency through its EMAP-Estuaries Program, it has not been subjected to Agency review, and therefore does not necessarily reflect the views of the Agency and no official endorsement should be inferred."

2. INVESTIGATOR INFORMATION

2.1 Principal Investigator

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2.2. Investigation Participant-Sample Collection

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2.3 Principal Investigator-Sample Processing

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3. DATA SET ABSTRACT

3.1 Abstract of the Data Set

The BENTHIC SPECIES data set presents summary data on each benthic taxon identified across all acceptable grabs collected at a station. A count of organisms of the taxon identified from all grabs (generally 3) is recorded. The mean abundance and standard deviation of the mean abundance is also reported. Each taxon is identified by a unique code which can be cross-referenced to the taxon phylogeny. Physical constraints or quality assurance problems precluded the collection or analysis of all samples at a few stations.

3.2 Keywords for the Data Set

   Benthic Species, Mean Species Abundance, Species Abundance,
   Species Composition, Taxon Abundance, Benthic Taxon
   Abundance, Mean Benthic Taxon Abundance

4.   OBJECTIVES AND INTRODUCTION

  4.1 Program Objective

     The Environmental Monitoring and Assessment Program (EMAP)
     was designed to periodically estimate the status and trends
     of the Nation's ecological resources on a regional basis.
     EMAP provides a strategy to identify and bound the extent,
     magnitude and location of environmental degradation and
     improvement on a regional scale based on randomly located
     station sites. The randomly located stations were called
     Base Sampling Sites (BASE).

  4.2 Data Set Objective

     The objective of the Benthic Species data set is to provide
     summary data for each taxon or species of bottom dwelling
     (benthic) organism identified from each station sampled in
     the Virginian Province in 1990.

  4.3 Data Set Background Information

     Benthic invertebrates are important secondary consumers in
     most estuarine systems, represent the largest living
     reservoir of organic carbon in many estuarine systems,
     contain many commercially and recreationally important
     species and are prey for critical life stages of other
     commercially and recreationally important species.

     Benthic invertebrate assemblages are sensitive to
     disturbance and stress from both natural and anthropogenic
     origins because of their taxonomic diversity, wide range of
     physiological tolerances to stress and multiple feeding
     modes and trophic levels. The condition of these
     communities is a reflection of local environmental
     conditions (since members of benthic assemblages generally
     have limited mobility). The communities respond to both
     sediment and water column conditions and contain long-lived
     species relative to most invertebrate communities in the
     water column. Consequently, benthic community studies have
     been used in many regional estuarine monitoring programs and
     have proven to be an effective indicator for describing the
     extent and magnitude of pollution impacts in estuarine
     ecosystems.

     Benthic monitoring data describing species composition,
     abundance and biomass were used as indicators of the
     biological conditions in the estuaries of the Virginian
     Province. These descriptions, along with additional
     measurements in other data sets describing habitat
     indicators (depth, salinity) and pollution exposure
     indicators (oxygen concentrations, sediment toxicity,

sediment contaminant concentrations) are being used to develop a benthic index of environmental condition for the Province.

4.4 Summary of Investigation Parameters

Benthic species diversity, abundance and biomass were counted or measured from the grabs, generally three, collected at a station. Summary data were calculated from these laboratory data.

5. DATA ACQUISITION AND SAMPLING METHODS

5.1 Data Acquisition

5.1.1 Sampling Objective

Collect sediment grab samples suitable for the analysis of benthic assemblages and biomass. Three replicate sediment samples were expected to be taken at each station.

5.1.2 Sample Collection Methods Summary

The grab sampler was lowered through the water column such that travel through the last 5 meters was no faster than 1 m/sec. The grab penetrated the sediment by gravity releasing a trigger allowing the jaws to close. When the grab was pulled from the sediment using the winch, the jaws closed, encapsulating the sediment sample. After the sampler was retrieved, it was lowered into an on-board cradle.

5.1.3 Sampling Start Date

19 July 1990

5.1.4 Sampling End Date

30 September 1990

5.1.5 Platform

Sampling was conducted from 8 m (24 ft), twin-engine Chesapeake style work boats.

5.1.6 Sampling Gear

A 1/25 m2, stainless steel, Young-modified Van Veen Grab sampler was used to collect sediment grabs for benthic analyses. This grab sampled a sample area of 440 cm2 and a maximum depth of penetration in the sediment of 10 cm. Samples were sieved through a 0.5 mm round stainless steel sieve.

5.1.7 Manufacturer of Sampling Equipment

Young's Welding, Sandwich, MA

5.1.8 Key Variables

At the time of sample collection, the number of grabs collected was recorded.

5.1.9 Collection Method Calibration

The sampling gear did not require any calibration. It required inspection for deformities incurred due to mishandling or impact on rocky substrates.

5.1.10 Sample Collection Quality Control

To ensure the integrity of the sediment samples collected, the interior surfaces of the grab sampler (including the underside of the hinged top) were rinsed prior to use to assure that no sediment remained from the previous station. To minimize the effects of bow wave disturbance to surficial sediments, the speed of grab through the water column was reduced as it neared the bottom. To minimize the chance of sampling the exact same location twice, after three (3) grabs were taken, the boat was moved five (5) meters downstream by letting out the appropriate length of anchor line. Sediment grabs used for benthic samples were randomly interspersed with the grabs used for sediment chemistry/toxicity samples.

A successful grab had relatively level, intact sediment over the entire area of the grab and a sediment depth at the center of at least 5 centimeters. Unacceptable grabs included those: substrates or grossly slumped surfaces. Grabs completely filled to the top, where the sediment was in direct contact with the hinged top, were also unacceptable.

The sieve was inspected immediately following the removal of the sample to ensure no organisms were left clinging to the sieve. Any organisms found were placed in the sample jar. The sieve was also thoroughly scrubbed with a stiff brush between samples.

5.1.11 Sample Collection Method Reference

Strobel, C.J. 1990. Environmental Monitoring and Assessment Program-Near Coastal Component: 1990 Demonstration Project Field Operations Manual. U.S. EPA NHEERL-AED, Narragansett, RI. October 1990.

5.1.12 Sample Collection Method Deviations

NA

5.2 Data Preparation and Sample Processing

5.2.1 Sample Processing Objective

Process sediment samples to accurately identify and enumerate all macrobenthic organisms found to the lowest taxonomic category which was possible.

5.2.2   Sample Processing Methods Summary

5.2.2.1   Field Summary

A clear plastic core was inserted into a random location in
the grab. The sediment within the core was extruded into
a "Whirl Pack" for benthic grain size analysis.

The sample was processed for benthic community
analysis. Each grab was placed separately into a frame
holding a 500 um sieve. The sieve was placed into a
sieve box containing water from the sampling station.
The sieve was agitated to wash away sediments and leave
organisms, detritus, sand particles and pebbles larger
than 500 um. This method was used to minimize
mechanical damage to fauna. A gentle flow of water
over the sample was also acceptable.

The contents on the sieve were gently rinsed, using a
funnel, into a bottle or bottles. The sieve was
inspected for remaining organisms. These were removed
by forceps and placed in the bottle. Benthic infauna
(final concentration of approximately 10% formalin).
The samples were again mixed by inversion and placed in
the dark. After processing each grab, the sieve was
vigorously cleaned with water and a brush to prevent
cross-contamination of samples.

5.2.2.2   Laboratory Summary

BENTHIC SAMPLES: The samples were washed through 500 um
mesh sieves. Benthic fauna were sorted from the
sediments, identified to species, if possible, and
enumerated. Benthic fauna identified included those
commonly termed 'macrofauna', i.e., those metazoan
organisms retained by a 0.5 mm mesh sieve.
'Meiofaunal' groups were not identified or enumerated.
These groups included: nematodes, ostracods,
turbellarians, harpacticoid copepods and foraminifera.
In addition to meiofauna, taxonomic groups having only
planktonic forms were excluded from the identification
process. Examples of these groups were copepods and
cladocerans.

Benthic fauna were identified to the lowest practical
taxonomic level. Macrobenthos were identified to
species, except for the following groups: class
anthozoa (class), subclass copepoda (order), phylum
nemertinea (phylum), subclass ostracoda (subclass) and
class turbellaria (class). For samples collected in
low salinity (less than 5 ppt) water, oligochaetes and
chironomids were identified to species, where possible.
Above 5 ppt salinity, individuals of these groups from
higher salinities were not further differentiated.

BIOMASS: Identified and counted organisms were grouped
by categories of taxonomic and ecologically

significance to be used in biomass determinations, placed in vials and preserved.

Biomass was determined using formaldehyde dry weight. Soft-bodied organisms and those having significant inorganic body parts were treated separately. The dry weight biomass of soft-bodied organisms was directly measured after drying. However, hard-bodied organisms (e.g., bivalves, gastropods, and echinoderms) were acidified prior to measuring dry weight in order to remove calcium carbonate (bivalves >2 cm in length were shucked rather than acidified). Biomass measurements were made using an analytical balance with an accuracy of 0.1 mg. Biomass was determined as shell-free dry weight after drying to a constant weight at 60 degrees C.

In the data base, biomass data are reported along with an abundance value (the number of organisms included in the sample). Data base records with a biomass value greater than zero but with an abundance equal to zero indicate that organism fragments were included in the sample.

SILT/CLAY: The procedure used to determine per cent silt/clay content is summarized below. The sediment sample was stirred, homogenized in a clean beaker and sieved using a 63 um mesh sieve. The fraction retained on the sieve (> 63 um) was transferred to a tared evaporating dish, dried in an oven and weighed as the sand weight. The filtrate fraction (< 63 um) was transferred to a 1 liter graduated cylinder, shaken to evenly distribute the particles and a set volume removed to a tared evaporating dish. The sample was dried and weighed as the silt/clay weight.

MOISTURE: A summary of the procedure used for the determination of moisture contents follows. The sample was brought to room temperature and homogenized in a beaker. An aliquot of wet sediment was placed in a tared evaporating dish and weighed immediately. The sample was dried and weight again.

5.2.3 Sample Processing Method Calibration

NA

5.2.4 Sample Processing Quality Control

To ensure that measurements were standardized, biomass measurements were made only after samples had been preserved for a minimum of two months. Samples were not transferred to ethanol prior to sorting.

5.2.5 Sample Processing Method Reference

U.S. EPA. 1995. Environmental Monitoring and Assessment Program (EMAP): Laboratory Methods Manual-Estuaries, Volume 1: Biological and Physical Analyses. U.S. Environmental Protection Agency, Office of Research and Development, Narragansett, RI. EPA/620/R-95/008.

5.2.6 Sample Processing Method Deviations

To ensure that measurements were standardized, biomass
measurements were made only after samples had been preserved
for a minimum of two months. Samples were NOT transferred
to ethanol prior to sorting.

6. DATA ANALYSIS AND MANIPULATIONS

  6.1 Name of New or Modified Value

          BSPECABN   Organisms of the Taxon:Total #
          BSPEC_MA   Organisms of the Taxon:Mean #/Grab
          BSPECSTD   Organisms of the Taxon:STD of Mean/Grab

  6.2 Data Manipulation Description

    Measurements on a 'per grab' basis were received from
    taxonomic laboratories. Values in this data set were calculated
    by 1) Summimg replicate abundance over 'n' grabs, 2) taking
    the mean of the abundance across 'n' replicates and 3)
    generating a standard deviation based on the replicate
    abundances for each taxon.

  6.3 Data Manipulation Examples

    6.3.1 Total abundance for a taxon:

        Abundance counts for a taxon were summed for all
        replicates collected at a station.

    6.3.2 Mean and Standard Deviation (SD) values for abundance

        The mean for each taxon identified at a station was
        calculated by summing the replicate abundances and
        dividing by the number of grabs collected. The SD was
        then calculated.

7. DATA DESCRIPTION

  7.1 Description of Parameters

      Parameter Data   Parameter
    # SAS Name Type Len Format   Label
----
  1 STA_NAME Char 8   8.   The Station Identifier
  2 VST_DATE Num   8 YYMMDD6.   The Date the Sample was Collected
  3 SPECCODE Char 8 $8.   EMAP Taxon Code
  4 BSPECABN Num   8   6.   Organisms of the Taxon:Total #
  5 BSPEC_MA Num   8   8.2   Organisms of the Taxon:Mean #/Grab
  6 BSPECSTD Num   8   6.2   Organisms of the Taxon:STD of Mean/Grab
----

    7.1.6 Precision to which values are reported

    Total abundance is reported as a whole number.
    Mean abundance and standard deviation (SD) are reported to 2
    decimal places.

7.1.7 Minimum Value in Data Set

```
BSPECABN        1
BSPEC_MA        0.33
BSPECSTD        0
```

7.1.7 Maximum Value in Data Set

```
BSPECABN        9882
BSPEC_MA        3294.00
BSPECSTD        1933.11
```

7.2 Data Record Example

7.2.1 Column Names for Example Records

```
STA_NAME     VST_DATE     SPECCODE     BSPECABN     BSPEC_MA     BSPECSTD
```

7.2.2 Example Data Records

OBS	STA_NAME	VST_DATE	SPECCODE	BSPECABN	BSPEC_MA	BSPECSTD
1	VA90-021	900721	ACTECANA	2	0.67	1.15
2	VA90-021	900721	AMPEABDI	1	0.33	0.58
3	VA90-021	900721	AMPELISC	3	1.00	1.00
4	VA90-021	900721	AMPHARCT	2	0.67	0.58
5	VA90-021	900721	AMPHARTD	2	0.67	1.15

8. GEOGRAPHIC AND SPATIAL INFORMATION

8.1 Minimum Longitude

-77 Degrees 17 Minutes 4.80 Decimal Seconds

8.2 Maximum Longitude

-70 Degrees 04 Minutes 18.60 Decimal Seconds

8.3 Minimum Latitude

36 Degrees 49 Minutes 54.60 Decimal Seconds

8.4 Maximum Latitude

41 Degrees 38 Minutes 33.00 Decimal Seconds

8.5 Name of area or region

Virginian Province

Stations were located in estuaries along the East Coast of the
United States from Cape Cod, Massachusetts, to Cape Henry, Virginia,
at the mouth of the Chesapeake Bay. The area includes the District
of Columbia and the States of Virginia, Maryland, New Jersey,
Delaware, Pennsylvania, New York, Connecticut, Rhode Island and
Massachusetts.

9.   QUALITY CONTROL/ QUALITY ASSURANCE

     9.1 Measurement Quality Objectives

     Measurement quality objectives were outlined in the Quality
     Assurance Project Plan (Valente et al., 1990). Accuracy
     goals are outlined below:

Benthic Community Composition	Accuracy Goal	Precision Goal	Completion Goal
Sorting	10 %		90%
Counting	10 %		90%
Taxonomic Identification	10 %		90%
Biomass		10 %	

     9.2 Quality Assurance/Control Methods

          9.2.1 Sample Collection Quality Control

     Following sieving, the sieve was carefully inspected to
     ensure that no organisms remained.

     Each crew was visited during the sampling period by the QA
     Coordinator or Logistics coordinator. Part of the review
     included observing sample collection procedures to ensure
     samples were being processed properly.

          9.2.2 Sample Processing Quality Control

     Quality control for processing grab samples involves both
     sorting and counting check systems. A check on the
     efficiency of the sorting process was required to document
     the accuracy of the organism extraction process. Checks on
     the accuracy of sample counting were conducted in
     conjunction with taxonomic identification and used the same
     criteria.

     The Quality control check on each technician's efficiency at
     sorting (i.e., separating organisms from sediment and
     debris) consists of a independent re-sort by a second,
     experienced sorter. To pass QC, the sorter's efficiency
     must be at least 90%, meaning no more than 10% of the
     organisms in the sample were missed. A minimum of 10
     percent of samples processed by a given sorter should be
     subjected to a QC sort at regular intervals during sample
     processing. If a sorter fails QC sorts, then all samples
     processed from the last successful QC check were resorted
     and any additional organisms found were added to each
     sample. If QC sorting passes, but some organisms were
     found, these animals WERE NOT added to the original sample
     sort.

     As organisms were identified and corrected, a voucher
     specimen collection was compiled. This specimen collection
     can be used as a quality cross check by sending specimens to
     a separate laboratory for identification. All specimens

were to be taxonomically confirmed by an outside source and
any discrepancies resolved. Identification and enumeration
accuracy were checked internally by a second taxonomist for
at least 10 percent of the samples processed by a given
technician. There should be no more than 10 percent total
error (for all species) in identification or enumeration in
any sample. The same procedures for sample reprocessing
that are used for sorting apply to identification and
counting.

Biomass determination procedures involve drying and weighing
a sample. Duplicate weight measurements by a separate
technician were taken before and after drying of 10 % of the
samples to control and document the precision of this
measurement process. If the two technicians' results differ
by more than 10 percent, the source of error was identified
and corrected before analysis proceeded. A series of blanks
(no less than 5% of the number of samples being processed)
were also included in the set of samples being dried as an
additional QC check. The weight of these blanks should have
varied by no more than 0.1 mg. If greater variations were
found, the balance and the procedures used by the technician
in its operation were checked and corrective action taken,
if necessary.

9.3   Quality Assessment Results

Two QA steps were required by the EMAP-VP 1990 QA Project Plan: 10%
recounts and independent verification of species identification.
The recounts (multiple types - see Table 9-3) and preliminary species
verification were performed by the laboratory responsible for the
analyses. These in-house QC measures met the requirements established
in the QA Plan. Definitive verification of species identification
was performed by an independent laboratory and the results are
described below.

External reviews of the taxonomic reference collections (i.e.,
voucher specimens) maintained by both Versar and Cove were completed
in 1990. Taxonomic experts at SAIC's Woods Hole office performed
the review of the Cove Corporation reference collection of marine
macroinvertebrates. This review disclosed that less than 5% of
the total number of species had been misidentified. The species
misidentifications subsequently were corrected in the
EMAP-E database and the taxonomic experts at Cove Corp. used these
results to improve their future accuracy for the species in
question.

Table 9-3. Results of recounts performed by the laboratory processing benthic
           infauna samples in 1990. Approximately 10% of all samples were
           processed in duplicate.

Measurement	Mean Error	Range of Error
Benthic sorting	3.06%	0 - 10%
Species identification and enumeration	1.37%	0 - 7.7%
Biomass	0.23%	0 - 1.24%
Weighing blanks for biomass	<0.0001g	0 - 0.0013g

9.4 Unassessed Errors

The methods used to process benthic samples require that a
small number of representative specimens of each species be
set aside in a taxonomic reference collection. However, the
biomass of specimens saved for the reference collection could
not be measured or estimated. In most cases, specimens in the
reference collection were estimated to represent a small
percentage of the total macrofaunal biomass. Nonetheless, the
total biomass is underestimated for those samples from which
reference specimens were taken.

Total macrofaunal biomass was also potentially underestimated
for samples from tidal fresh and oligohaline salinity regions
where the number of chironomids or the number of oligochaetes
was less than 20. Where oligochaetes and chironomids were
present in sufficient numbers (>20), half were mounted on
slides to complete taxonomic identifications and half were
used for biomass measurements. In those instances where the
number of oligochaetes or chironomids was <20, all specimens
were mounted for identification and no biomass measurements
were made. This procedure generally has a negligible effect
on biomass estimates.

An additional source of error results from the process of
removing an aliquot of sediment from each grab for grain size
analysis. This sample (a 2 cm core) was removed from each
grab prior to sieving. No attempt was made to "correct" for
the animals potentially lost to this sample.

10. DATA ACCESS

  10.1 Data Access Procedures

     Data can be downloaded from the WWW server.

  10.2 Data Access Restrictions

  10.3 Data Access Contact Persons

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  10.4 Data Set Format

     Data can be downloaded in several formats from the web application and
     web site.

10.5 Information Concerning Anonymous FTP

    Not accessible

10.6 Information Concerning WWW

    Data can be downloaded from the WWW server.

10.7 EMAP CD-ROM Containing the Data Set

    Data not available on CD-ROM.

11. REFERENCES

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