



M E C BIOLOGICAL PROJECT
SAN ONOFRE NUCLEAR GENERATING STATION
MONITORING STUDIES ON
MYSIDS AND SOFT BOTTOM BENTHOS
FINAL REPORT
APPENDICES

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APPENDIX A

Glossary and Documentation

APPENDIX A.1

Glossary of Special Use Terminology

APPENDIX A.1

Glossary of Special Use Terminology

The following list of terms and definitions is intended to cover special or particular uses of terms which are either peculiar to the MRC contractor language, have meanings in the SONGS context differing from normal use or have evolved specific or restricted meanings over the course of this project. It is not intended to cover all technical terms used in this report. Some of these terms are further defined in context within this report and its appendices, or in prior MEC reports. For terms whose definitions have changed over time, the meaning presented here refers to this report.

After: the time period of monitoring sample collection following initial full power operation of Unit 3 (Unit 2 had already been brought up to full power) and with or without operation of Unit 1; the actual dates vary by organism assemblage because they are based on a presumption of whether the organisms might respond immediately (instantaneous) or in integrated fashion (cumulative) to SONGS conditions. For ichthyoplankton and macrozooplankton the After period begins 1 July 1983 for mysids the period begins after September 1984, and for benthos the period begins January 1984. The After period, often referred to as the "Operational Period" is a continuous time span from its initiation noted above through the present and into the future.

Before: the time period of monitoring sample collection before December 1981, with or without operation of Unit 1. After that time, Unit 2 cooling operations comprised both circulation through the cooling system and a heated discharge; the length of the Before period varies by monitoring group (see Section 2); for some groups it includes both preconstruction and construction period sampling, with construction referring to that of the ocean portion of the cooling systems of Units 2 and 3.

Control Area: the most proximate and similar habitat for monitoring sampling to the Impact Area which is sufficiently remote from the intake/discharge structures of Units 2 and 3 to be (hypothetically) beyond their withdrawal, entrainment or discharge influences; the locations vary by monitoring group; Control areas for MEC mysids and benthos projects are given in Section 2.

Cooling System: the complete once-through circulating seawater system at SONGS including the intake structures, conduits, screenwells, pumps, condensers, discharge structures and all the additions to and removals from that system including the additions of waste heat, chemicals and radionuclides.

Delta: the difference between the Control and Impact values of each of a set of cells during each survey; this is the basic variate of the BACI analysis; the means of the Before and After Deltas are the values compared in the BACI t-test. The cells are abundance values of individual taxa, functional subsets of taxa or pools of taxa; the composition of cells vary with each monitoring group.

Entrainment: the process of capturing and relocating parcels of water (the "entrained water") and portions of those parcels' biota by the flow of discharged water through the receiving water in the immediate vicinity of the discharge ports. Entrainment results from the friction between the relatively high speed of the discharged water and the relatively low speed and differing direction of the receiving water; see "Withdrawal" for comparison; at SONGS Units 2 and 3 Entrainment results in the upward and offshore translocation of near-bottom water and midwater and some of its biota.

Impact: a regionally significant result of a SONGS effect (equals significant effect).

Impact Area: Potential Impact Area the area for monitoring sampling within the definable withdrawal, entrainment or discharge influence of the SONGS Units 2 and 3 intake and discharge structures; the locations of Impact Area stations vary with monitoring group; Impact Areas for MEC mysids and benthos projects are given in Section 2.

Interim: referring to the period between commencement of the sample collections following the first persistent heat generating operations of Unit 2 in January 1982 and the first qualifying sample period following startup of Unit 3 Interim dates are between 31 December 1981 and 1 October 1983 for mysids and between 1 December 1981 and 1 January 1984 for benthos.

Mechanism: the physical, chemical and/or biological changes in the entrained or receiving water body produced by the plant source, including the biological process by which the changes act to create the potential effects.

Monitoring Group: the taxonomic or functional group comprising one of the four MEC subprojects, i.e., zooplankton, ichthyoplankton, mysids and soft-bottom benthos.

Net Relative Effect: a measurable change in one or more Impact Area populations as determined by the BACI analysis resulting from one or any combination of SONGS operations related mechanisms. Net relative change can result from a change in the mean abundance at Control in the operational period unaccompanied by a change in SONGS abundances, as well as changes in After SONGS abundances.

Operational: referring to the specific periods after 1 October 1983 for mysids and 1 January 1984 for benthos or to surveys during the After Period. Unit 1 may or may not have been operating in the period leading up to any given Operational sample collection.

Plant: the physical power plant facility including the reactor, turbines and cooling system.

Plant Source: the design or operational feature which produces the potential effect.

Potential Effect: the translation of the mechanism on the biota to a gain or loss in population of affected species; by MRC definition, the result would be a BACI effect if the change were statistically significant on a local scale; it would be an impact if it were also significant on a regional scale.

Preoperational Monitoring: referring to the period before the first persistent heat generating operations of Unit 2; the duration backward in time varies with monitoring group; specific dates of the Preoperational samples are given for each group in Section 2.

Preoperational: refers to Preoperational Monitoring samples and to baseline and Unit 1 effects studies samples which were not taken in the SONGS/Control configuration and are therefore not appropriate or needed for the BACI analysis; the number and dates vary with monitoring group.

Significant BACI Effect: a significant t-test result of the difference of means of the Before and After pools of Deltas. Type one (= alpha) errors are set at 0.05 or 0.10 depending on the predetermined power of the test. The t-test is two-tailed for mysids and benthos.

SONGS Effect: a detectable change in the Impact Area populations which can be ascribed to a Plant source and/or mechanism.

SONGS Operations: partial or complete, normal or non-normal working of the cooling system including such aperiodic operations as heat treatment and chlorination.

Taxa: taxonomic groupings and/or pools of taxa used in the BACI analysis.

Trophic Motility (TM) group: a group of species that resemble one another in their feeding mode and general scale of movement. Grouping was performed within and across taxonomic categories (polychaetes, crustacea, mollusks, etc.).

Withdrawal: the capture of parcels of water (the "withdrawn water") and portions of their included biota at the intake structures as a result of the operation of the circulating seawater pumps of the cooling system.

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Documentation of Computer Programs
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APPENDIX A.2

Documentation of Computer Programs

APPENDIX A.2

Documentation of Computer Programs

This Appendix contains flow charts to document all SAS software used to derive data presented in tables or figures contained within this report. Each figure shows the flow from the MRC data base(s) through SAS software to the final table or figure presentation. All SAS programs listed herein have been documented in the MRC computer system by the software in the Disk Inventory Control System. The location of the documented SAS software is shown on each figure.

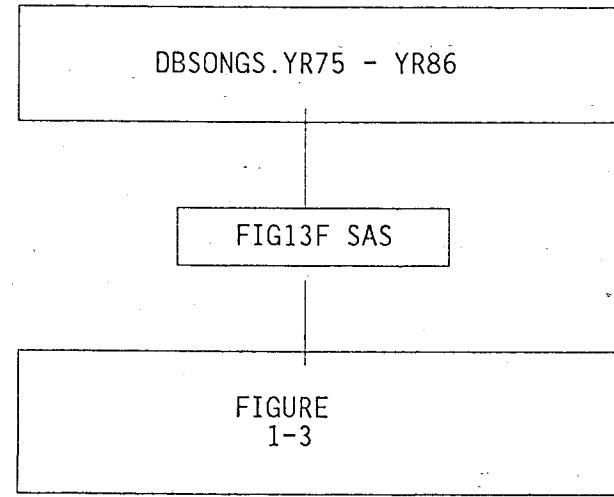
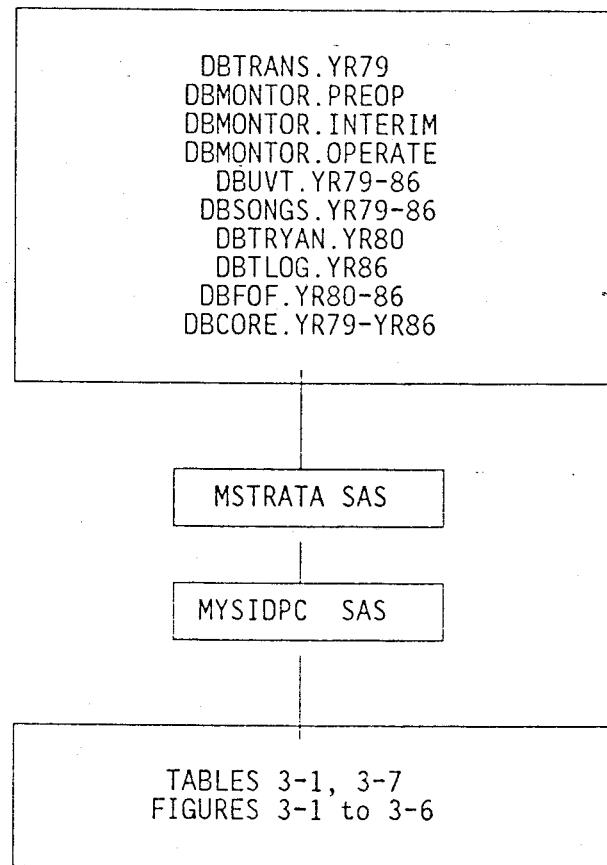


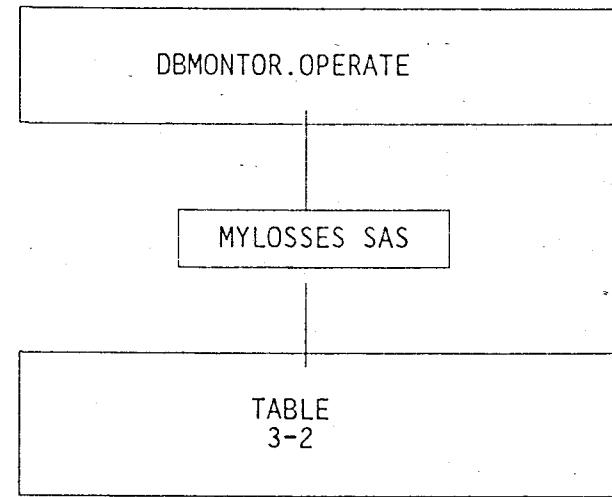
FIG13F SAS computes and plots the weekly average number of pumps for SONGS Units 1, 2, and 3

Figure A.2-1. Documentation of program used to generate Figure 1-3.
The SAS program has been placed on the ichthyoplankton report disk.



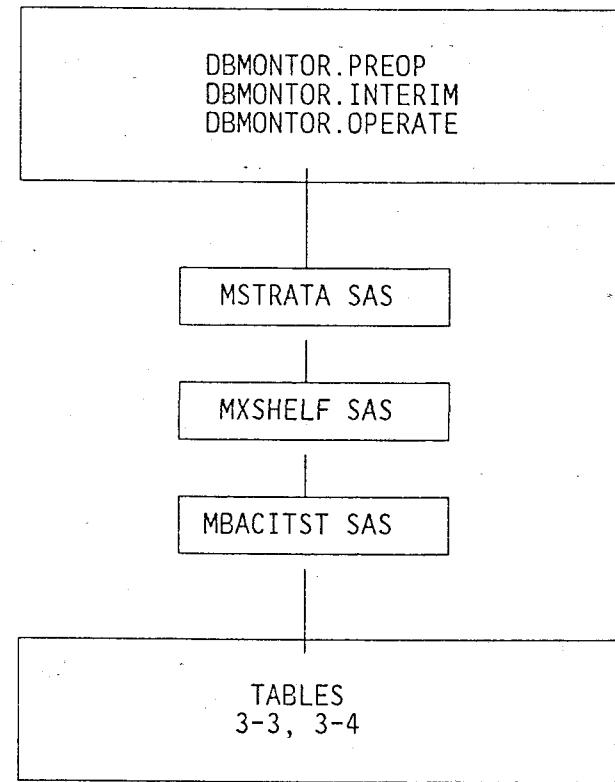
-
- MSTRATA SAS selects selected species from data base,
outputs number per tow for each stage and for all stages combined e
- MXSHELF SAS computes the weighted mean number per cubic meter in the cross-shelf transect
- MYSIDPC SAS collects physical/chemical data from MRC data bases
plots physical/chemical data
runs multiple regressions on mysid abundance with p/c data
-

Figure A.2-2. Documentation of programs used to generate tables and figures presented in Section 3.1. The SAS programs listed have been placed on the mysid report disk.



MYLOSSSES SAS selects selected species from data base,
computes average daily intake loss percentage, and
also estimates of possible diffuser entrainment losses

Figure A.2-2. (cont.)

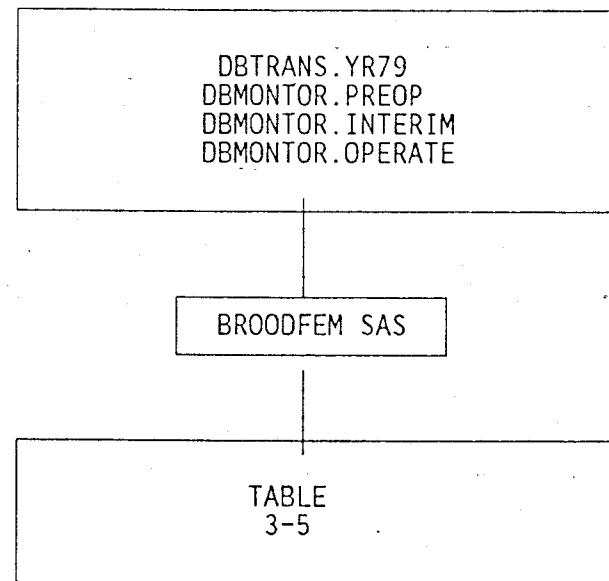


MSTRATA SAS selects selected species from data base,
outputs number per stratum for each taxon

MXSHELF SAS computes the weighted mean number per cubic meter in the
cross-shelf transect

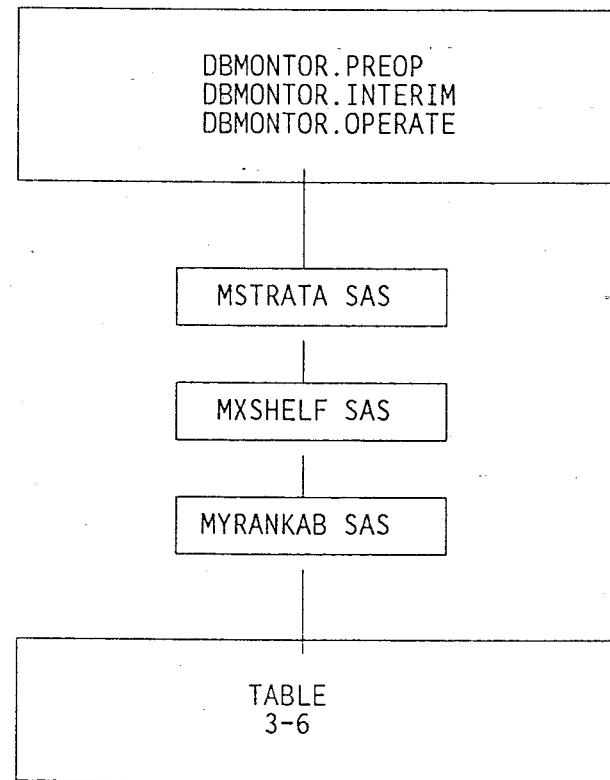
MBACITST SAS runs assumption tests on Before data
runs BACI t-test on Before and After data
computes percent change in abundance at SONGS

Figure A.2-2. (cont.)



BROODFEM SAS selects selected species from data base,
calculates the reproductive index and
runs ANCOVA on the data

Figure A.2-2. (cont.)

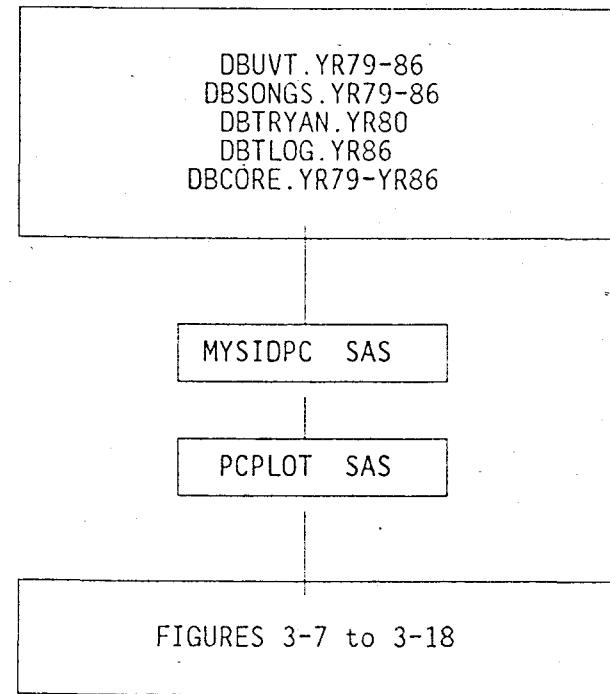


MSTRATA SAS selects selected species from data base,
outputs number per stratum for each taxon

MXSHELF SAS computes the weighted mean number per cubic meter in the
cross-shelf transect

MYRANKAB SAS ranks the species by abundance
runs a t-test on Before and After ranks

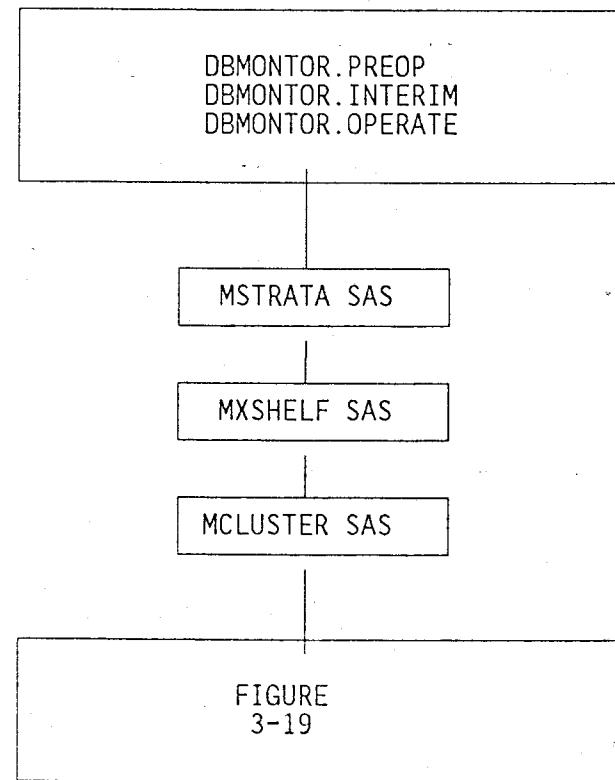
Figure A.2-2. (cont.)



MYSIDPC SAS collects physical/chemical data from MRC data bases
plots physical/chemical data
runs multiple regressions on mysid abundance with p/c data

PCPLOT SAS plots contours for quarterly means

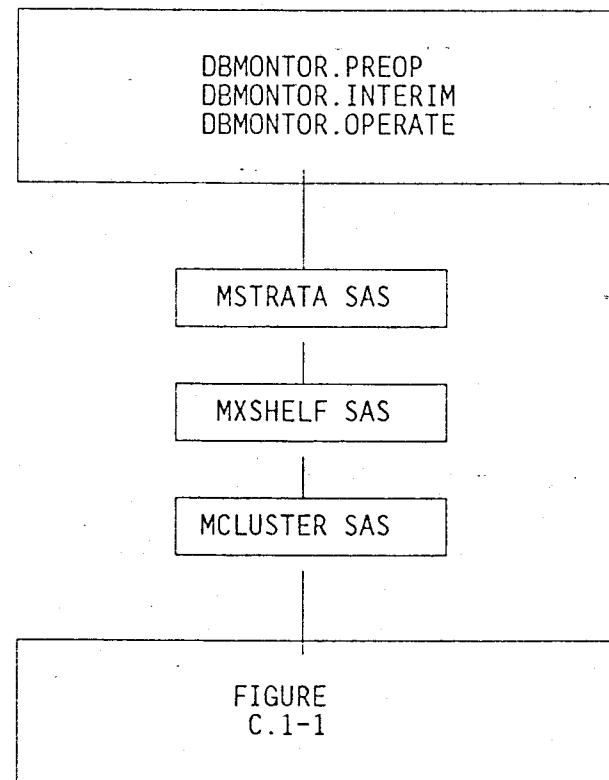
Figure A.2-2. (cont.)



MSTRATA SAS selects selected species from data base,
outputs number per stratum for each taxon

MCLUSTER SAS clusters the species and date/stations by abundance

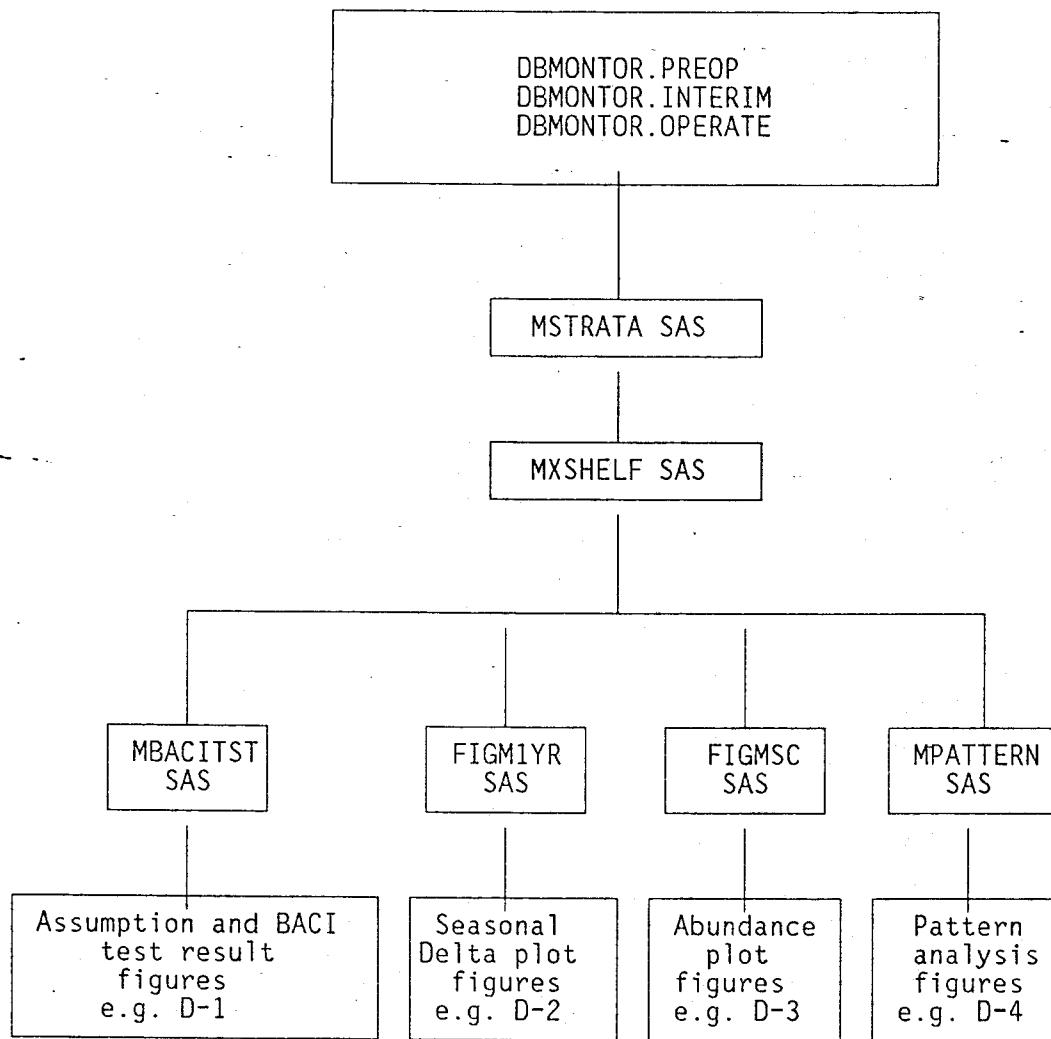
Figure A.2-2. (cont.)



MSTRATA SAS selects selected species from data base,
outputs number per stratum for each taxon

MCLUSTER SAS clusters the species and date/stations by abundance

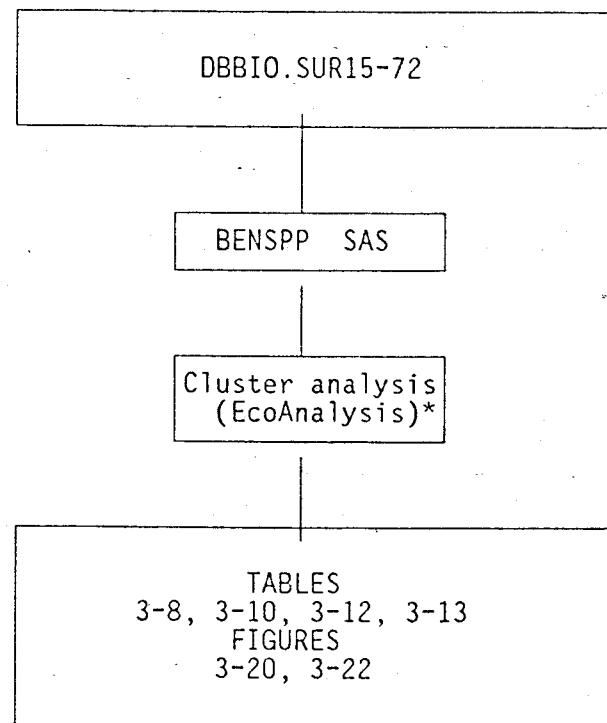
Figure A.2-3. Documentation of programs used to generate figures presented for mysids in Appendix C.1. The SAS programs listed have been placed on the mysid report disk.



MSTRATA SAS selects selected species from data base,
outputs number per stratum for each taxon

MXSHELF SAS computes the weighted mean number per cubic meter in the
cross-shelf transect

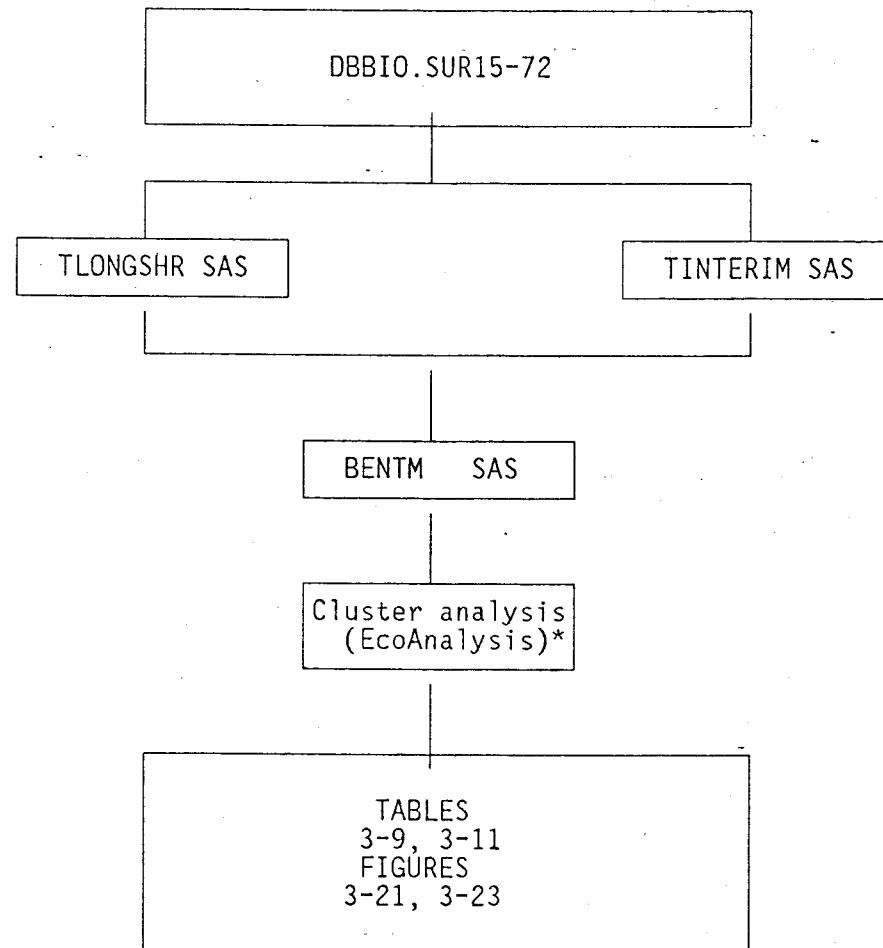
Figure A.2-4. Documentation of programs used to generate figures presented for mysids in Appendix D. The SAS programs listed have been placed on the mysid report disk.



BENSPP SAS filters species and stations to be used in cluster analysis
outputs data base

*Cluster analyses were run by EcoAnalysis because, due to the number of
variables and observations, they could not be run on the MRC computer.

Figure A.2-5. Documentation of programs used to generate tables and figures presented in Section 3.3. The SAS programs listed have been placed on the benthos report disk.



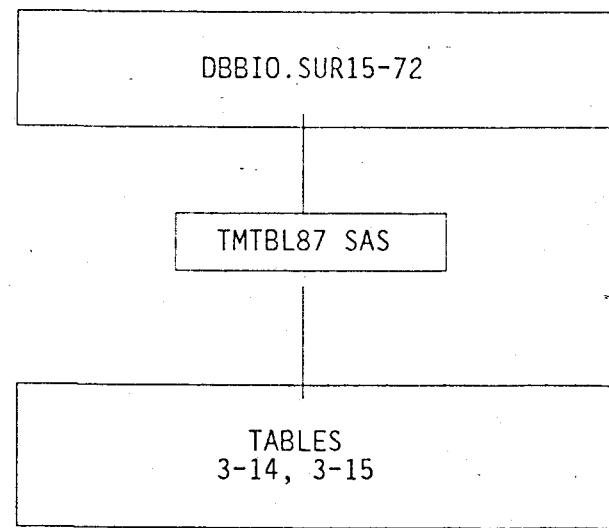
TLONGSHR SAS collects trophic-motility groups and stations for Before and After periods

TINTERIM SAS collects trophic-motility groups and stations for Interim period

BENTM SAS output trophic-motility groups and stations to be used in cluster analyses into data bases

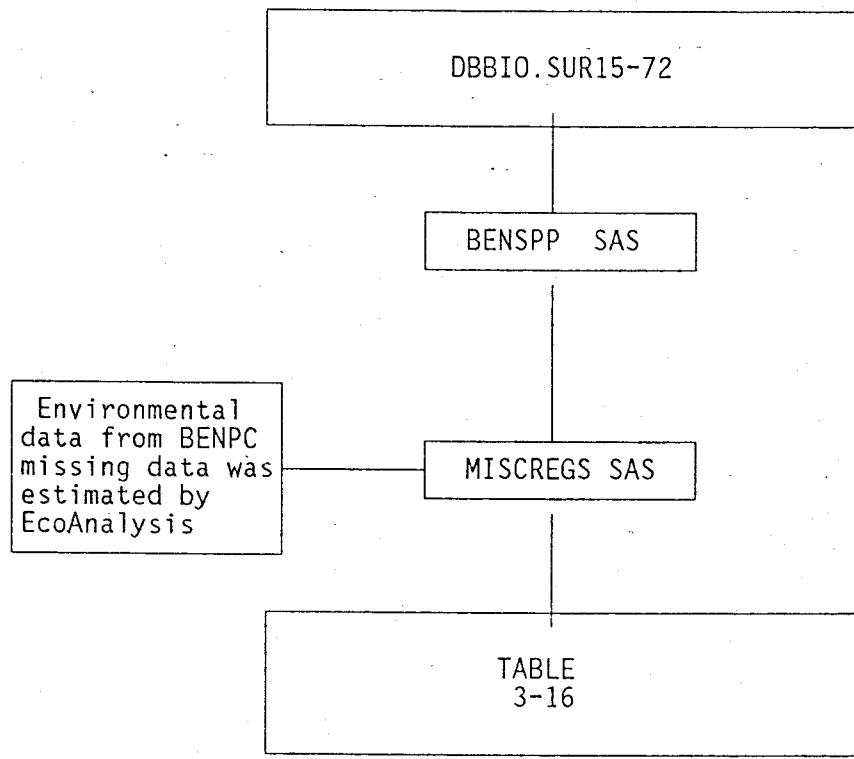
*Cluster analyses were run by EcoAnalysis because, due to the number of variables and observations, they could not be run on the MRC computer

Figure A.2-5. (cont.)



TMTBL87 SAS puts species into trophic-motility groups and creates tables

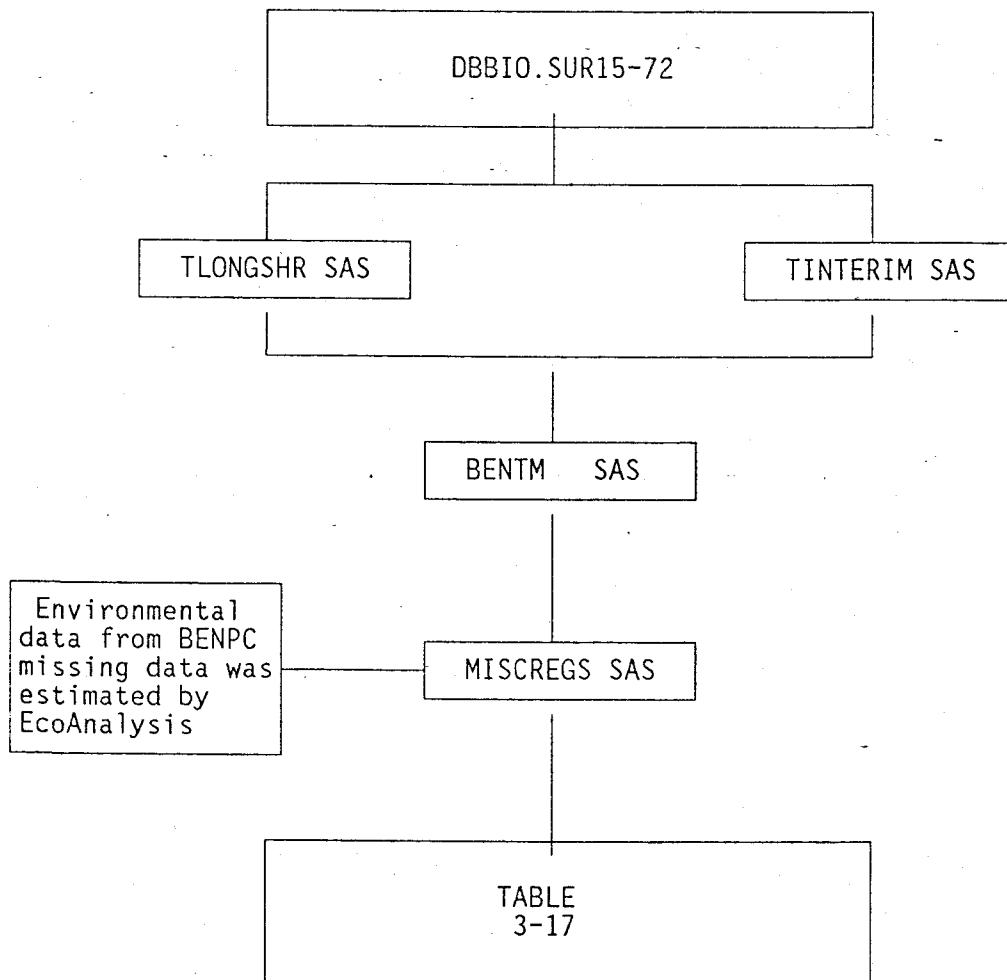
Figure A.2-5. (cont.)



BENSPP SAS filters species and stations to be used in cluster analysis
outputs data base

MISCREGS SAS runs multiple regressions on selected species with
environmental data

Figure A.2-5. (cont.)



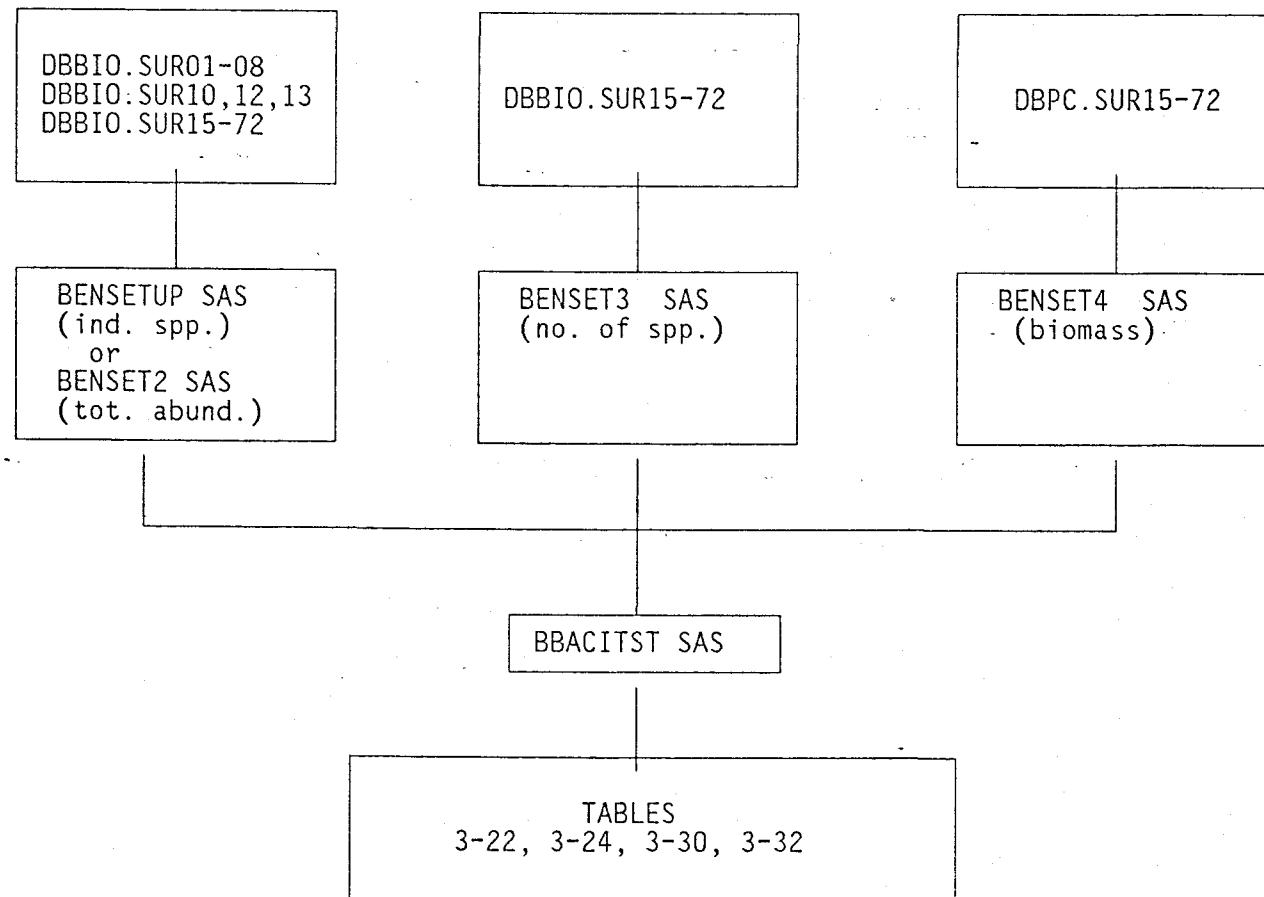
TLONGSHR SAS collects trophic-motility groups and stations for Before and After periods

TINTERIM SAS collects trophic-motility groups and stations for Interim period

BENTM SAS output trophic-motility groups and stations to be used in cluster analyses into data bases

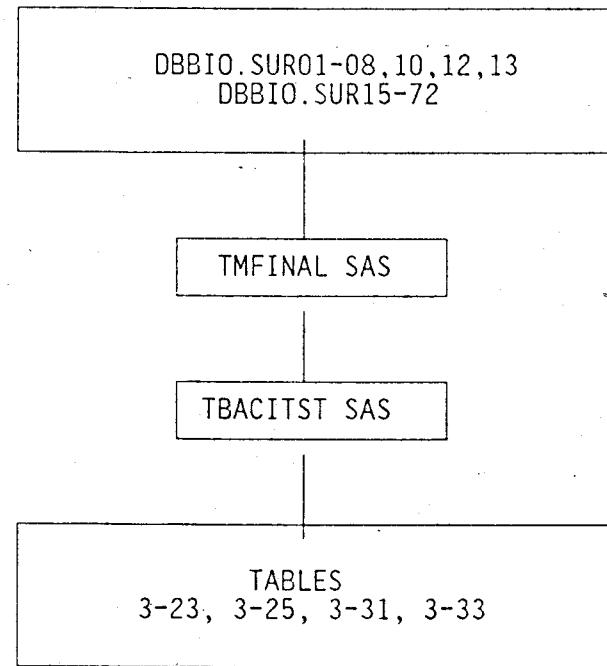
MISCREGS SAS runs multiple regressions on selected species with environmental data

Figure A.2-5. (cont.)



BENSETUP SAS selects individual taxa for BACI testing
 BENSET2 SAS computes total abundance for each location
 BENSET3 SAS computes number of species for each location
 BENSET4 SAS computes total biomass for each location
 BBACITST SAS runs assumption tests on Before data
 runs BACI t-test on Before and After data
 computes percent change in abundance at SONGS

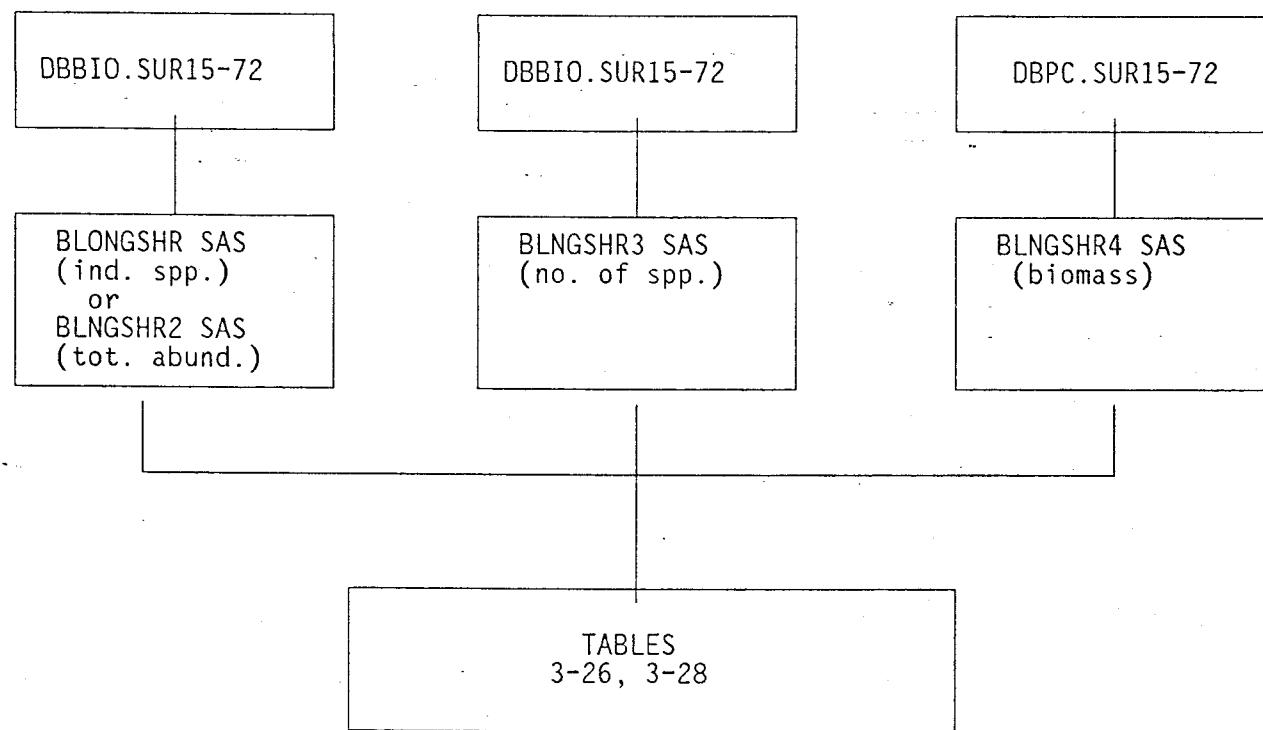
Figure A.2-5. (cont.)



TMFINAL SAS puts species into trophic-motility groups and outputs number per location for each group and subset

TBACITST SAS runs assumption tests on Before data
runs BACI t-test on Before and After data
computes percent change in abundance at SONGS

Figure A.2-5. (cont.)



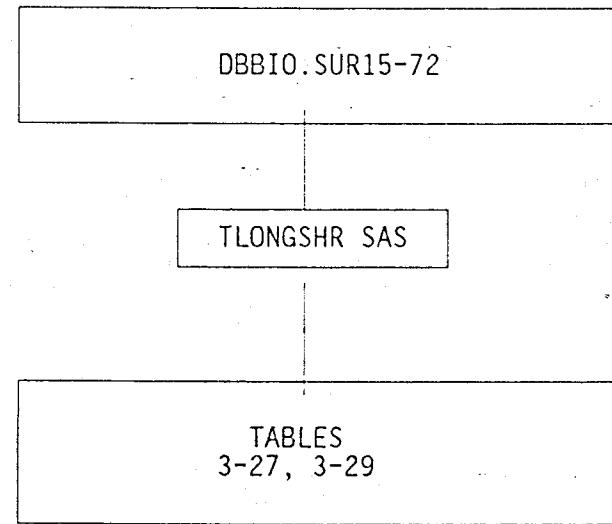
BLONGSHR SAS selects individual taxa and runs longshore pattern tests

BLNGSHR2 SAS computes total abundance and runs longshore pattern tests

BLNGSHR3 SAS computes number of species and runs longshore pattern tests

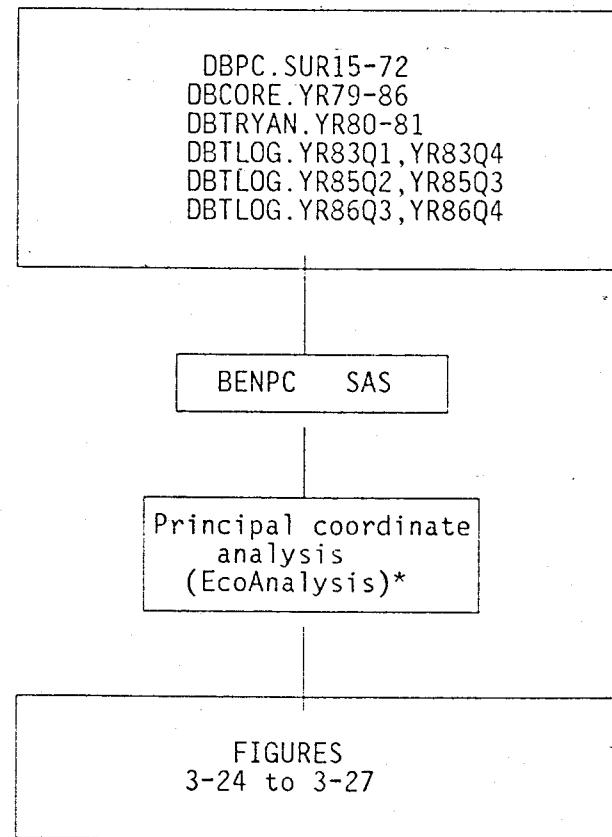
BLNGSHR4 SAS extracts total biomass and runs longshore pattern tests

Figure A.2-5. (cont.)



TLONGSHR SAS puts species into trophic-motility groups and
runs longshore pattern analyses

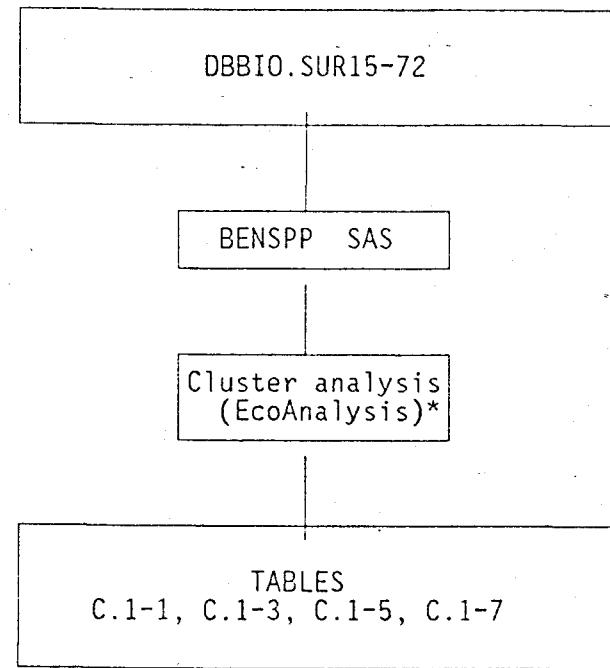
Figure A.2-5. (cont.)



BENPC SAS collects physical-chemical data and outputs a data base to be used in principal coordinate analyses

*Principal coordinate analyses were run by EcoAnalysis because, they were run in conjunction with the cluster analyses which could not be run on the MRC computer

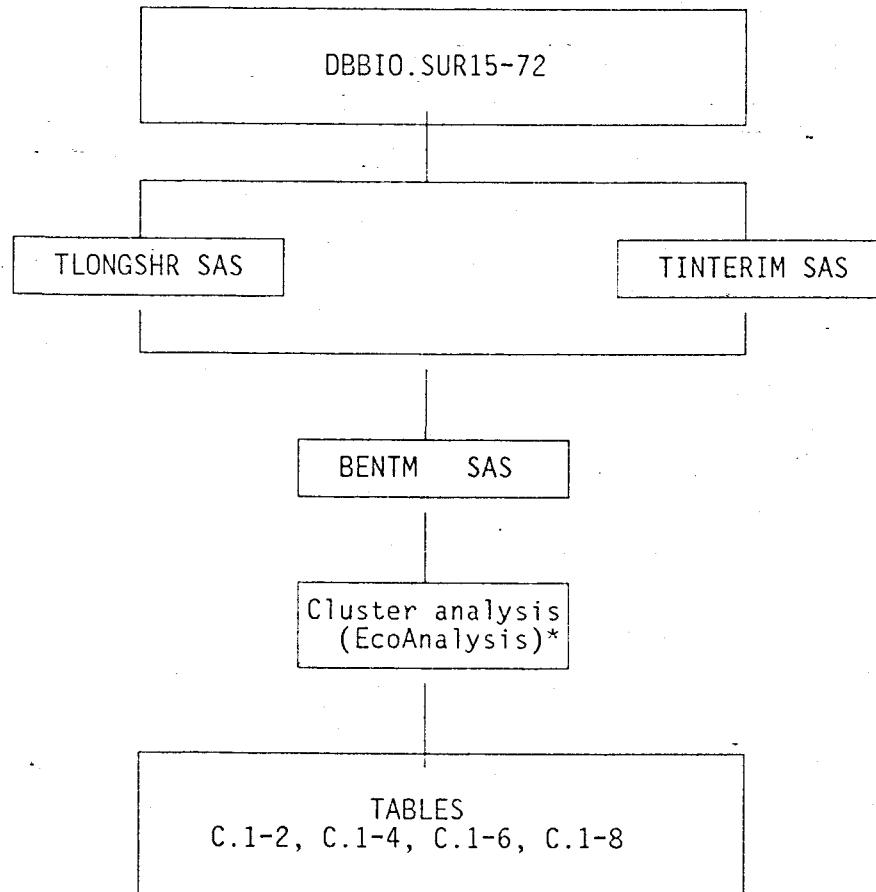
Figure A.2-5. (cont.)



BENSPP SAS filters species and stations to be used in cluster analysis
outputs data base

*Cluster analyses were run by EcoAnalysis because, due to the number of
variables and observations, they could not be run on the MRC computer

Figure A.2-6. Documentation of programs used to generate tables presented
in Appendix C.1. The SAS programs listed have been placed
on the benthos report disk.



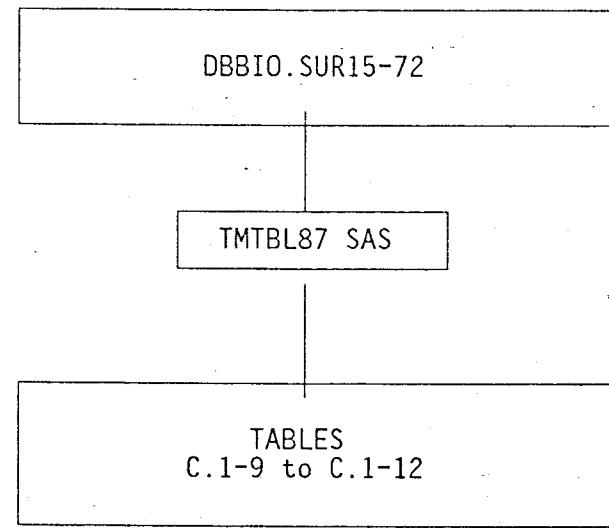
TLONGSHR SAS collects trophic-motility groups and stations for Before and After periods

TINTERIM SAS collects trophic-motility groups and stations for Interim period

BENTM SAS output trophic-motility groups and stations to be used in cluster analyses into data bases

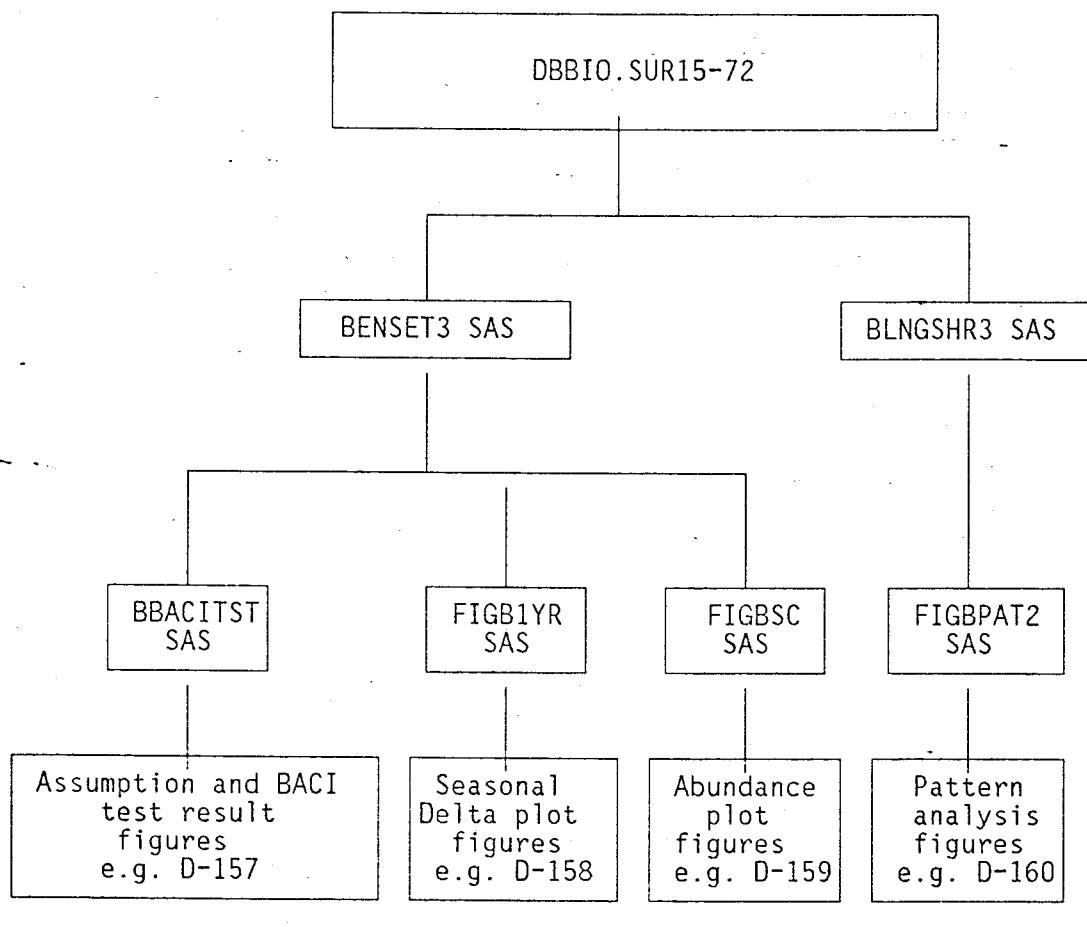
*Cluster analyses were run by EcoAnalysis because, due to the number of variables and observations, they could not be run on the MRC computer

Figure A.2-6. (cont.)



TMTBL87 SAS puts species into trophic-motility groups and creates tables

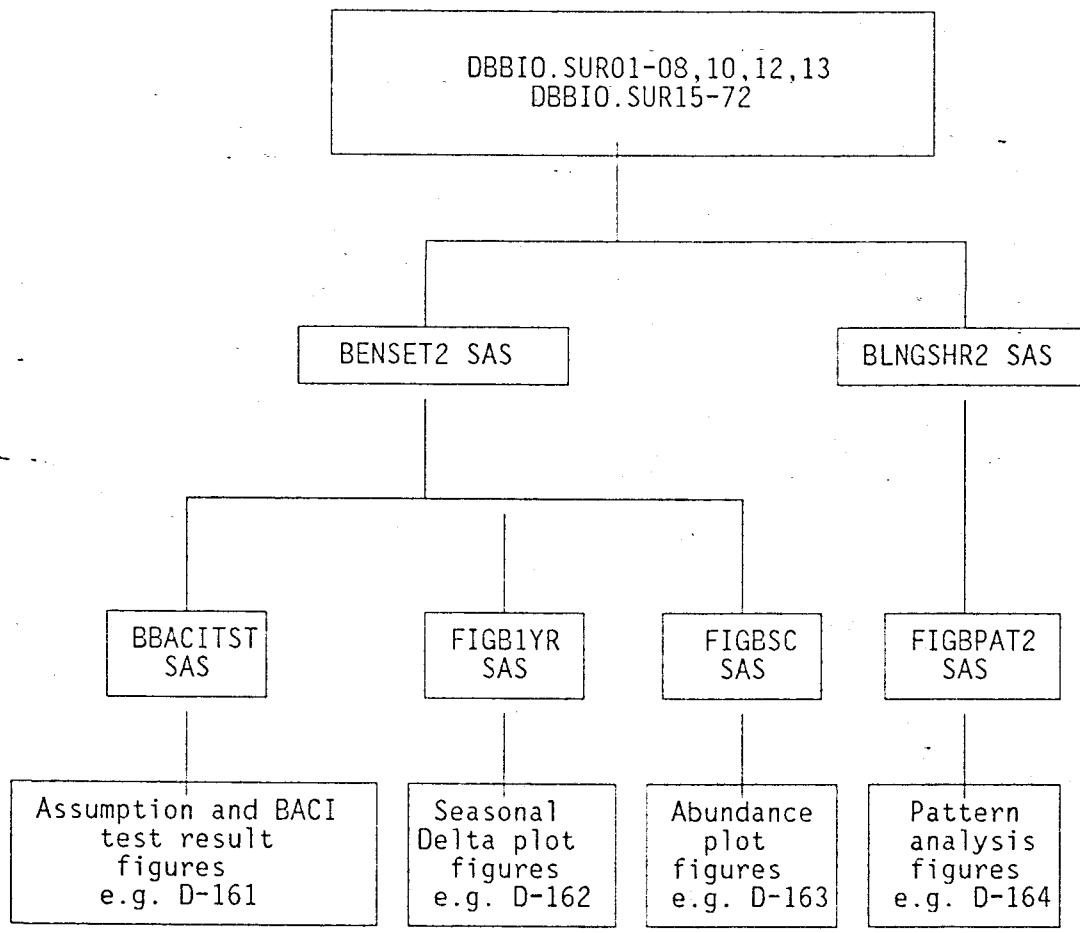
Figure A.2-6. (cont.)



BENSET3 SAS computes number of species for each location, SONGS and Control

BLNGSHR3 SAS computes the number of species for each station

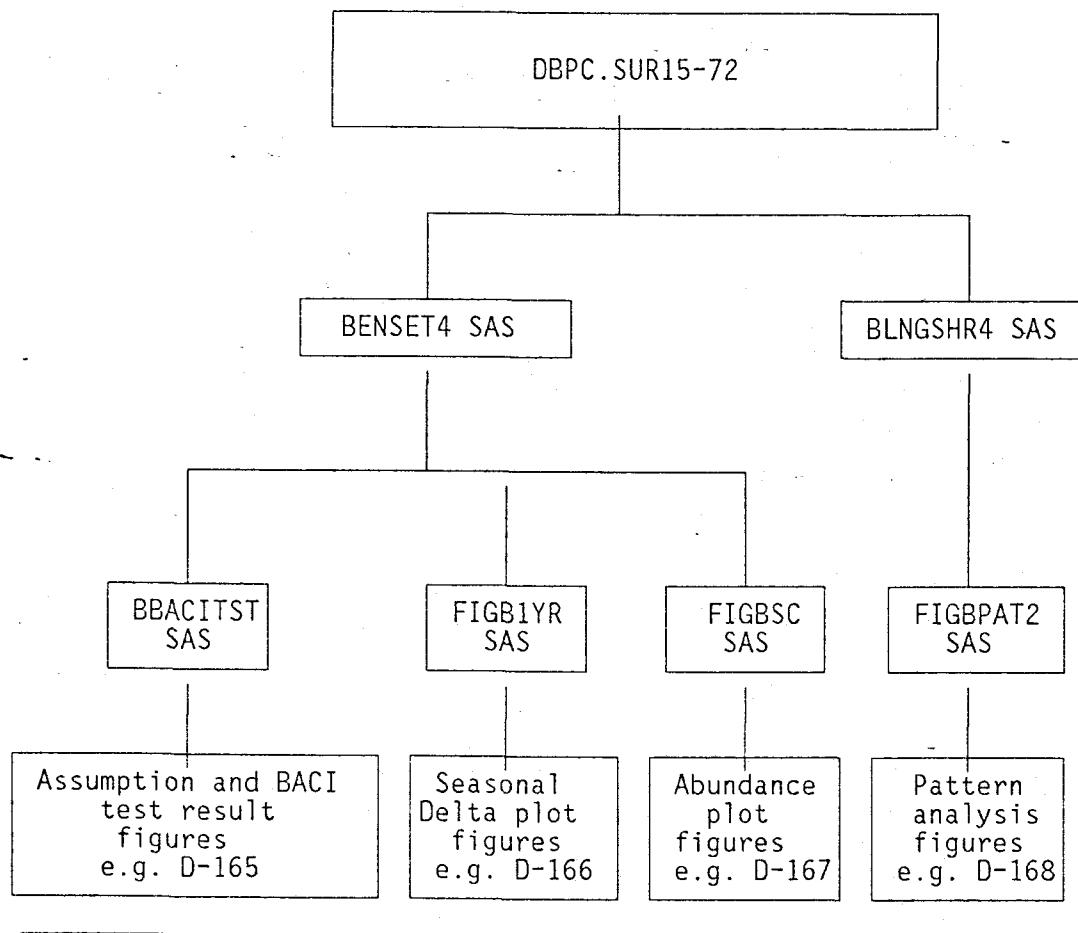
Figure A.2-7. Documentation of programs used to generate figures presented for benthic number of species in Appendix D. The SAS programs listed have been placed on the benthos report disk.



BENSET2 SAS computes total abundance for each location, SONGS and Control

BLNGSHR2 SAS computes the total abundance for each station

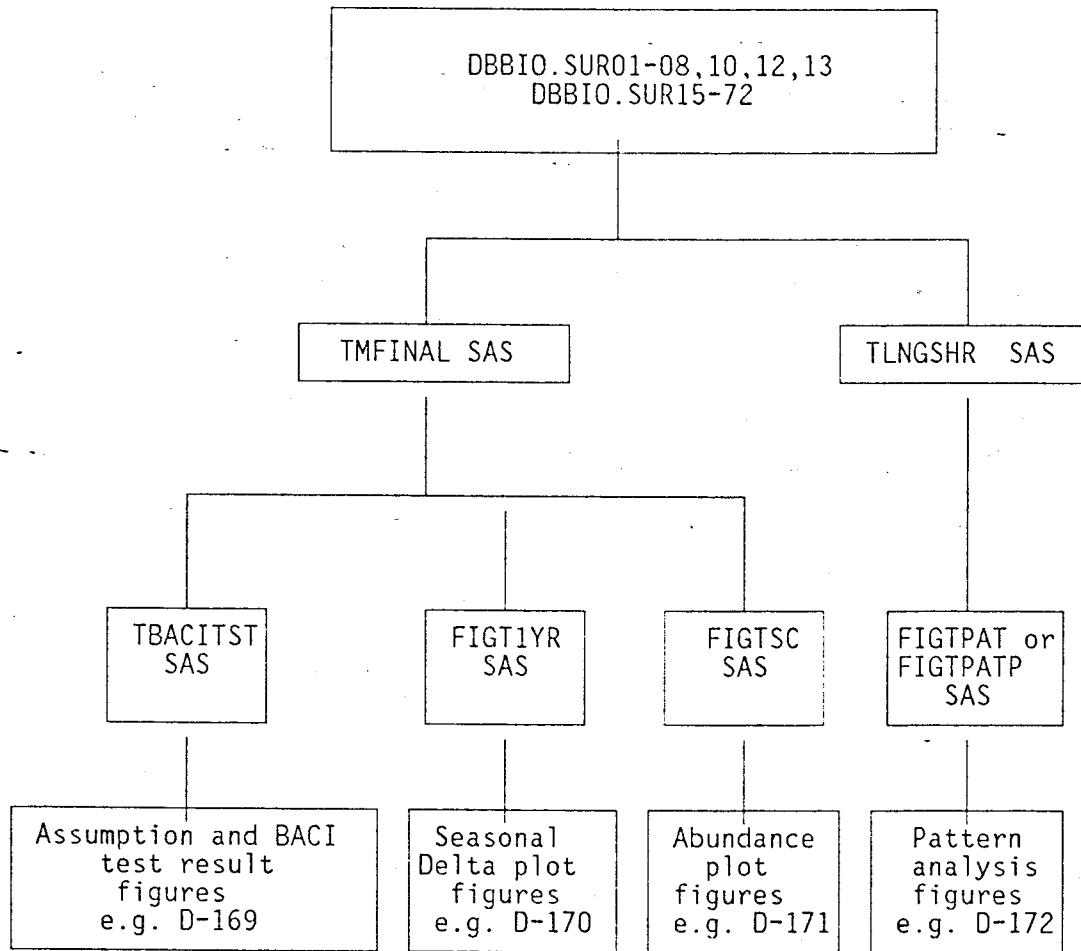
Figure A.2-7. (cont.)



BENSET4 SAS computes total biomass for each location, SONGS and Control

BLNGSHR2 SAS computes the total biomass for each station

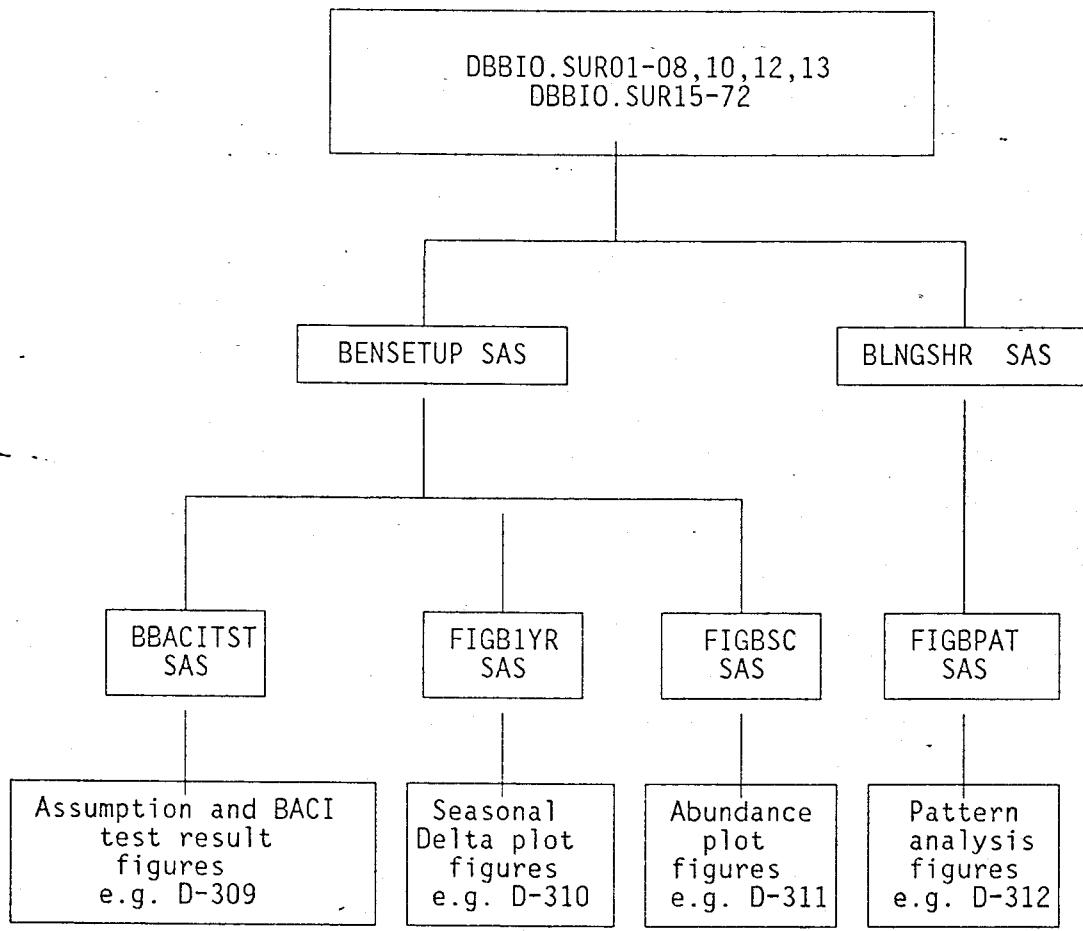
Figure A.2-7. (cont.)



TMFINAL SAS puts species into trophic motility groups and computes the abundance for each at SONGS and Control

TLNGSHR SAS puts species into trophic-motility groups and computes the abundance at each station

Figure A.2-7. (cont.)



BENSETUP SAS selects species to be used in analyses and computes the abundance for each at SONGS and Control

BLNGSHR SAS selectes species to be used in analyses and computes the abundance at each station

Figure A.2-7. (cont.)

APPENDIX B

Field and Laboratory Protocol

APPENDIX B
Field and Laboratory Protocol

B.1 MYSIDS

B.1.1 Field Sampling

A. Mobilization

1. Schedule cruise dates so as to avoid conflicts with other programs for use of the vessel and equipment.
 - a. Reserve Mini-Ranger as soon as the cruise dates have been established. Sign up for the Mini-Ranger, the auxiliary transponder, and the battery power source at ECO-M. If the miniranger has already been signed out by another group, either reschedule the mysid survey or request that the other group reschedule theirs.
 - b. Reserve the use of the vessel Lo-An. If a scheduling conflict exists, either reschedule the mysid cruise or investigate the possibility that the other cruise be rescheduled.
 - c. Reserve vehicles as soon as the cruise dates have been established. Sign up for the MEC stakebed truck for the boat loading day and for the second day of the cruise, and sign up for the MEC pick-up truck for the first day of the cruise.
2. Notify boat captain and crew as soon as the cruise dates have been established. The field crew consists of 3 crew members and the boat captain.
3. The week before the cruise, notify California Fish and Game (237-7311) and Camp Pendleton (725-4007) of the cruise. Fish and Game will request the following information: collector's permit number, the boat's name and size, the number of crew, what will be caught, what kind of gear will be used, the cruise dates, hours of collection, and locations to be sampled. Camp Pendleton will want to know the cruise dates and the locations to be sampled. If Camp Pendleton advises that marine activities are scheduled that would prohibit the sampling activities, reschedule the cruise.
4. Check SONGS operational status within 2 hours of scheduled departure; Shift Supervisor (714 - 492-7700 x 56412 or x 86144).
5. Calibrate flowmeters.
 - a. Coordinate the timing of this procedure with the Ichthyoplankton project so that meters used for both cruises can be calibrated at the same time.
 - b. Take flowmeters, flowmeter calibration sticks, a stopwatch, and some data paper on a clipboard to Y Dock at Oceanside Harbor.
 - i. Find the marked 20 meter length on Y Dock.
 - ii. Attach two flowmeters to the flowmeter calibration stick. Note their serial numbers and their start readings. Lower them into the water at one of the 20 meter markings; while keeping them horizontal, briskly walk to the other 20 meter marking. The walk will be timed with a stopwatch by another

- technician. The walk should take about 11 seconds. Record the end meter reading. Do not allow the flowmeters (especially TSK) to spin while in the air.
- iii. Repeat step ii until you have ten readings for each meter used by the mysid and ichthyoplankton subprojects.
- c. Flowmeter serial numbers, beginning to ending readings for each repetition, and elapsed time for each 20 m walk are recorded and entered into the flowmeter calibration data base upon return to the laboratory.
6. The day before the cruise, place auxiliary transponder at Don Lite.
- Access to Don Lite is via the Las Pulgas Gate with a Camp Pendleton Base Permit.
 - Once past the entrance gate, take the first road left that parallels the freeway heading north. Take another left approximately 1.8 miles from guard gate onto a dirt road leading under the freeway and follow it, as far as is prudent, to the Don Lite structure on the cliffs overlooking the ocean.
 - Fasten the transponder to the wood structure. Connect the two batteries to each other in series (positive to negative), then to the transponder (negative to the black clip, positive to the red clip on the transponder). Point the rounded portion of the antenna offshore and a few degrees downcoast.
7. Arrange for one of the crew to bring the miniranger console, cable and antenna to the boat with them on the morning of the cruise.
8. Load the boat with the gear listed on the "mysid cruise equipment list". The boat is usually loaded the day before the cruise. The gear is stored in the MRC storage area with the following exceptions:
- wedge block with shackles--kept on boat,
 - diving gear--personal property of one of the crew members and loaded morning of cruise,
 - foul weather gear and boots--kept by the crew members and loaded morning of cruise,
 - thermometer--use temperature probe that is used by the MRC Fish Project or get one from ECO-M,
 - field forms, paper towels, and drinking water--kept in MEC office,
 - miniranger and equipment--in ECO-M shop area.
9. Load sled (epibenthic sampler) on Lo-An.
- Temporarily moor Lo-An at the launch ramp.
 - Deploy sled at the northern launch ramp.
 - Attach sled to Lo-An winch cable, walk the sled out past the launch dock, and winch it on board the boat.
- B. Depart harbor for sampling site
- Fit and bolt chafing gear and net onto sampling sled.
 - Mount flowmeters onto the sampling sled with the mounting screw (Do not over-tighten), one inside the mouth ("inner") on bungie cords, one above the mouth frame ("upper") with the mounting screw, and the third above the right sled runner ("outer"). Record the flowmeter serial numbers on the field sampling log sheet.

3. Attach net tag line to the lower portion of frame.
4. Formalize at least six cases of quart jars to be used during the cruise. To do this, fill each jar about 10% full (approximately one inch) with formalin from the carboy labeled "formalin pH 7.0".
5. Prepare inside and top labels. Cruise number and date can be filled in at this time.
6. Set up miniranger equipment (console and antennae) in the pilot house. The miniranger derives its power from the boat's generator.

C. Arrive at sampling location

1. Sampling cannot begin until 1 hour after sunrise.
2. The cruise leader records starting flowmeter readings on the field sampling notes.
3. Check net cod end, make sure knots (2-3 overhand knots) are tight and secure, and clip with cod end buoy. Roll net up towards mouth.
4. Let out net tag line.
5. Move epibenthic sled onto the transom, being careful not to damage the "upper" flowmeter with the winch cable.
 - a. One crew member operates the hydraulic controls for the U-frame and winch.
 - b. One crew member guides the sled by putting one foot on the front midpoint of the lower frame of the sled while pulling the upper frame toward him. This causes the sled runners to lift up from the deck; the weight of the crew member provides stability while the sled is moved to the stern. The hydraulics operator moves the sled carefully by moving the U-frame and keeping an even tension on the winch cable. When the sled is resting on the transom, the rider disembarks but still steadies the sled.
6. Upon a signal from the skipper that the boat is on course and at proper speed (ca. 1 m/s or 2 knots-Lo-An 1800 RPM), sampling commences.
 - a. Six transects--three near SONGS and three located from 17.5 to 18.5 km south of SONGS--are sampled. At each transect, six tows are taken.
 - b. Lower the sled into the water.
 - i. One crew member operates the hydraulic controls for the U-frame and winch.
 - ii. One crew member stays at the stern to assist if the sled begins to turn before it enters the water or if other problems arise.
 - iii. The third crew member measures the cable released using a hand held meter wheel. The amount of cable released is equal to three times the maximum depth sampled for the tow. The cable is then marked, using duct tape, to indicate the end point required for each tow (Tow 1 = 1 strip of duct tape, Tow 2 = 2 strips, etc.)
 - c. Hydraulics are turned off during the tow.
 - d. The cruise leader notes the station and time the tow began in standard (PST) time on the field sampling notes.

- e. The boat captain notes the time, fathometer, and miniranger readings for the start of the tow on the cruise tow data sheet.
 - f. The sled is towed (offshore, at about 220°) between isobaths (Tow 1 = 6-8 m, Tow 2 = 8-12 m, Tow 3 = 12-15 m, Tow 4 = 15-23 m, Tow 5 = 23-30 m, Tow 6 = 30-37 m). The boat captain keeps track of the bottom depth.
 - g. The boat captain signals when the maximum tow depth has been reached and the sled is retrieved.
 - i. The hydraulics are turned on.
 - ii. The sled is brought onto the boat.
 - a) One crew member operates the hydraulics.
 - b) Two crew members guide the sled forward on the deck (they are attempting to get as much of the net on the deck as possible).
 - c) If the net contains a lot of sand, the sample is discarded and the tow repeated. Excessive sand damages the mysids beyond recognition.
7. The cruise leader records the finish flowmeter readings on the field sampling notes. He/she visually identifies the water color and estimates the percent cloud coverage, wind direction, wind velocity, swell height, and direction. For all but the last tow for each transect, the cruise leader measures and records the bottom temperature using the temperature probe and determines the water clarity by using the Secchi disk (water clarity = depth at which Secchi disk is no longer visible).
8. The other two crew members wash down the net after each tow, beginning at the mouth and working towards the cod end. When necessary, one crew member will hold up areas of the net while the other crew member washes them. When all of the sample has been washed to the cod end, the end is held over a five gallon bucket, untied, and carefully washed into the bucket. The bucket is transferred to the sample preservation station. The cod end is retied, the cod end buoy reattached, and the net rolled to the mouth in preparation for the next tow.
9. At the preservation station, a crew member washes the tow sample through a .333 mm mesh screen, removes the larger pieces of algae and detritus, and stores the sample in as many quart jars as needed or in a five gallon bucket when required. If the quart jars do not already contain formalin or if a bucket is used, formalin is added to the sample to make up a 10% formalin solution. Each jar or bucket is labelled inside and out with the cruise number, date, sample time, sample location, jar number, and total number of jars (or buckets) required to store the sample. The field sampling notes will also contain this information.

D. Proceed to the next transect

1. Repeat sampling steps D2-9 above, at next transect line with the following exception: the cable markings which were measured and taped for each tow on the first transect line, are used for the cable length for the tows on the other five transect lines. The tape markers are removed from the cable during each tow on the last transect to be sampled.
2. The transect lines for the first day of sampling are at MRC x LOC = 2500, 3000, 3500 and for the second day at 17,500, 18,000, and 18,500.

3. Transect lines can be offset up to several hundred meters to avoid kelp plants, gill nets, etc.

E. Return to harbor

1. At the end of sampling on the first day, the flowmeters are removed from the sled, rinsed with fresh water, and stored for the night. The sampling net is suspended by the cod end from the U-frame to dry, and the miniranger is returned to the MEC facility for overnight storage.
2. At the end of sampling on the second day, the flowmeters are removed from the sled, rinsed with fresh water, and returned to their storage boxes; the net is removed from the sled and placed in its storage bag.
3. Upon return to the harbor on the second day, all gear and samples are offloaded and returned to the laboratory.
4. The sled is rinsed off at the harbor boat wash area (but you must bring your own hose).

F. Demobilization

1. Return miniranger equipment to the ECO-M storage site.
 - a. Retrieve auxiliary transponder from remote site.
 - b. Return console, cable, and antenna from Lo-An to ECO-M.
2. Wash used nets and bags. Inspect nets for tears, repair small rips. Badly torn nets should be delivered to Ullman Sails in San Diego for repair.
3. Empty and replace the fresh water in the flowmeters.
4. Replace any lost or broken cruise gear.
5. Prepare cruise report for project investigator.

B.1.2 Laboratory Analysis

A. Sample preparation

1. In the wet laboratory, clean the sample to remove formalin, sand, and detritus. Save the formalized sea water and sample label. Rinse any large, non-mysid animals over the sample and save them. They will be returned to the sample after it is sorted. Specific cleaning techniques vary depending on the condition of the sample, as follows:
 - a. Samples without sand or detritus - pour sample through a sieve of .333 mm or smaller mesh. Rinse thoroughly with fresh water.
 - b. Sand samples - transfer a portion of the sample to a clean quart jar, fill jar with tap water (sample to water ratio = 1 to 5), swirl, and pour water and suspended material through a sieve of .333 mm or smaller mesh. Repeat until only sand remains in jar (this process usually requires at least five water rinses). Discard sand, and repeat process with another portion of the sandy sample. Repeat procedure until the entire sample has been cleaned.
 - c. Red algae or other large detritus samples - stack a 4.75 mm mesh metal screen on top of a .300 mm mesh metal screen. Transfer a small portion of the sample to the top screen and wash it with the water sprayer. After a thorough rinsing, manually remove the contents from the large mesh screen, inspect to ensure that there are no trapped mysids, discard, and repeat the procedure with

another portion of sample. When cleaning red algae, make sure the rinsed algae only forms a thin layer on the top screen; stacks or thick layers of algae should not be allowed to form. Turn algae frequently so that all of it is exposed to the spray. Continue procedure until sample is as clean as possible. The less red algae left in the sample, the easier it will be to take reliable subsamples; this procedure can be time consuming, but it is essential.

2. Put clean sample into calibrated (by 4000 ml increments) 5 gallon bucket. Add a measured volume of fresh water to desired volume, minimum 4000 ml, maximum 18,000 (attained by filling to 16,000 ml mark and adding 2,000 ml). The desired volume is an educated guess; enough water is needed to enable ease of stirring, while too much water dilutes the sample to the point where too few animals are found in the standardized subsamples. The goal is to have a dilution volume whereby either 50 Metamysidopsis elongata or 100 total mysids may be obtained in no less than 2 subsamples. The dilution volume may be adjusted if inspection of the first subsample indicates that an alternate volume would be more suitable in attaining the stated goal.
3. Stir the diluted sample (in all directions), then smoothly and quickly remove a subsample using the standardized 10 ml scoop. Place subsample into a small beaker. Stir and remove a second subsample and place it into the same beaker.

B. Sample analysis

1. Take subsamples and sample label to the dry laboratory. Before sorting, gather the following: a dissecting microscope, light source, forceps, sorting tray, 2 vials with poly-seal caps, 2 wash bottles (one with fresh water and one with seawater), and an empty jar for sorted subsamples.
2. Record the label information, number of subsamples (2), and the dilution volume on the laboratory field sample examination sheet.
3. Rinse a portion of the subsample into the sorting tray and examine under microscope at 12X power. Remove mysids and place M. elongata and "others" in separate vials containing seawater. Keep track of the number of M. elongata and "others" removed. Scan sorting tray twice before pouring the sorted subsample into the empty jar. Continue this step until all of the subsample has been sorted and counted. (If the first examination of the sample reveals vastly more mysids than is needed, return the subsample to the sample and increase the dilution.)
4. After sorting the first two subsamples, calculate approximately how many more subsamples will be needed to obtain either 50 M. elongata or 100 total mysids. Remove additional subsamples from the sample, if necessary, and sort them. Keep track of the number of subsamples and number of sorted mysids. If the computed number of subsamples requires more effort than is necessary, and the sample permits (i.e., large dilution, small sample), condense sample and start over. Note that the dilution volume is kept constant, once it is decided upon, during the analysis of the sample.

5. After sorting enough subsamples (never stop sorting in the middle of a sample), label the vials with the sample label information (on top) and this information plus the subsample size and final sample dilution volume (inside). The inside label is made using 100% rag paper (bioform) and a pen with waterproof ink. A dot label is used on the cap of the vial. Add buffered formalin to the vials to bring them up to a 10% formalin-seawater solution. Record the subsample volume and final dilution volume on the laboratory field sample examination sheet and note how many M. elongata and "others" were removed from the sample.
6. A qualified mysid taxonomist will: identify sorted mysids to the lowest practicable taxon, count each species according to sex and developmental stage, and record information on laboratory data sheet.

C. Data management

1. Transcribe field collection and laboratory analysis information for each sample onto computer keypunch sheets.

D. Sample curation

1. Return sorted subsamples to sample and condense sample (using .333 mm screen or finer) into quart jars with 5-10% buffered (pH = 6.5-7.0) formalin in seawater. Make sure all jars are labeled inside and out. If a different number of jars than that which was used in the field are needed, make sure new jar number information appears on both the top and inside labels. Place jars in storage box.
2. Place sorted and identified mysids in a single vial, if possible, labeled with information specified in step B5. Fill vial with 5-10% buffered Formalin-seawater and seal with a poly-seal cap. Place vial(s) in storage box.
3. Record the number of jars the sample is stored in, the box number the jars are in, and the sample identification information on the MRC Curation Bottle Inventory Computer keypunch sheets. The same information is recorded for the vial(s) containing the identified mysids, however, the vial(s) is considered the last jar(s) of the sample for inventory purposes.

B.2 BENTHOS

B.2.1 Field Sampling

A. Mobilization

1. A month before the cruise, sign up for the miniranger, Better Benthos, and Ford truck.
2. A week before the cruise, schedule mobilization and field crews and notify people selected.
3. A day or two before the cruise, notify California Department of Fish and Game, Ecosystems Management, Inc. and prep for cruise.
 - a. California Department of Fish and Game (237-7311) requires cruise dates, estimated time in field each date, location each date, vessel name and length, gear used, animals sampled (benthic invertebrates), number of persons in field each day and scientific collecting permit number of cruise leader.
 - b. Notify Ecosystems Management, Inc. of sampling dates and expected date of custody transfer of chemical environmental samples.
 - c. Cruise prep consists of field gear check, making labels, glassware supply check, wet lab gear check and chemical supply check.
 - i. Check and organize field gear (see field gear check list).
 - ii. Make labels for biological and environmental samples.
 - a) Biological labels are written on bioform paper in pencil and include station, depth, survey, core number, screen size and date.
 - b) Environmental labels are written on bioform paper and include station, depth, survey, analysis (grain size/TOC or chemistry) and date.
 - c) Each environmental label is stapled to the upper inside corner of a small ziploc bag.
 - iii. Check and organize wet lab glassware supply.
 - a) Four dozen clean 2 oz. jars with lids.
 - b) Six each clean 4, 8, and 16 oz. jars with lids.
 - iv. Check and organize wet lab gear.
 - a) Green trash buckets, 0.5 mm Tyler screens, H₂O squirt bottles and funnels.
 - b) Environmental core extruder, low green pail and spatula.
 - v. Check and organize wet lab chemicals.
 - a) Straight buffered formalin carboy and squirt bottle.
 - b) 70% isopropyl alcohol carboy and squirt bottle.
 4. Check operational status averaged over a period of six months. Levels should be 55% of total capacity and 4 pumps per day. If these levels are not met, receive written authorization to conduct survey from MRC advisor Dr. J. Kastendiek.

5. Before the cruise, gas up "Better Benthos" and Ford truck.

B. Transport to field

1. Load boat with field and diving gear.
2. Proceed to Oceanside Harbor and launch boat (need \$2 in quarters for parking).
3. Motor to first sample location.

C. Arrive at sample location.

1. Divers suit up and organize dive gear.
2. Sampling gear organized for first station.
 - a. Red goodie bag with 4 biological cores, 5 core lids and 10 meter clip line.
 - b. Blue goodie bag with 3 environmental cores, 4 sets of bungs (top and bottom) and thermometer clipped to bag.

D. Benthic sampling

1. When divers and sampling gear are ready either tie-up to station marking buoy, anchor near station marking buoy or live boat.
2. Two-man diving team enters water with sampling gear (one goodie bag each) and proceeds to bottom following buoy line.
3. Ten meter clip line is attached to bottom of buoy line.
4. Divers swim out 5-10 meters of line in a random direction and take the first set of cores (1 biological and 1 environmental).
 - a. Taking biological cores
 - i. The biological core is slowly placed on the sediment surface and pushed completely into the sediment.
 - ii. A core lid is used to dig out the biological core until the lid can be slid into the bottom of the core.
 - iii. Entirely remove biological core from sediment and secure lid onto bottom.
 - b. Taking environmental cores.
 - i. The environmental core is slowly placed on the sediment surface with the top bung securely in place and pushed into the sediment up to the marking lines just below the top of the core.
 - ii. With a finger over the hole in the top bung to provide suction, pull the core straight up out of the sediment.
 - iii. Place bottom bung on bottom of core and secure with a twisting motion.
5. Divers swim a random distance along an arc with the clip line and take the second set of cores.
6. Step 5 is repeated for the third set of cores.
7. Step 5 is repeated for the fourth biological core. A bottom temperature reading to the nearest tenth of a degree celcius is made.
8. Divers return to the buoy line winding up clip line.
9. Divers ascend to surface cleaning the buoy line and buoy of fouling organisms and checking for failing parts in the buoy array.
10. Once onboard the boat, the biological and environmental cores are placed in a labeled bag and put into a styrofoam cooler for transport back to the lab.

11. Divers bottom times, visibility, bottom temperature and comments are recorded in the diving log book.
12. New biological cores and lids and environmental cores and bungs are put into the red and blue goodie bags respectively.
13. Motor to the next station and repeat steps 1-12 until all stations scheduled for that day have been sampled.

E. Motor to Oceanside Harbor, trailer boat, and wash down boat and diving gear.

F. Return to lab.

G. Biological core sample processing.

1. Biological cores are washed with fresh water through a .5 mm Tyler screen into the green trash bucket. Sediment retained in the bucket is discarded.
2. Material retained on the .5 mm screen is transferred to an appropriate size jar with label.
3. Straight buffered formalin is added to the water and material in the jar to make a 5-10% formalin solution for fixing the animals.
4. After 48-72 hours in formalin, the material in each jar is rinsed and transferred to 70% isopropyl alcohol for preservation of the animals.

H. Environmental core sample processing.

1. The environmental core extruder is placed in the low green pail. The environmental cores (3) from each station are individually extruded and longitudinally split with the spatula.
2. Half cores (3) from each station are combined and homogenized to produce two composite environmental samples. One composite goes in the ziploc bag labeled Grain size/TOC; the other goes in the ziploc bag labeled chemistry.
3. Samples are frozen.
4. Within a week after sampling, chemistry samples are transferred to Ecosystems Management, Inc. for processing and long-term storage.
5. Grain size/TOC samples are held by MEC for processing then transferred to Ecosystems Management, Inc. for long-term storage.

B.2.2 Laboratory Analysis

A. Sorting of biological core samples.

1. Three of the four collected replicate cores are sorted under a dissecting microscope into four major taxonomic groups (polychaetes, crustaceans, mollusks, and "others") and placed into labeled vials with 70% isopropyl alcohol. Nematodes are counted for each core but not retained for long-term storage.
2. The fourth core is a reserve and is held in storage for possible future use.

B. Identification of biological core samples.

1. Sorted samples are distributed to taxonomists for identifications to the lowest taxa practicable (target -

species level) and enumeration. Taxa and counts are entered on identification sheets by core for each station.

2. Cores are lumped together by station within each major taxonomic group after identification. This is done to facilitate wet weight biomassing.

C. Wet weight biomassing.

1. Wet weight biomassing of lumped replicate samples is performed on the four major taxonomic groups by station. Excess alcohol is removed by vacuum pump for 10 seconds and wet weights are read to the nearest one hundredth of a gram on a Sartorius model #1212MP electronic balance.

D. Macrodetritus measurement.

1. The remaining material from the three sorted replicates per station are combined. The macrodetritus is swirled into suspension and poured off into a preweighed filter. Macrodetritus is identified to categories of old (anoxic) and new terrestrial particles, marine macrophytic particles, animal tubes, and inorganic particles, and the percent (+ 10%) composition of each category is visually estimated and recorded. The filter is then dried at 80°C for 10-12 hours and weighed (to .01 gram). The dry weight of this combined macrodetritus is then divided by three to yield an estimated macrodetritus dry weight per core.

E. Data management of biological core samples.

1. Taxa, taxa computer code and core counts are entered onto computer keypunch sheets for each station. Station information (i.e., station name, survey number, sampling date, bottom temperature, core size, number of replicates, and missing or bad data) is also included on the keypunch sheets.

F. Data management of physical/chemical data.

1. Macrodetritus and biomass data are entered onto Benthos physical/chemical computer keypunch sheets by station for each survey.

G. Sample curation.

1. Identified core samples and reserve cores are stored in alcohol by survey in jars with lids secured with tape for long-term storage. Alcohol levels are checked each year to prevent drying out of samples. The sample information is coded and entered onto MRC Curation Bottle Inventory computer keypunch sheets.
2. When a new species is encountered at SONGS, a representative specimen is vialled and properly labeled and stored in the MEC benthic laboratory. A voucher collection computer keypunch sheet is used to enter classification information, station location, sample date, author, date, and taxonomic reference information for each species in the collection.

B.2.3 Laboratory Analysis for ECO-M

B.2.3.1 Sediment Grain Size Analysis

- A. Equipment - for determination of median grain size, silt/clay fraction, coarse fraction, skewness, and dispersion of sediments.
 - 1. 8 oz. numbered plastic deflocculent bottles
 - 2. 0.025N (38.25g per 15 liters deionized water) sodium hexametaphosphate (deflocculent)
 - 3. 38 or 63 micron sieve
 - 4. Stainless steel evaporating dish
 - 5. Preweighed and numbered Coors dishes
 - 6. Numbered 1000ml graduated cylinders
 - 7. Watchglasses to cover graduated cylinders
 - 8. 3" sections of pipe (used to weigh down 1000 ml graduated cylinders in water bath)
 - 9. Plunging device (for agitating silt and clay solution)
 - 10. 25 ml Lowy Automatic Pipette with markings at 7, 8, 10 and 20 cm
 - 11. Preweighed and numbered 50ml beakers
 - 12. 24°C water bath
 - 13. Drying Oven (110° + 20°C)
 - 14. Eleven U.S.A. Standard Testing Sieves (A.S.T.M. E-11 specification) and bottom catch plate; Sieve numbers 10, 14, 18, 25, 35, 45, 60, 80, 120, 170, 230
 - 15. Sieve shaker
 - 16. Sartorius milligram balance

B. Initial treatment

- 1. Thaw frozen samples.
- 2. Mix wet sample thoroughly in its container or transfer to a suitable large container to mix. Immediately (while still homogeneous) weigh 20-50 gm wet sediment into 8 oz. deflocculent bottles.
- 3. Record on data sheet Sample ID, analyzed by: date, sieve size for sand/silt-clay separation, deflocculent bottle number, sample color and sample composition.
- 4. To sediment in 8 oz. bottles, add 150 ml of sodium hexameta-phosphate (deflocculent), shake well, and let stand 8 hours.

C. Separate fine particles (silt & clay) from sand

- 1. Place 63 (or 38) micron screen in evaporating dish in order to catch all wash water.
- 2. Shake sample, let settle 10-15 seconds and decant suspended fine particles through sieve into a collecting pan. Add deionized water to sample remaining in the bottle.
- 3. If necessary, wash fine particles through sieve with deionized water into a collecting pan.
- 4. Repeat steps 5 and 6 until most fine particles removed.
- 5. Transfer remaining sample from bottle to sieve using squirt bottle with deionized water.
- 6. Using light finger pressure and squirt bottle, wash remaining fine particles through sieve.
- 7. Periodically wash the bottom of the sieve to remove adhering particles.
- 8. Wash sand remaining in the sieve with deionized water to remove excess sodium hexametaphosphate and salts.

9. Carefully concentrate sand against bottom lip of sieve with squirt bottle. Scrape and wash sand into numbered Coors dish and record sand dish number on data sheet.

D. Prepare sand

1. Let sand settle and decant most overlying water (not particles).
2. Dry sand in oven at 70°C.

E. Prepare silt & clay

1. Transfer silt-clay solution from evaporating dish to a numbered 1000 ml graduated cylinder with a funnel and fill to 1000 ml with deionized water.
2. Record cylinder number and silt/clay beaker number on data sheet.
3. Agitate silt-clay solution with plunger for one minute.
4. 15 seconds after stopping agitation, take a 25 ml aliquot from a depth of 20 cm with pipette.
5. Cover the top of the cylinder with a watchglass and set the cylinder aside until such time as it is decided that the silt/clay fraction of the sample is no longer needed.
6. Transfer 25 ml aliquot to a 50 ml numbered beaker.
7. Rinse pipette before reuse.
8. Dry silt-clay solution in oven.
9. Allow silt-clay and sand fractions to come to room temperature in dessicators and weigh on balance.
10. Determine percent sand and percent silt and clay contained in the total sample weight.

F. Sieve analysis for sand

1. Transfer sand from Coors dish to top sieve in sieve stack.
2. Gently shake sieve stack and break-up aggregates on top 1-3 sieves.
3. Place sieve stack in sieve shaker and shake for 15 minutes.
4. Starting with top sieve, invert each sieve on a large piece of paper and rap sieve firmly on table top to remove all sand.
5. Examine particles on successive sieves and the bottom catch plate and make notes in comments section of data sheet if shell, aggregates, twigs, metal, etc., are present.
6. Initially tare out the empty weight of plastic weighing dish (dish wt. to = 0.001 gm).
7. Transfer sand to tare plastic dish on balance; record cumulative weight with each successive sieve.
8. The difference in the successive cumulative weights is the contribution of each phi size.

G. Pipette analysis for silt-clay fraction

1. Record sample with batch number on data sheet.
2. Place numbered graduated cylinders (from Part E 1 above) in water both with pipe sections (up to 10 cylinders at a time). Be sure watchglasses are covering graduate cylinders.
3. Agitate each sample for one minute with plunger and take six additional 25 ml aliquots from each cylinder at different depths and different times. Plunging times, withdrawal times and withdrawal depths are provided on a chart.
4. Record beaker numbers to be used on the data sheet.

5. Transfer aliquots to numbered 50 ml beakers, dry, and weigh (as in Part E 6-8).
6. Calculations (Part H below) will give the weight contributed for each Ø size.

H. Calculations

1. Total Sand = (weight of Coors dish + sand) - weight of Coors dish.
2. Weight of silt and clay fractions = (weight of silt and clay + beaker) - weight of beaker.
Multiply this weight by 40.08 to obtain the total weight in 1000 ml.
($25 \text{ ml}/1000 \text{ ml} = 1/40$; .08 is a correction factor because the pipette does not deliver exactly 25 ml at 24°C). From this subtract .3825 grams (the weight of sodium hexametaphosphate in 150 ml of a .025N solution).
Total weight of silt and clay = $\{\text{wt. of beaker containing dry silt/clay} - \text{wt. of beaker}\} \times 40.08 - .3825 \text{ gms.}$
3. Total sand + total silt-clay = total sample weight
4. Total sand/Total sample weight = % sand
5. Total silt-clay/Total sample weight = % silt and clay
6. Computer is used to calculate individual and cumulative percents, median and mean grain size and grain size distribution moments.

B.2.3.2 Sediment Total Organic Carbon Analyses

A. Equipment

1. The MEC chemistry lab uses an Oceanography International model 524-B total organic carbon system for the determination of total organic carbon in sediments. This system utilizes a Horiba model PIR 2000 infrared gas analyzer and an ampule sealing unit manufactured by Oceanography International. The method used is that recommended by the manufacturers with modifications.

B. Calibration procedure

1. Dry Potassium Biphthalate at 120°C for 2 hours and allow to cool in a dessicator.
2. Weigh out an appropriate amount to micrograms and dissolve in reagent water of low carbon content to make up a stock solution ($.21252 \text{ g}/100 \text{ ml} = 1\mu\text{gC}/\mu\text{l}$). This solution should be used the same day it is prepared.
3. Amounts of the standard solution covering the range of carbon expected in the samples are dispensed into pre-combusted ampules with a 10-100 microliter Eppendorf pipette.
4. 0.2 ml of a 10% v/v Phosphoric acid solution is added to the ampules containing the standards and added to empty ampules for zero determinations.
5. Add 2.0 ml reagent water to the ampules (washing down the sides).
6. The following is done in groups of eight ampules in one minute intervals:
 - a. Add 0.2 g Potassium Persulfate with dipper.
 - b. Add 2.0 ml water (washing the granules of Persulfate down the sides of the ampule).

- c. Purge for 8 min. with O₂ and seal.
 7. The standards and zeros are oxidized with a batch of samples and used to generate a standard curve for only that batch.
- C. Sample procedure
1. Dry 20-50 g subsample at 70°C for at least 12 hours.
 2. Grind samples to a homogeneous powder.
 3. Dry powder for 8 hours then cool in a dessicator.
 4. Weigh precombusted ampules to the nearest 0.00001 g.
 5. Add sample (5-50 mg) to the preweighed ampules.
 6. Reweigh the ampules containing the samples to obtain weight of unknown sediment.
 7. Add 1.0 ml Phosphoric acid (10% v/v) to each of the sample and reagent blank ampules.
 8. Add 2.0 ml of water to samples and blanks.
 9. Allow to stand for at least 30 minutes.
 10. The following is done in groups of eight samples in one minute intervals:
 - a. Add 0.2 g Potassium Persulfate to each sample.
 - b. Add 2.0 ml water to wash down the sides of the ampule.
 - c. Purge for 8 minutes with O₂ and seal.
 11. Convert organic material to CO₂ by placing the sealed ampules in an 130°C autoclave for at least four hours.
 12. Measure carbon content from the amount (moles) of CO₂ liberated.
 13. Amount of CO₂ released by unknowns minus amount released by reagent blanks is compared to generated standard curve in section B.7 to obtain carbon content of samples.

APPENDIX C

Supporting Information

APPENDIX C.1

Step-by-Step Procedure for Examining Assumption Testing and BACI Testing Computer Outputs (Protocol Specifics)

APPENDIX C.1

Step-by-Step Procedure for Examining Assumption Testing and BACI Testing Computer Outputs (Protocol Specifics)

1. Examine the "NOTRANSFORM" row of the "Before" data set for additivity and trends (Figure C.1-1). The two values should be greater than 0.05. The serial correlation column should be labeled "NS". For the After data set serial correlation should also be "NS". If in compliance, go to (14).
2. If the trends column (Figure C.1-1) of the Before data indicates a trend with time go to (6).
3. If there are no trends, but if additivity is not in compliance, run the additivity test on the untransformed data without observations of zero. If the untransformed data is additive (Figure C.1-2) go to (5).
4. If the untransformed data with zeros omitted is not additive, check the table of Deltas vs. Sums regression (Figure C.1-3) for untransformed data. If there are values in the last (Sum of Betas) column ≥ 2.0 indicating an influence point, rerun the additivity test on the untransformed and $\log(x + 0)$ transformation with the single or highest two (if more than 1) influence date(s) removed. If the untransformed data are now additive (Figure C.1-4) go to (5). If not go to (6).
5. If the additivity and trends are in compliance check for serial correlation (Figure 3.1-1). If there is a significant serial correlation, go to (12). If not, accept the NOTRANSFORM option, use the non-parametric Wilcoxon rank sum test and go to (14).

6. Examine the $\log(x + 0)$ assumption test results (Figure C.1-1) for compliance with assumptions. If the assumptions are all met and fewer than 10% of the untransformed delta values (i.e. surveys) are dropped because of zero values, accept the $\log(x + 0)$ transformation, use the BACI t-test and go to (14). If more than 10% of the untransformed delta values are dropped, go to (10).
7. If not, and if there is a significant trend in the data (Figure 3.1-1) go to (10).
8. If not, and if additivity is not in compliance, look at the zeros and Delta vs. Sums checks of additivity on $\log(x + 0)$ transformation (Figure 3.1-4) as in steps (3) and (4). If additivity is still not in compliance go to (10). Otherwise go to (9).
9. If serial correlation is significant, go to Step (12) select an α level, and use the AUTOREG procedure. If not accept the $\log(x + 0)$ option and go to (14).
10. Examine the output of the χ^2 test (Figure C.1-5) for the H_0 that the number of zero data points are distributed equally in each of the four BACI cells at $\alpha = 0.05$. If the zeros are equally distributed, go to (11). If not, go to (13).
11. Examine the power columns (Figure C.1-1) for $\alpha = 0.05$ and $\alpha = 0.10$ for any of the $\log(x + c)$ rows (where $c > 0$), which meet all BACI assumptions. If more than one transformation meets all assumptions or if only serial correlation is significant, then select the transformation with the highest power rating. If only one transformation meets the conditions, use that transformation. Proceed to (14) if all assumptions are met or to (12) if only serial correlation is significant. If none of the $\log(x + c)$ transformations meets these assumptions, go to (13).

12. Select an α level (see Step 14) and use the AUTOREG procedure on the appropriate transformation, then go to (15). In AUTOREG accept the model which minimizes at least two of the values for ROOT MSE, AIC, and SBC. If the accepted model is not significant then use the test results for the BACI t-test and Wilcoxon rank sum test rather than the AUTOREG results. An adjustment must be made to the p-level from the AUTOREG computer output for one-tailed tests (Ichthyoplankton) because this printout is always a 2-tailed test. This adjustment is made as follows:
- a) If the parameter estimate of the SONGS effect (Figure C.1-6) is negative indicating a relative decrease at SONGS, then take one-half of the given p-level for the one-tailed p-level.
 - b) If the parameter estimate of the SONGS effect is positive, then take one-half of the given p-level and add .5 for the one-tailed p-level. Rejection of the null hypothesis for the one-tailed test for a relative decrease at SONGS is never possible when there is a relative increase at SONGS.
13. Use the results of the binomial $p = S/(S + C)$ test. Then proceed to Step (15).
14. When the power column ($\alpha = 0.05$) for the selected data form (untransformed, $\log(x + 0)$ or one of the $\log(x + c)$ transformations; Figure C.1-1) is ≤ 0.80 , set $\alpha = .10$; otherwise set $\alpha = 0.05$.
15. Using the selected data form and α level, determine whether the p-value for the BACI t-test (for untransformed and $\log(x + c)$ transformations; Figure C.1-8), Wilcoxon rank sum test (Figure C.1-8), the AUTOREG test (Figure C.1-6), or the binomial test

(Figure C.1-7) has a value $\leq \alpha$. If so, reject H_0 . If not, accept H_0 .

16. Prepare an interpretation of the results.
17. Examine the suite of untransformed and transformed BACI analysis results (Figure C.1-9) for their descriptive and potential corroborative value, keeping in mind their compliance with, or violation of BACI assumptions. If Chi² test was significant, if two (log + constant) transformations complied with the BACI assumptions, both transformations may be examined. Also examine the results of the binomial $p = S/(S + C)$ test for its descriptive and potential corroborative value.
18. To the extent that these examinations add to the understanding of the outcome of (15), prepare an addendum to the interpretation.

BACI TESTING PROGRAM
USING THE DATA SET `BACI.XSHELL` -- ALL DATES, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE CONTROL
RESULTS OF BACI ASSUMPTION TESTING --

SPCODE

	NUMBER OF SURVEYS BEFORE	NUMBER OF SURVEYS AFTER	P-LEVEL FOR ADDITIVITY*	P-LEVEL FOR SYMMETRY**	SERIAL CORREL. SIGNIFICANCE*** BEFORE	SERIAL CORREL. SIGNIFICANCE*** AFTER	P-LEVEL FOR TRENDS**** BEFORE
TRANSFORMATION BEFORE							
INV(X+0, 1)	25	16	0.839	0.795	NS	NS	0.431
INV(X+0)	8	4	0.078	0.034	NS	NS	0.190
INV(X+1)	25	16	0.998	0.050	NS	NS	0.811
INV(X+10)	25	16	0.033	0.080	NS	NS	0.344
LOG(X+0, 1)	25	16	0.892 11	0.857	NS 11	NS 11	0.728 11
LOG(X+0)	8 4 6	0.384 6,8	0.966	NS 6,9	NS 6,9	0.929 6,7	
LOG(X+1)	25	16	0.287 11	0.934	NS 11	NS 11	0.671 11
LOG(X+10)	25	16	0.007 11	0.913	NS 11	NS 11	0.261 11
NOTTRANSFORM	25	16	0.001 1	0.913	NS 1,5	NS 1,5	0.197 1,2
TRANSFORMATION AFTER							
INV(X+0, 1)	0.756	10.3	17.9	1.979	3.443	14.910	42.598
INV(X+0)	0.285	47.0	60.9	1.057	16.471	106.715	368.615
INV(X+1)	0.849	12.1	20.7	0.053	0.164	0.009	0.128
INV(X+10)	0.628	15.4 11	25.5 11	0.001	0.002	0.000	0.000
LOG(X+0, 1)	0.983	12.1 20.7	-0.146	-0.352	0.074	0.074	0.563
LOG(X+0)	0.473	18.8 29.8	-0.073	-0.614	0.132	0.132	0.817
LOG(X+1)	0.859	14.2 23.7	-0.025	-0.079	0.002	0.002	0.062
LOG(X+10)	0.571	16.2 26.4	-0.003	-0.006	0.000	0.000	0.002
NOTTRANSFORM	0.522	16.8 27.2	-0.066	-0.094	0.014	0.014	1.698

C.1-5

* IF $< .05$ THEN THE TRANSFORMATION IS NON-ADITIVE.
 ** IF $< .05$ THEN THE TRANSFORMATION IS NOT SYMMETRICAL.
 *** SIG INDICATES THAT THE TRANSFORMATION HAS SIGNIFICANT SERIAL CORRELATION AT THE .05 P-LEVEL USING VON NEUMANN'S TEST.
 **** IF $< .05$ THEN THE TRANSFORMATION HAS A LINEAR TREND WITH TIME.

Figure C.1-1. Example of BACI assumption testing output. Numbered items refer to steps in text.

BACI TESTING PROGRAM
USING THE DATA SET IBACI.XSHELF -- OCCURENCES OF ZERO DELETED, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE CONTROL
RESULTS OF ADDITIVITY TESTS

SPCODE	
TRANS	P1
	8
LOC(X+0)	0.384
NOTTRANSFORM	0.021
	3

Figure C.1-2. Example of additivity testing without observations of zero. Numbered items refer to steps in text.

BACI TESTING PROGRAM
USING THE DATA SET 1BACI.XSHELF -- ALL DATES, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE CONTROL
REGRESSION OF DELTA VERSUS SUM WITH INFLUENCE STATISTICS

SPCODE TRANS=NOTTRANSFORM PERIOD=BEFORE

DEP VARIABLE: DELTA
ANALYSIS OF VARIANCE

SOURCE	DF	SUM OF SQUARES	MEAN SQUARE	F VALUE	PROB>F
MODEL	1	7.13954443	7.13954443	14.014	0.0011
ERROR	23	11.71259237	0.50946054		
C TOTAL	24	18.85113680			

ROOT MSE 0.713765
DEP MEAN -0.0791664
C.V. -901.601

R-SQUARE 0.3786
ADJ R-SQ 0.3516

PARAMETER ESTIMATES

VARIABLE	DF	PARAMETER ESTIMATE	STANDARD ERROR	T FOR H0: PARAMETER=0	PROB > T
INTERCEP	1	-0.36952381	0.16246351	-2.275	0.0326
SUM	1	0.40381560	0.10787061	3.744	0.0011

OBS	ID	RESIDUAL	RSTUDENT	HAT	DIAG	COV RATIO	DFFITS	INTERCEP DFBETAS	SUM DFBETAS
1	24JUL79	0.3037	0.4278	0.0462	1.1270	0.0941	0.0934	-0.0344	
2	22AUG79	0.3384	0.4784	0.0511	1.1282	0.1110	0.1110	-0.0517	
3	21SEP79	-2.0806	-3.8095	0.0705	0.4269	-1.0492	-0.3649	-0.6902	
4	10MAR80	0.6501	0.9274	0.0414	1.0560	0.1928	0.1834	-0.0356	
5	24MAR80	0.1219	0.1713	0.0467	1.1435	0.0379	0.0377	-0.0144	
6	04APR80	0.8980	1.3040	0.0406	0.9817	0.2684	0.2179	0.0337	
7	05MAY80	0.3046	0.4301	0.0503	1.1318	0.0990	0.0990	-0.0449	
8	26MAY80	0.3477	0.4910	0.0481	1.1234	0.1104	0.1101	-0.0453	
9	09JUN80	0.3839	0.5436	0.0510	1.1214	0.1261	0.1260	-0.0586	
10	17JUN80	0.1692	0.2377	0.0457	1.1394	0.0520	0.0515	-0.0184	
11	24JUL80	0.1927	0.2734	0.0646	1.1606	0.0719	0.0285	0.0443	
12	07JUL80	0.4276	0.6058	0.0488	1.1117	0.1372	0.1370	-0.0583	
13	14JUL80	0.2926	0.4130	0.0501	1.1330	0.0948	0.0948	-0.0425	
14	04AUG80	-0.0446	-0.0625	0.0441	1.1430	-0.0134	-0.0132	0.0041	
15	11AUG80	-0.3698	-0.5206	0.0408	1.1119	-0.1074	-0.1008	0.0155	
16	18AUG80	-0.0224	-0.0313	0.0444	1.1437	-0.0668	-0.0066	0.0021	
17	01SEP80	0.2921	0.4122	0.0501	1.1330	0.0946	0.0946	-0.0424	
18	08SEP80	-0.6527	-0.9306	0.0400	1.0539	-0.1900	-0.1663	-0.0013	
19	22SEP80	-1.7428	-2.8817	0.0541	0.6090	-0.6892	-0.3527	-0.3518	
20	26SEP80	-0.2220	-0.3114	0.0420	1.1309	-0.0652	-0.0628	0.0143	
21	29SEP80	-0.6731	-0.9610	0.0401	1.0487	-0.1964	-0.1676	-0.0100	
22	06OCT80	-0.2021	-0.2835	0.0422	1.1329	-0.0595	-0.0574	0.0437	
23	07JUL81	0.9292	4.6745	0.8521	1.8603	11.2208	-3.0936	10.9543	4
24	15SEP81	0.3840	0.5437	0.0510	1.1214	0.1261	0.1261	-0.0286	
25	17NOV81	-0.0257	-0.0360	0.0438	1.1429	-0.0077	-0.0075	0.0023	

C.1-7

Figure C.1-3 Example of delta versus sum regression output. Numbered items refer to steps in text.

BACI TESTING PROGRAM
USING THE DATA SET IBACI.XSHELF -- 7JUL81 DELETED, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE' CONTROL
RESULTS OF ADDITIVITY TESTS

SPCODE	
TRANS	P1
	8
	LOG(X+0)
	NOTRANSFORM 0.980
	0.033 4

Figure C.1-4. Example of additivity testing with influential date(s) deleted. Numbered items refer to steps in text.

CHI SQUARE TEST ON BACI DATA

SPCODE

TABLE OF ABUND BY PERLOC

ABUND

PERLOC

FREQUENCY	PERCENT	ROW PCT		COL PCT		AFTER_CO_NTROL		AFTER_SO_NCS		BEFORE_CONTROL		BEFORE_SO_NGCS		TOTAL
		AFTER	CO	NTROL	SO	NCS	C	BEFORE	S	ONGS	ONGS	ONGS	ONGS	
0	6	7.32		7.32	6	6	5	12	14.63	14.63	12	29	29	
		20.69		20.69	20.69	6.10	17.24	41.38	41.38	41.38	35.37	35.37		
		37.50		37.50	37.50	20.00	20.00	48.00	48.00	48.00				
1	10	12.20		12.20	10	10	20	13	15.85	15.85	13	53	53	
		18.87		18.87	18.87	24.39	37.74	24.53	24.53	24.53	64.63	64.63		
		62.50		62.50	62.50	80.00	80.00	52.00	52.00	52.00				
TOTAL	16	19.51		19.51	16	25	25	82	82	82				
					30.49	30.49	30.49	100.00	100.00	100.00				

STATISTICS FOR TABLE OF ABUND BY PERLOC

STATISTIC	DF	VALUE	PROB
CHI-SQUARE	3	4.392	0.2222-10
LIKELIHOOD RATIO CHI-SQUARE	3	4.570	0.206
MANTEL-HAENSZEL CHI-SQUARE	1	0.200	0.655
PHI		0.231	
CONTINGENCY COEFFICIENT		0.225	
CRAMER'S V		0.231	

SAMPLE SIZE = 82

Figure C.1-5. Example of chi square test for equal distribution of zero data points. Numbered items refer to steps in text.

BACI TESTING PROGRAM
USING THE DATA SET IBACI.XSHELLF -- ALL DATES, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE CONTROL

SPCODE TRANS=LOG(X+0.1)

A U T O R E G P R O C E D U R E

DEPENDENT VARIABLE = DELTA

ORDINARY LEAST SQUARES ESTIMATES

	SSE	DFE	ROOT MSE	46
MSE	0.225495	0.4748631		
SBC	70.42368	66.68128		
REG RSQ	0.1526	0.1526		
DURBIN-WATSON	1.6466			

VARIABLE DF B VALUE STD ERROR T RATIO APPROX PROB

INTERCPT	1	-0.128264130	0.096931023	-1.323	0.1923
PERVAR	1	-0.394557987	0.137081168	-2.878	0.0060

ESTIMATES OF AUTOCORRELATIONS

LAG	COVARIANCE	CORRELATION	-1	9	8	7	6	5	4	3	2	1	0	1	2	3	4	5	6	7	8	9	1
0	0.216099	1.000000												*****	*****	*****	*****	*****	*****	*****	*****	*****	*****
1	0.0345996	0.160110												***	***	***	***	***	***	***	***	***	***
2	0.0112067	0.051859												#	#	#	#	#	#	#	#	#	#
3	-0.060909	-0.281857												*****	*****	*****	*****	*****	*****	*****	*****	*****	*****

PRELIMINARY MSE= 0.1911909

LAG	COEFFICIENT	STD ERROR	T RATIO	VARIABLE DF	B VALUE	STD ERROR	T RATIO	APPROX PROB
1	-0.1639420	0.1456814	-1.127718	INTERCPT	1	-0.114107063	0.089543616	0.2094
2	-0.07399774	0.14706985	-0.503147	PERVAR	1	-0.417438046	0.127805404	0.0021
3	0.30220596	0.14536814	2.078901	A(1)	1	-0.174582825	0.143778929	0.2313
				A(2)	1	-0.0923333760	0.149375967	0.6118
				A(3)	1	0.333444222	0.152066169	0.0338

MAXIMUM LIKELIHOOD ESTIMATES

	SSE	DFE	ROOT MSE	43	VARIABLE DF	B VALUE	STD ERROR	T RATIO	APPROX PROB
MSE	0.2088978	0.4570534							
SBC	75.51565	66.15964							
REG RSQ	0.1989	0.2662							
DURBIN-WATSON	2.0603								

INTERCPT	1	-0.144107063	0.089470756	-1.275	0.2090
PERVAR	1	-0.417438046	0.127760691	-3.267	0.0021

12,15

Figure C.1 - 6. Example of AUTOREG test output. Numbered items refer to steps in text.

RESULTS OF BINOMIAL TEST ON RATIOS OF SONGS/(SONGS+CONTROL)

SPCODE	STAGE	ZAMNSB	PROB2TL	PROB1TL
		0.285	0.776	0.612 15

Figure C.1-7. Example of the binomial testing output. Numbered items refer to steps in text.

BACI TESTING PROGRAM
USING THE DATA SET IBACI.XSHELF -- ALL DATES, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE CONTROL
SUMMARY OF BACI TEST RESULTS

SPCODE	TRANSFORMATION	BEFORE N	AFTER N	AFTER MEAN	DELTA AFTER-BEFORE	PERCENT CHANGE SONGS	PERCENT CHANGE CONTROL	Prob>T	PROB>Z
				MEAN DELTA	DELTA				
LOG(X+1)		25	16	-.051	-.014	0.037	-36.11	-50.87	0.824 (0.872)

Figure C.1-8. Example of BACI test results. Numbered items refer to steps in text.

BACI TESTING PROGRAM
USING THE DATA SET 'BACI_XSHELL' -- ALL DATES, THE SONGS VARIABLE SONGS AND THE CONTROL VARIABLE CONTROL
SUMMARY OF BACI TEST RESULTS

SPCODE	TRANSFORMATION	BEFORE N	BEFORE MEAN	AFTER MEAN	DELTA AFTER-BEFORE	PERCENT CHANGE SONGS	PERCENT CHANGE CONTROL	Prob>T	PROB>Z
			DELTA	MEAN	DELTA				
		N	DELTA	DELTA					
	INV(X+0, 1)	25	16	2.682	1.452	-1.23	-36.11	-50.87	0.213
	INV(X+0)	8	4	10.69	17.02	6.328	-36.11	-50.87	0.691
	INV(X+1)	25	16	0.106	0.042	-.064	-36.11	-50.87	0.778
	INV(X+10)	25	16	0.001	0.000	-.001	-36.11	-50.87	0.134
	LOG(X+0, 1)	25	16	-.245	-.112	0.133	-36.11	-50.87	0.237
	LOG(X+0)	8	4	-.411	-.443	-.032	-36.11	-50.87	0.838
	LOG(X+1)	25	16	-.051	-.014	0.037	-36.11	-50.87	0.473
	LOG(X+10)	25	16	-.004	-.000	0.004	-36.11	-50.87	0.399
	NOTTRANSFORM	25	16	-.079	0.008	0.088	-36.11	-50.87	0.872

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Figure C.1-9. Example of BACI analysis results for the suite of transformations. Numbered items refer to steps in text.

APPENDIX C.2

Cluster Analysis Output

Table C.2-1.

Two-way coincidence table of soft bottom benthic species along the 8 m isobath during the San Onofre monitoring studies. Brackets show the species clusters and survey/station groups identified from the species and survey/station dendograms generated by the cluster analysis. Numerals refer to the survey/station groups discussed in the text (Section 3.3.2). Surveys are: 15-32=Before, 33-40=interim, 41-72=After. Station locations are given directly below survey numbers; these are: 700 and 1100=Impact sites, 1900 and 3350=intermediate sites, 6700 and 9400=Control sites. Standardized abundances are given by symbols: blank=0, .>0 to 0.25, -->0.25 to 0.50, +->0.50 to 0.75, *->0.75.

Table C-2-2.

Two-way coincidence table of soft bottom benthic trophic-motility groups along the 8 m isobath during the San Onofre monitoring studies; brackets show the trophic-motility group clusters and the survey/station groups identified from the trophic-motility group and survey/station dendograms generated by the cluster analysis. Numerals refer to the survey/station groups discussed in the text (Section 3.3.2). Surveys are: 15-32=Before 33-40=interim, 41-72=After. Station locations are given directly below survey numbers; these are: 700 and 1100=impact sites, 1900 and 3350=intermediate sites, 6700 and 9400=control sites. Standardized abundances are given by symbols: blank=0, .=>0 to 0.25, ==>0.25 to 0.50, +=>0.50 to 0.75, *=>.75.

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Table C. 2-4.

Two-way coincidence table of soft bottom benthic trophic-motility groups along the 18 m isobath during the San Onofre monitoring studies. Brackets show the trophic-motility group clusters and the survey/station groups identified from the trophic-motility group and survey/station dendograms generated by the cluster analysis. Numerals refer to the survey/station groups discussed in the text (Section 3.3.2). Surveys are: 15-32=Before 33-40=interim, 41-72=After. Station locations are given directly below survey numbers; these are: 700 and 1100=impact sites, 1900 and 3200=intermediate sites, 6700 and 9400=control sites. Standardized abundances are given by symbols: blank=0, .=>0 to 0.25, -=>0.25 to 0.50, +=>0.50 to 0.75, *=>.75.

Table C.2-5. The 50 highest ranked species in the station groups formed by the cluster analysis of the 8 meter data. The values to the right are the standardized relative abundances (see Section 2.4.6).

GROUP NO. 1	OBS SPECIES	GROUP NO. 2	OBS SPECIES
1 Tiron biocellata	0.37	1 Thalenessa spinosa	0.29
2 Photis californica	0.35	2 Rhoxygnus sp. A	0.27
3 Rhopoxynius sp. juvenile	0.22	3 Leptociuma forsmanni	0.27
4 Gibberosus myersi	0.20	4 Scoloplos armiger	0.25
5 Monoculodes hartmannae	0.17	5 Aceta catherinae	0.23
6 Modiolus neglectus	0.16	6 Rhopoxynius sp. juvenile	0.22
7 Atylus tridens	0.16	7 Prionospio pygmaea	0.21
8 Jassa falcata	0.11	8 Rhopoxynius abronius	0.21
9 Amastigus acutus	0.06	9 Spiophanes bombyx	0.21
10 Acetes cataphracta	0.00	10 Neptys sp.	0.21
11 Acteocina harpa	0.00	11 Monoculodes hartmannae	0.18
12 Acuminateutopus heterurus	0.00	12 Parapriionospio pinnata	0.18
13 Anaeana occidentalis	0.00	13 Dendraster excentricus	0.17
14 Amantis callosa	0.00	14 Ephilomedes longisetata	0.17
15 Ampelisca agassizii	0.00	15 Synchelidium shoemakeri	0.16
16 Archichthurus occidentalis	0.00	16 Olivella baetica	0.16
17 Ancinus granulatus	0.00	17 Goniada littorea	0.15
18 Acorides inermis	0.00	18 Diastylopsis tenuis	0.15
19 Argissa hamatipes	0.00	19 Paramenteres sp. A	0.15
20 Armandia bioculata	0.00	20 Jassa fallata	0.14
21 Asthenothaerus villosior	0.00	21 Paraonella platybranchiata	0.14
22 Baltis micans	0.00	22 Rhopoxynius menziesi	0.13
23 Callianassa sp. juvenile	0.00	23 Mediomasstus acutus	0.13
24 Campylaspis sp. C SCAMIT	0.00	24 Campylaspis sp. C SCAMIT	0.13
25 Caprella angusta	0.00	25 Onuphis eremita	0.11
26 Chaetozone setosa	0.00	26 Photis californica	0.11
27 Cooperella subdiaphana	0.00	27 Phoronis spp.	0.11
28 Crepidula coei	0.00	28 Eohaustorius washingtonianus	0.11
29 Cyclospis nubila	0.00	29 Pectinaria californiensis	0.11
30 Cyclostremella californica	0.00	30 Leitoscoloplos elongatus	0.11
31 Dendraster excentricus	0.00	31 Tellina modesta	0.11
32 Diastylopsis tenuis	0.00	32 Glyceria convoluta	0.10
33 Diopatra splendidissima	0.00	33 Caprella angusta	0.10
34 Dioplopuncinata	0.00	34 Edotea sublittoralis	0.09
35 Ecotela subtortularis	0.00	35 Ophiuroidea juvenile	0.09
36 Eohaustorius washingtonianus	0.00	36 Typosyllis hyalina	0.09
37 Etenea diatae	0.00	37 Spiophanes missionensis	0.09
38 Ephilomedes carcharodontata	0.00	38 Periploma planisculum	0.09
39 Ephilomedes longisetata	0.00	39 Magelona pitalkai	0.09
40 Flatworm 1	0.00	40 Lumbrineris sp.	0.08
41 Flatworm 3	0.00	41 Amastigus acutus	0.08
42 Gottidia albida	0.00	42 Nephtys caecoides	0.08
43 Glycera convoluta	0.00	43 Tubulanidae sp. B	0.08
44 Glycera sp.	0.00	44 Sulcoretusa xystrum	0.08
45 Glycine armigera	0.00	45 Tiron biocellata	0.07
46 Gonioda littorea	0.00	46 Stenothoe estacola	0.07
47 Hemichordate unidentified	0.00	47 Munna ubiquita	0.07
48 Hemicilia plumbea	0.00	48 Mediomasstus californiensis/ambiseta	0.07
49 Lamprops carinata	0.00	49 Ampelisca agassizi	0.07
50 Leitoscoloplos elongatus	0.00	50 Ancinus granulatus	0.07

Table C.2-5. (cont.)

GROUP NO. 3	OBS SPECIES	GROUP NO. 4	OBS SPECIES
-3		-4	
1 Rhepoxyinius sp. A	1 Acesta catherinae	0.42	0.49
2 Leptocuma forsmanni	2 Rhepoxyinius sp. A	0.39	0.38
3 Paraoneilla platybranchiata	3 Spiophanes bombyx	0.35	0.37
4 Rhepoxyinius sp. juvenile	4 Rhepoxyinius abronius	0.32	0.37
5 Spiophanes bombyx	5 Synchelidium shoemakeri	0.30	0.33
6 Synchelidium shoemakeri	6 Pectinaria californiensis	0.29	0.33
7 Rhepoxyinius abronius	7 Rhepoxyinius sp. juvenile	0.27	0.33
8 Diastylopsis tenuis	8 Scoloplos armiger	0.26	0.29
9 Magelona sacculata	9 Pista disjuncta	0.25	0.28
10 Euphilomedes longisetata	10 Nephtys sp.	0.24	0.27
11 Prionospio pygmaea	11 Diastylopsis tenuis	0.24	0.27
12 Acesta catherinae	12 Paraoneilla platybranchiata	0.22	0.27
13 Paranemertes sp. A	13 Magelona sacculata	0.22	0.27
14 Nephtys sp.	14 Thalenessa spinosa	0.20	0.27
15 Campylaspis sp. C SCAMIT	15 Parasterope hulingsi	0.19	0.26
16 Amastigos acutus	16 Paranemertes sp. A	0.19	0.25
17 Dendraster excentricus	17 Olivella baetica	0.19	0.24
18 Rhepoxyinius menziesi	18 Photis californica	0.19	0.23
19 Tellina modesta	19 Acteinoma harpa	0.17	0.23
20 Scoloplos armiger	20 Rhepoxyinius daboios	0.17	0.21
21 Goniada littorea	21 Tellina modesta	0.17	0.21
22 Rhepoxyinius daboios	22 Phoronis spp.	0.16	0.21
23 Monoculoides hartmanae	23 Euphilomedes longisetata	0.15	0.21
24 Ampelisca agassizii	24 Campylaspis sp. C SCAMIT	0.15	0.20
25 Magelona pitelkai	25 Dendraster excentricus	0.15	0.20
26 Phoronis spp.	26 Phyllocoelae (Aponaitides) hartmanae	0.14	0.19
27 Tubulanidae sp. B	27 Parapriionospio pinnata	0.14	0.19
28 Ecotea sublittoralis	28 Lamprops carinata	0.14	0.19
29 Nemiomastus acutus	29 Leptocuma forsmanni	0.13	0.19
30 Neverita reclusiana	30 Priionospio cirrifera	0.13	0.18
31 Thalenessa spinosa	31 Anchicolarurus occidentalis	0.13	0.18
32 Pectinaria californiensis	32 Yoldia cooperi	0.13	0.17
33 Photis macrotaca	33 Gibberulus myersi	0.13	0.17
34 Gibberulus myersi	34 Goniada littorea	0.11	0.17
35 Olivella baetica	35 Monoculoides hartmanae	0.11	0.17
36 Macoma sp.	36 Cyclaspis nubila	0.10	0.16
37 Parasterope hulingsi	37 Mediomasustus acutus	0.10	0.16
38 Eohaustorius washingtonianus	38 Asthenothaerus villosior	0.10	0.16
39 Ancinus granulatus	39 Tubulanidae sp. B	0.10	0.16
40 Jassa faecata	40 Podakeopsis brevipalpa	0.10	0.15
41 Nephtys caecoides	41 Balcis micans	0.10	0.15
42 Tiron biocellata	42 Atylus tridens	0.10	0.15
43 Podakeopsis brevipalpa	43 Priionospio pygmaea	0.09	0.15
44 Parapriionospio pinnata	44 Edotea sublittoralis	0.09	0.14
45 Phyllocoelae (Aponaitides) hartmanae	45 Nassarius perquinus	0.09	0.14
46 Euphilomedes carcharodonta	46 Spiochaetopterus costarum	0.09	0.14
47 Lamprops carinata	47 Rhepoxyinius menziesi	0.09	0.14
48 Atylus tridens	48 Macoma sp.	0.09	0.14
49 Anchicolarurus occidentalis	49 Lissica agassizii	0.09	0.14
50 Typosyllis hyalina	50 Nunnia ubiquita	0.09	0.14

Table C.2-5. (cont.)

GROUP NO. 5	OBS SPECIES	GROUP NO. 6	OBS SPECIES
5	1 Nephtys sp.	1 Goniada littorea	0.47
	2 Parameretes sp. A	2 Tellina modesta	0.42
	3 Almastigos acutus	3 Zygopollia sp.	0.38
	4 Tubulanidae sp. B	4 Asthenothaerus vittiosior	0.36
	5 Zygeupolia sp.	5 Rheoxynius sp. juvenile	0.35
	6 Campylaspis pinnata	6 Edotea sublittoralis	0.31
	7 Parapriionospio pinnata	7 Diastylopsis tenuis	0.31
	8 Spiophanes bombyx	8 Typosyllis hyalina	0.31
	9 Tellina modesta	9 Ancinus granulatus	0.30
	10 Monoculodes hartmannae	10 Acesta catherinae	0.30
	11 Goniada littorea	11 Synchelidium shoemakeri	0.30
	12 Synchelidium shoemakeri	12 Paranemertes sp. A	0.29
	13 Priionospio pygmaea	13 Nephtys sp.	0.28
	14 Photis californica	14 Euphilomedes longisetosus	0.28
	15 Sulcoretusa xystrum	15 Parasterope huilensis	0.25
	16 Lumbrineris sp. D	16 Prionospio pygmaea	0.24
	17 Typosyllis hyalina	17 Amastigos acutus	0.24
	18 Edotea sublittoralis	18 Olivella baetica	0.24
	19 Thalenessa spinosa	19 Wenia collaris	0.23
	20 Acesta catherinae	20 Thalenessa spinosa	0.21
	21 Rheoxynius abronius	21 Photis californica	0.21
	22 Tiron biocellata	22 Lumbrineris californiensis	0.19
	23 Paraonella platybranchiata	23 Gibberosus myersi	0.19
	24 Rheoxynius sp. A	24 Rheoxynius sp. A	0.19
	25 Acteocina harpa	25 Campylaspis sp. C SCAMIT	0.17
	26 Ophiuroidea juvenile	26 Tiron tropakis	0.16
	27 Scoloplos sp.	27 Scoloplos sp.	0.16
	28 Diastylopsis tenuis	28 Yoldia cooperi	0.16
	29 Jassa faicata	29 Spiophanes bombyx	0.15
	30 Spiophanes missionensis	30 Monoculodes hartmannae	0.15
	31 Lumbrineris californiensis	31 Rheoxynius menziesii	0.13
	32 Scoloplos armiger	32 Tubulanidae sp. B	0.13
	33 Pectinaria californiensis	33 Lumbrineris sp.	0.12
	34 Flatworm 3	34 Nymphon cf. heterodonticulatum	0.11
	35 Phoronis spp.	35 Leptocuma forstmani	0.11
	36 Prionospio cirrifera	36 Cyclostremella californica	0.11
	37 Parasterope huilensis	37 Parapriionospio pinnata	0.09
	38 Leptocuma forstmani	38 Armandia bioculata	0.09
	39 Spiochaetopterus costarum	39 Euphilomedes carcharodonta	0.09
	40 Medioma stasys acutus	40 Glycera convoluta	0.08
	41 Magelona pitelkai	41 Lumbrineris sp. D	0.08
	42 Tubularia pelliculoides (red)	42 Pectinaria californiensis	0.08
	43 Olivella baetica	43 Medioma stasys californiensis/ambiseta	0.08
	44 Podakeopsis brevipalpa	44 Jassa fallacta	0.08
	45 Ancinus granulatus	45 Atylus tridens	0.08
	46 Rheoxynius sp. juvenile	46 Spiophanes sp.	0.08
	47 Gibberosus myersi	47 Leitoscoloplos elongatus	0.07
	48 Dendraster excentricus	48 Callianassa sp. juvenile	0.07
	49 Rheoxynius menziesii	49 Magelona sacculata	0.07
	50 Yoldia cooperi	50 Magelona sp.	0.07

Table C.2-6. The trophic-motility groups in the station groups formed by cluster analysis of the 8 meter data. The letters to the left of the columns indicate the taxonomic subset; C=cnidaria, P=crustacea, M=mollusc, E=echinoderm, O=other, PCAP=capitellid polychaete, PPAR=paraonid polychaete. The values to the right are the standardized relative abundances (see Section 2.4.8).

GROUP NO. 1	OBS SPECIES	GROUP NO. 2	OBS SPECIES	
1		2		
1	O-Surface carnivore-omnivore: Motile	0.47	1 C-Surface omnivore-deposit: Motile	0.44
2	C-Surface omnivore-deposit: Motile	0.41	2 O-Surface carnivore-omnivore: Motile	0.37
3	P-Surface carnivore-omnivore: Discrete	0.38	3 C-Surface deposit-detrital: Motile	0.33
4	P-Subsurface carnivore-deposit: Motile	0.35	4 P-Surface carnivore-omnivore: Discrete	0.32
5	M-Surface carnivore-omnivore: Motile	0.33	5 P-Subsurface carnivore-omnivore: Motile	0.31
6	C-Surface deposit-detrital: Motile	0.30	6 M-Surface carnivore-omnivore: Motile	0.30
7	C-Surface, suspension-deposit: Discrete	0.29	7 PPAR-Subsurface deposit feeder: Motile	0.30
8	PCAP-Subsurface deposit feeder: Motile	0.28	8 C-Surface, suspension-deposit: Discrete	0.27
9	C-Surface carnivore-omnivore: Discrete	0.28	9 P-Surface carnivore-omnivore: Motile	0.21
10	P-Surface, suspension-deposit: Discrete	0.26	10 P-Surface, suspension-deposit: Discrete	0.20
11	P-Surface carnivore-omnivore: Motile	0.25	11 P-Surface deposit-detrital: Discrete	0.20
12	C-Surface, suspension-deposit: Discrete	0.23	12 O-Surface omnivore-deposits: Discrete	0.19
13	PPAR-Subsurface deposit feeder: Motile	0.22	13 M-Surface, suspension-deposit: Discrete	0.19
14	O-Surface carnivore-omnivore: Discrete	0.19	14 PCAP-Subsurface deposit feeder: Motile	0.18
15	C-Surface, suspension-deposit: Motile	0.16	15 C-Surface, suspension-deposit: Motile	0.18
16	M-Suspension feeder: Sessile	0.15	16 E-Surface omnivore-deposits: Discrete	0.17
17	O-Suspension feeder: Sessile	0.13	17 P-Suspension feeder: Motile	0.17
18	P-Surface deposit-detrital: Discrete	0.13	18 M-Surface carnivore-omnivore: Discrete	0.16
19	E-Surface omnivore-deposit: Discrete	0.12	19 C-Surface carnivore-omnivore: Discrete	0.14
20	M-Surface deposit-detrital: Discrete	0.12	20 O-Surface carnivore-omnivore: Discrete	0.14
21	E-Multi-feeding strategy: Discrete	0.10	21 E-Multi-feeding strategy: Discrete	0.13
22	P-Suspension feeder: Motile	0.09	22 C-Surface, suspension-deposit: Sessile	0.11
23	C-Surface omnivore-deposit: Discrete	0.08	23 M-Suspension feeder: Discrete	0.11
24	M-Surface carnivore-omnivore: Discrete	0.07	24 M-Suspension feeder: Sessile	0.10
25	G-Surface, suspension-deposit: Sessile	0.07	25 P-Surface deposit-detrital: Sessile	0.10
26	C-Surface deposit-detrital: Discrete	0.06	26 M-Surface deposit-detrital: Discrete	0.09
27	M-Suspension feeder: Discrete	0.06	27 C-Surface deposit-detrital: Discrete	0.09
28	P-Suspension feeder: Sessile	0.04	28 O-Subsurface deposit feeder: Discrete	0.08
29	O-Surface deposit-detrital: Sessile	0.04	29 P-Surface, suspension-deposit: Sessile	0.08
30	G-Surface carnivore-omnivore: Motile	0.03	30 C-Surface carnivore-omnivore: Motile	0.08
31	E-Subsurface deposit feeder: Motile	0.03	31 C-Surface omnivore-deposits: Discrete	0.04
32	O-Subsurface deposit feeder: Discrete	0.03	32 P-Suspension feeder: Sessile	0.03
33	P-Surface, suspension-deposit: Sessile	0.03	33 M-Subsurface deposit feeder: Discrete	0.03
34	M-Surface omnivore-deposit: Motile	0.02	34 P-Subsurface deposit feeder: Sessile	0.03
35	P-Surface deposit-detrital: Motile	0.02	35 E-Surface deposit-detrital: Motile	0.03
36	P-Surface deposit-detrital: Sessile	0.02	36 E-Subsurface deposit feeder: Motile	0.03
37	O-Surface carnivore-omnivore: Sessile	0.02	37 O-Surface deposit-detrital: Sessile	0.03
38	P-Subsurface deposit feeder: Sessile	0.01	38 P-Surface deposit-detrital: Motile	0.03
39	C-Suspension feeder: Discrete	0.01	39 O-Surface, suspension-deposit: Motile	0.03
40	M-Subsurface deposit feeder: Discrete	0.01	40 M-Surface omnivore-deposits: Motile	0.02
41	M-Surface deposit-detrital: Motile	0.01	41 M-Surface deposit-detrital: Motile	0.02
42	O-Surface suspension-deposit: Motile	0.00	42 O-Surface suspension-deposit: Discrete	0.02
43	C-Suspension feeder: Sessile	0.00	43 C-Suspension feeder: Sessile	0.01
44	C-Suspension feeder: Motile	0.00	44 C-Suspension feeder: Motile	0.01
45	E-Surface carnivore-omnivore: Motile	0.00	45 E-Surface carnivore-omnivore: Sessile	0.01
46	E-Surface deposit-detrital: Motile	0.00	46 O-Surface carnivore-omnivore: Sessile	0.01
47	O-Surface, suspension-deposit: Discrete	0.00	47 C-Suspension feeder: Discrete	0.00

Table C.2-6, (cont.)

GROUP NO.	3	OBS SPECIES	_3
1	C-Surface omnivore-deposit:	Motile	0.42
2	O-Surface carnivore-omnivore:	Motile	0.37
3	P-Surface carnivore-omnivore:	Discrete	0.35
4	P-Subsurface carnivore-deposit:	Motile	0.33
5	M-Surface carnivore-omnivore:	Motile	0.32
6	PPAR-Subsurface deposit feeder:	Motile	0.30
7	C-Surface, suspension-deposit:	Discrete	0.26
8	G-Surface deposit-detrital:	Motile	0.23
9	P-Surface carnivore-omnivore:	Motile	0.23
10	M-Surface, suspension-deposit:	Discrete	0.20
11	M-Surface carnivore-omnivore:	Discrete	0.19
12	C-Surface, suspension-deposit:	Motile	0.19
13	O-Suspension feeder:	Sessile	0.18
14	O-Surface carnivore-omnivore:	Discrete	0.17
15	P-Surface, suspension-deposit:	Discrete	0.17
16	PCAP-Subsurface deposit feeder:	Motile	0.16
17	E-Surface omnivore-deposit:	Discrete	0.16
18	G-Surface carnivore-omnivore:	Discrete	0.15
19	P-Surface deposit-detrital:	Sessile	0.14
20	M-Suspension feeder:	Sessile	0.12
21	P-Surface deposit-detrital:	Discrete	0.12
22	C-Surface deposit-deposit:	Discrete	0.11
23	M-Surface deposit-detrital:	Discrete	0.10
24	P-Surface deposit-detrital:	Motile	0.10
25	G-Surface suspension-deposit:	Sessile	0.10
26	P-Suspension feeder:	Motile	0.09
27	P-Surface, suspension-deposit:	Sessile	0.09
28	E-Multi-feeding strategy:	Discrete	0.08
29	M-Suspension feeder:	Discrete	0.08
30	O-Subsurface deposit feeder:	Discrete	0.07
31	E-Subsurface deposit feeder:	Motile	0.06
32	C-Surface carnivore-omnivore:	Motile	0.05
33	P-Suspension feeder:	Sessile	0.05
34	O-Surface deposit-detrital:	Sessile	0.05
35	C-Surface deposit-detrital:	Discrete	0.04
36	M-Surface omnivore-deposit:	Motile	0.03
37	O-Surface, suspension-deposit:	Motile	0.02
38	M-Surface deposit-detrital:	Motile	0.01
39	P-Subsurface deposit feeder:	Sessile	0.01
40	E-Surface deposit-detrital:	Motile	0.01
41	C-Suspension feeder:	Discrete	0.00
42	C-Suspension feeder:	Motile	0.00
43	C-Suspension feeder:	Sessile	0.00
44	E-Surface carnivore-omnivore:	Motile	0.00
45	M-Subsurface deposit feeder:	Discrete	0.00
46	O-Surface carnivore-omnivore:	Sessile	0.00
47	O-Surface, suspension-deposit:	Discrete	0.00

Table C.2-7. The 50 highest ranked species in the station groups formed by the cluster analysis of the 18 meter data. The values to the right are the standardized relative abundances (see Section 2.4.8).

GROUP NO. 1	OBS SPECIES	GROUP NO. 2	OBS SPECIES
1 <i>Synchelidium shoemakeri</i>	0.58	1 <i>Prionospio pygmaea</i>	0.49
2 <i>Aricidea wassi</i>	0.50	2 <i>Nephtys cornuta franciscana</i>	0.48
3 <i>Acuminodeutopus heteroropus</i>	0.48	3 <i>Euphilomedes carcharodonta</i>	0.46
4 <i>Rhepoxygnius stenodes</i>	0.47	4 <i>Glycinde armigera</i>	0.45
5 <i>Rhepoxygnius menziesi</i>	0.46	5 <i>Mediomastus californiensis/ambiseta</i>	0.44
6 <i>Acesta catherinae</i>	0.46	6 <i>Acesta catherinae</i>	0.40
7 <i>Nebalia pugettensis</i>	0.44	7 <i>Cossura cf. candida</i>	0.39
8 <i>Nephtys cornuta franciscana</i>	0.41	8 <i>Parapriionospio pinnata</i>	0.38
9 <i>Cirrophorus furcatus</i>	0.40	9 <i>Acuminodeutopus heteroropus</i>	0.37
10 <i>Ampelisca brevisimilata</i>	0.39	10 <i>Ampelisca brevisimilata</i>	0.37
11 <i>Ampelisca cristata microdentata</i>	0.39	11 <i>Chone vereronis</i>	0.36
12 <i>Tellina modesta</i>	0.39	12 <i>Aricidea wassi</i>	0.36
13 <i>Euphilomedes carcharodonta</i>	0.38	13 <i>Rhepoxygnius menziesi</i>	0.35
14 <i>Priionospio pygmaea</i>	0.36	14 <i>Spiophanes missionensis</i>	0.35
15 <i>Cossura cf. candida</i>	0.36	15 <i>Paramenterites sp. A</i>	0.35
16 <i>Parapriionospio pinnata</i>	0.35	16 <i>Synchelidium shoemakeri</i>	0.34
17 <i>Paramenterites sp. A</i>	0.33	17 <i>Cirrophorus furcatus</i>	0.34
18 <i>Pachynus barnardi</i>	0.33	18 <i>Euchone hancocki</i>	0.33
19 <i>Cume la sp. A SCAMIT</i>	0.33	19 <i>Tellina modesta</i>	0.32
20 <i>Sulcoretusa xystrum</i>	0.32	20 <i>Rhepoxygnius stenodes</i>	0.31
21 <i>Leptocheilia dubia</i>	0.32	21 <i>Tauberia gracilis</i>	0.29
22 <i>Rutiderma rostrata</i>	0.32	22 <i>Hemilamprops californica</i>	0.29
23 <i>Thalenessa spinosa</i>	0.32	23 <i>Diastylops tenuis</i>	0.29
24 <i>Tauberia gracilis</i>	0.30	24 <i>Goniada littorea</i>	0.28
25 <i>Oxyurostyliis pacifica</i>	0.29	25 <i>Argissa hamatipes</i>	0.28
26 <i>Spiophanes missionensis</i>	0.28	26 <i>Rhepoxygnius abronius</i>	0.28
27 <i>Mediomastus californiensis/ambiseta</i>	0.28	27 <i>Podaecopsis brevipalpa</i>	0.27
28 <i>Goniada littorea</i>	0.27	28 <i>Monoculodes hartmanae</i>	0.27
29 <i>Harmothoe cf. lunulata</i>	0.27	29 <i>Ampelisca cristata microdentata</i>	0.27
30 <i>Foxiphilus golensis/obtusidens</i>	0.27	30 <i>Ampelisca cristata</i>	0.26
31 <i>Tharyx sp.</i>	0.27	31 <i>Chaetozone setosa</i>	0.26
32 <i>Pista disjuncta</i>	0.26	32 <i>Tharyx sp.</i>	0.26
33 <i>Monoculodes hartmanae</i>	0.26	33 <i>Heimichordate unidentified</i>	0.25
34 <i>Rhepoxygnius sp. juvenile</i>	0.26	34 <i>Gloottidia albida</i>	0.24
35 <i>Chaetozone setosa</i>	0.25	35 <i>Pachynus barnardi</i>	0.24
36 <i>Olivella baetica</i>	0.25	36 <i>Parasterope huilingi</i>	0.24
37 <i>Campylaspis rubromaculata</i>	0.24	37 <i>Mageiora sacculata</i>	0.24
38 <i>Glycinde armigera</i>	0.24	38 <i>Lumbrineris sp.</i>	0.24
39 <i>Nephtys caecoides</i>	0.23	39 <i>Nebalia pugettensis</i>	0.24
40 <i>Rhepoxygnius daboiius</i>	0.23	40 <i>Phylodoce (Aponaitides) hartmanae</i>	0.23
41 <i>Munnogonium tiliare</i>	0.23	41 <i>Tubulariidae sp. B</i>	0.23
42 <i>Parilucina tenuisculpta</i>	0.22	42 <i>Munnogonium tiliare</i>	0.22
43 <i>Phylodoce (Aponaitides) papillosa</i>	0.22	43 <i>Olivella baetica</i>	0.22
44 <i>Podakeopsis brevipalpa</i>	0.21	44 <i>Nassarius perpinquis</i>	0.22
45 <i>Ophiuroidea juvenile</i>	0.21	45 <i>Sulcoretusa xystrum</i>	0.22
46 <i>Lumbrineris sp.</i>	0.21	46 <i>Phoronis spp.</i>	0.22
47 <i>Harmothoe priops</i>	0.21	47 <i>Thalienna spinosa</i>	0.21
48 <i>Phoronis spp.</i>	0.20	48 <i>Meliphisana bolla</i>	0.21
49 <i>Phylodoce (Aponaitides) hartmanae</i>	0.20	49 <i>Lumbrineris sp. D</i>	0.20
50 <i>Edwardsia sp. A (orange w/ white base)</i>	0.20	50 <i>Ophiuroidea juvenile</i>	0.20

Table C.2-7. (cont.)

GROUP NO. 3	OBS SPECIES	GROUP NO. 4	OBS SPECIES
-3		-4	
1 <i>Tellina modesta</i>	0.46	1 <i>Nephtys</i> sp.	0.57
2 <i>Parapriionopis pinnata</i>	0.42	2 <i>Ampelisca cristata</i>	0.51
3 <i>Syncheliidium shoemakeri</i>	0.40	3 <i>Mediomastus californiensis/ambiseta</i>	0.51
4 <i>Oxyurostylis pacifica</i>	0.35	4 <i>Acuminodeutopus hetereuropus</i>	0.47
5 <i>Acesta catherinae</i>	0.35	5 <i>Aricidea wassi</i>	0.46
6 <i>Euphilomedes carcharodontae</i>	0.35	6 <i>Rutiderma rostrata</i>	0.45
7 <i>Rutiderma rostrata</i>	0.34	7 <i>Tharyx</i> sp.	0.44
8 <i>Sulcoretusa xystrum</i>	0.32	8 <i>Hemicladoredate unidentified</i>	0.44
9 <i>Rhepoxynius menziesi</i>	0.31	9 <i>Tellina modesta</i>	0.44
10 <i>Mediomastus californiensis/ambiseta</i>	0.29	10 <i>Tubulanidae</i> sp. B	0.40
11 <i>Tauberia gracilis</i>	0.29	11 <i>Prionospio pygmaea</i>	0.39
12 <i>Jassa falicata</i>	0.29	12 <i>Parapriionopis pinnata</i>	0.39
13 <i>Leitoscoloplos elongatus</i>	0.26	13 <i>Rhepoxynius menziesi</i>	0.39
14 <i>Rhepoxynius stenodes</i>	0.26	14 <i>Euphilomedes carcharodontae</i>	0.39
15 <i>Tharyx</i> sp.	0.26	15 <i>Tauberia gracilis</i>	0.38
16 <i>Nephtys cornuta franciscana</i>	0.26	16 <i>Typosyllis hyalina</i>	0.38
17 <i>Monoculodes hartmanna</i>	0.25	17 <i>Synchelidium shoemakeri</i>	0.37
18 <i>Acuminodeutopus hetereuropus</i>	0.25	18 <i>Anottomastus gordiodes</i>	0.35
19 <i>Aricidea wassi</i>	0.25	19 <i>Ampelisca brevisimulata</i>	0.34
20 <i>Glottidia albida</i>	0.25	20 <i>Chaetozone setosa</i>	0.33
21 <i>Ampelisca cristata</i>	0.25	21 <i>Paranemertes</i> sp. A	0.33
22 <i>Ampelisca brevisimulata</i>	0.24	22 <i>Sulcoretusa xystrum</i>	0.33
23 <i>Macoma</i> sp.	0.24	23 <i>Nereis provera</i>	0.33
24 <i>Lumbrineris</i> sp.	0.23	24 <i>Harmothoe priops</i>	0.32
25 <i>Onuphis iridescentis</i>	0.23	25 <i>Aestea catherinae</i>	0.31
26 <i>Rhepoxynius</i> sp. juvenile	0.22	26 <i>Rhepoxynius</i> sp. juvenile	0.31
27 <i>Nebatia pugettensis</i>	0.22	27 <i>Glycinde armigera</i>	0.30
28 <i>Prionospio pygmaea</i>	0.21	28 <i>Podakeopsis brevipalpa</i>	0.29
29 <i>Chaetozone setosa</i>	0.21	29 <i>Amphideutopus oculatus</i>	0.29
30 <i>Sphaerodrotopsis biserialis</i>	0.21	30 <i>Leptocheilia dubia</i>	0.28
31 <i>Tubulanidae</i> sp. B	0.20	31 <i>Goniada littorea</i>	0.28
32 <i>Typosyllis hyalina</i>	0.20	32 <i>Olivella baetica</i>	0.27
33 <i>Paranemertes</i> sp. A	0.20	33 <i>Spiophanes missionensis</i>	0.26
34 <i>Spiophanes missionensis</i>	0.20	34 <i>Prionospio cirrifera</i>	0.26
35 <i>Argissa hamatipes</i>	0.19	35 <i>Parilucina tenuisculpta</i>	0.25
36 <i>Goniada littorea</i>	0.19	36 <i>Lumbrineris</i> sp.	0.25
37 <i>Cirrophorus furcatus</i>	0.19	37 <i>Cumella</i> sp. A SCAMIT	0.24
38 <i>Cumella</i> sp. A SCAMIT	0.19	38 <i>Cirrophorus furcatus</i>	0.23
39 <i>Driloneurus falcata</i>	0.19	39 <i>Rhepoxynius dabolus</i>	0.22
40 <i>Cossura cf. candida</i>	0.18	40 <i>Edwardsia</i> sp. B (white w/white base)	0.21
41 <i>Munna ubiquita</i>	0.18	41 <i>Lumbrineris</i> sp. D	0.21
42 <i>Rudilimboides stenopropodus</i>	0.18	42 <i>Nuculana taphira</i>	0.21
43 <i>Nuculana taphira</i>	0.18	43 <i>Rhepoxynius variatus</i>	0.21
44 <i>Ophiuroidea juvenile</i>	0.17	44 <i>Leitoscoloplos elongatus</i>	0.20
45 <i>Nephtys caecoides</i>	0.17	45 <i>Munnogonium tillerae</i>	0.20
46 <i>Rhepoxynius variatus</i>	0.17	46 <i>Ruditemboides stenopropodus</i>	0.19
47 <i>Solen sicarius</i>	0.17	47 <i>Spiochaetopterus costarum</i>	0.19
48 <i>Hemimoprops californica</i>	0.17	48 <i>Oxyurostylum pacifica</i>	0.19
49 <i>Diasyloopsis tenuis</i>	0.17	49 <i>Eteone</i> sp.	0.19
50 <i>Goniada maculata</i>	0.17	50 <i>Goniada maculata</i>	0.19

Table C.2-7. (cont.)

GROUP NO. 5	OBS SPECIES	-5-
1	Hemichordate unidentified	0.46
2	<i>Typosyllis hyalina</i>	0.44
3	<i>Prionospio pygmaea</i>	0.43
4	<i>Nephtys</i> sp.	0.42
5	<i>Rutiderma rostrata</i>	0.41
6	<i>Hemilamprus californica</i>	0.41
7	<i>Rhepoxy尼us menziesi</i>	0.37
8	<i>Aricidea wassi</i>	0.35
9	<i>Mediomastus californiensis/ambisseta</i>	0.35
10	<i>Coniada littorea</i>	0.34
11	<i>Tubulanus nothus</i> (black)	0.32
12	<i>Parapriionospio pinnata</i>	0.32
13	<i>Lumbrineris</i> sp.	0.31
14	<i>Tauberia gracilis</i>	0.31
15	<i>Edwardsia</i> sp. A (orange w/ white base)	0.30
16	<i>Rhepoxy尼us</i> sp. juv.	0.30
17	<i>Parameristes</i> sp. A	0.30
18	<i>Anoplissa cristata</i>	0.29
19	<i>Euphilomedes carcharodonta</i>	0.28
20	<i>Harmothoe priops</i>	0.27
21	<i>Tetilla modesta</i>	0.27
22	<i>Macoma yoldiformis</i>	0.26
23	<i>Anotomastus gordioides</i>	0.25
24	<i>Synchelidium shoemakeri</i>	0.25
25	<i>Cooperella subdiphyhana</i>	0.24
26	<i>Onuphis iridescentis</i>	0.24
27	<i>Lumbrineris</i> sp. D	0.24
28	<i>Owenia collaris</i>	0.23
29	<i>Rhepoxy尼us daboious</i>	0.23
30	<i>Rhepoxy尼us variatus</i>	0.22
31	<i>Acesta catherinae</i>	0.21
32	<i>Nereis provera</i>	0.21
33	<i>Thalenessa spinosa</i>	0.21
34	<i>Tharyx</i> sp.	0.20
35	<i>Mysella tumida</i>	0.20
36	<i>Rhepoxy尼us stenodes</i>	0.20
37	<i>Phylodoce (Aponaitides) hartmanna</i>	0.18
38	<i>Eteone</i> sp.	0.18
39	<i>Cumella</i> sp. A SCAMIT	0.18
40	<i>Zygepolia</i> sp.	0.18
41	<i>Driloneurus falcata</i>	0.17
42	<i>Glycinde armigera</i>	0.17
43	<i>Macoma</i> sp.	0.17
44	<i>Glycera convoluta</i>	0.17
45	<i>Sulcoretusa xystrum</i>	0.17
46	<i>Ancistrosyllis hamata</i>	0.17
47	<i>Olivella baetica</i>	0.17
48	<i>Meliphisana bola</i>	0.16
49	<i>Tubulanidae</i> sp. B	0.16
50	<i>Glottidia albida</i>	0.16

Table C.2-8. The trophic-motility groups in the station groups formed by cluster analysis of the 18 meter data. The letters to the left of the columns indicate the taxonomic subset; C=crustacea, P=mollusc, E=echinoderm, O=other, PCAP=capitellid polychaete, PPAP=paragonid polychaete. The values to the right are the standardized relative abundances (see Section 2.4.8).

GROUP NO. 1	OBS SPECIES	-1	GROUP NO. 2	OBS SPECIES	-2	
1	C-Surface omnivore-deposit:	Motile	1	C-Surface omnivore-deposit:	Motile	
2	P-Subsurface carnivore-deposit:	Motile	0.61	2	M-Surface carnivore-omnivore:	Motile
3	P-Surface carnivore-omnivore:	Motile	0.57	3	PPAR-Subsurface deposit-feeder:	Motile
4	C-Surface suspension-deposit:	Discrete	0.56	4	C-Surface, suspension-deposit:	Motile
5	M-Surface, suspension-deposit:	Discrete	0.55	5	O-Surface carnivore-omnivore:	Discrete
6	M-Surface carnivore-omnivore:	Motile	0.51	6	P-Surface carnivore-omnivore:	Motile
7	PCAP-Subsurface deposit feeder:	Motile	0.50	7	C-Surface, suspension-deposit:	Sessile
8	P-Surface carnivore-omnivore:	Discrete	0.50	8	M-Surface, suspension-deposit:	Discrete
9	O-Surface carnivore-omnivore:	Discrete	0.48	9	P-Subsurface deposit feeder:	Sessile
10	PPAR-Subsurface deposit feeder:	Motile	0.47	10	C-Surface deposit-detrital:	Motile
11	P-Surface deposit-detrital:	Motile	0.43	11	M-Surface carnivore-omnivore:	Discrete
12	O-Subsurface deposit feeder:	Discrete	0.42	12	M-Suspension feeder:	Sessile
13	C-Surface, suspension-deposit:	Sessile	0.41	13	P-Surface deposit-detrital:	Discrete
14	E-Multi-feeding strategy:	Discrete	0.39	14	O-Suspension feeder:	Sessile
15	H-Suspension feeder:	Sessile	0.39	15	P-Surface deposit-detrital:	Sessile
16	P-Surface deposit-detrital:	Discrete	0.38	16	C-Surface omnivore-deposit:	Discrete
17	O-Surface carnivore-omnivore:	Motile	0.38	17	P-Subsurface carnivore-deposit:	Motile
18	C-Surface omnivore-deposit:	Discrete	0.35	18	O-Surface carnivore-omnivore:	Discrete
19	C-Surface deposit-detrital:	Discrete	0.31	19	PCAP-Subsurface deposit feeder:	Motile
20	C-Surface deposit-detrital:	Motile	0.30	20	P-Surface, suspension-deposit:	Discrete
21	P-Surface, suspension-deposit:	Discrete	0.29	21	P-Suspension feeder:	Motile
22	M-Surface carnivore-omnivore:	Discrete	0.29	22	P-Surface deposit-detrital:	Motile
23	P-Subsurface deposit-feeder:	Sessile	0.26	23	P-Surface carnivore-omnivore:	Discrete
24	P-Surface, suspension-deposit:	Sessile	0.26	24	M-Surface deposit-detrital:	Discrete
25	P-Suspension feeder:	Motile	0.25	25	C-Surface, suspension-deposit:	Motile
26	O-Suspension feeder:	Sessile	0.22	26	C-Surface deposit-detrital:	Discrete
27	M-Surface deposit-detrital:	Discrete	0.21	27	P-Suspension feeder:	Sessile
28	C-Surface, suspension-deposit:	Motile	0.18	28	C-Surface carnivore-omnivore:	Discrete
29	M-Suspension feeder:	Discrete	0.17	29	O-Subsurface deposit feeder:	Discrete
30	P-Suspension feeder:	Sessile	0.15	30	M-Suspension feeder:	Discrete
31	M-Subsurface deposit-feeder:	Discrete	0.14	31	E-Multi-feeding strategy:	Discrete
32	C-Surface carnivore-omnivore:	Discrete	0.12	32	E-Surface deposit-detrital:	Motile
33	P-Surface deposit-detrital:	Sessile	0.12	33	P-Surface, suspension-deposit:	Sessile
34	O-Subsurface deposit-detrital:	Sessile	0.08	34	M-Surface deposit-detrital:	Motile
35	E-Surface carnivore-omnivore:	Motile	0.07	35	E-Surface carnivore-omnivore:	Motile
36	O-Surface carnivore-omnivore:	Sessile	0.07	36	O-Surface deposit-detrital:	Sessile
37	M-Surface deposit-detrital:	Motile	0.07	37	P-Suspension feeder:	Discrete
38	E-Surface deposit-detrital:	Sessile	0.04	38	M-Subsurface deposit feeder:	Discrete
39	P-Suspension feeder:	Discrete	0.04	39	C-Surface carnivore-omnivore:	Motile
40	E-Subsurface deposit-feeder:	Motile	0.02	40	E-Surface omnivore-deposit:	Motile
41	O-Surface, suspension-deposit:	Motile	0.02	41	M-Surface omnivore-deposit:	Motile
42	G-Surface carnivore-omnivore:	Motile	0.02	42	O-Surface carnivore-omnivore:	Sessile
43	C-Suspension feeder:	Discrete	0.00	43	C-Suspension feeder:	Discrete
44	G-Suspension feeder:	Motile	0.00	44	C-Suspension feeder:	Motile
45	E-Surface deposit-detrital:	Motile	0.00	45	E-Subsurface deposit-feeder:	Motile
46	E-Surface omnivore-deposit:	Motile	0.00	46	E-Surface deposit-detrital:	Sessile
47	M-Surface omnivore-deposit:	Motile	0.00	47	O-Surface suspension-deposit:	Discrete
48	O-Surface, suspension-deposit:	Discrete	0.00	48	O-Surface, suspension-deposit:	Motile

Table C.2-8. (cont.)

GROUP NO. 3	OBS SPECIES	-3	OBS SPECIES	-4
GROUP NO. 4	OBS SPECIES			
1 C-Surface omnivore-deposit: Motile	0.55	1 C-Surface omnivore-deposit: Motile	0.63	
2 PPAR-Subsurface deposit feeder: Motile	0.54	2 C-Surface deposit-detrital: Motile	0.47	
3 P-Surface carnivore-omnivore: Motile	0.51	3 M-Surface, suspension-deposit: Discrete	0.41	
4 P-Surface deposit-detrital: Discrete	0.50	4 M-Surface carnivore-omnivore: Motile	0.39	
5 P-Subsurface carnivore-deposit: Motile	0.46	5 N-Surface carnivore-omnivore: Motile	0.37	
6 O-Surface carnivore-omnivore: Motile	0.46	6 P-Surface carnivore-omnivore: Motile	0.37	
7 P-Surface, suspension-deposit: Discrete	0.46	7 O-Surface carnivore-omnivore: Discrete	0.36	
8 PCAP-Subsurface deposit feeder: Motile	0.45	8 PPAR-Subsurface deposit feeder: Motile	0.36	
9 O-Surface carnivore-omnivore: Discrete	0.44	9 C-Surface, suspension-deposit: Discrete	0.32	
10 C-Surface deposit-detrital: Motile	0.43	10 C-Surface, suspension-deposit: Sessile	0.29	
11 P-Surface carnivore-omnivore: Discrete	0.41	11 O-Suspension feeder: Sessile	0.28	
12 M-Surface carnivore-omnivore: Motile	0.40	12 P-Surface deposit-detrital: Discrete	0.28	
13 P-Subsurface deposit feeder: Sessile	0.39	13 P-Surface carnivore-omnivore: Discrete	0.28	
14 C-Surface, suspension-deposit: Sessile	0.37	14 P-Subsurface carnivore-deposit: Motile	0.27	
15 P-Suspension feeder: Motile	0.36	15 P-Surface deposit-detrital: Sessile	0.26	
16 M-Surface, suspension-deposit: Discrete	0.35	16 P-Surface, suspension-deposit: Discrete	0.26	
17 O-Suspension feeder: Sessile	0.34	17 PCAP-Subsurface deposit feeder: Motile	0.25	
18 C-Surface, suspension-deposit: Discrete	0.31	18 M-Suspension feeder: Sessile	0.25	
19 P-Surface deposit-detrital: Motile	0.29	19 O-Subsurface deposit feeder: Discrete	0.21	
20 M-Surface carnivore-omnivore: Discrete	0.26	20 P-Surface deposit-detrital: Motile	0.19	
21 C-Surface, suspension-deposit: Motile	0.26	21 P-Subsurface deposit feeder: Sessile	0.17	
22 P-Suspension feeder: Sessile	0.25	22 C-Surface, suspension-deposit: Motile	0.16	
23 O-Subsurface deposit feeder: Discrete	0.24	23 P-Suspension feeder: Motile	0.16	
24 M-Suspension feeder: Sessile	0.19	24 C-Surface omnivore-deposit: Discrete	0.15	
25 P-Surface deposit-detrital: Sessile	0.17	25 P-Suspension feeder: Sessile	0.12	
26 E-Multi-feeding strategy: Discrete	0.13	26 M-Suspension feeder: Discrete	0.11	
27 C-Surface omnivore-deposit: Discrete	0.12	27 M-Surface carnivore-omnivore: Discrete	0.07	
28 M-Surface deposit-detrital: Discrete	0.11	28 E-Surface deposit-detrital: Motile	0.06	
29 M-Suspension feeder: Discrete	0.07	29 E-Surface carnivore-omnivore: Motile	0.05	
30 P-Surface, suspension-deposit: Sessile	0.07	30 E-Multi-feeding strategy: Discrete	0.05	
31 O-Surface carnivore-omnivore: Sessile	0.07	31 O-Surface deposit-detrital: Sessile	0.05	
32 O-surface deposit-detrital: Sessile	0.06	32 P-Surface, suspension-deposit: Sessile	0.04	
33 C-Surface carnivore-omnivore: Discrete	0.05	33 M-Surface deposit-detrital: Discrete	0.04	
34 E-Surface carnivore-omnivore: Motile	0.04	34 C-Suspension feeder: Discrete	0.03	
35 M-Subsurface deposit feeder: Discrete	0.03	35 E-Subsurface deposit feeder: Motile	0.03	
36 C-Surface deposit-detrital: Discrete	0.03	36 O-Surface carnivore-omnivore: Sessile	0.03	
37 E-Subsurface deposit feeder: Motile	0.03	37 M-Subsurface deposit feeder: Discrete	0.02	
38 C-Surface carnivore-omnivore: Motile	0.02	38 C-Surface deposit-detrital: Discrete	0.02	
39 E-Surface deposit-detrital: Motile	0.02	39 C-Surface carnivore-omnivore: Discrete	0.02	
40 E-Surface omnivore-deposit: Motile	0.02	40 C-Surface carnivore-omnivore: Motile	0.01	
41 C-Suspension feeder: Motile	0.01	41 M-Surface deposit-detrital: Motile	0.01	
42 O-Surface, suspension-deposit: Discrete	0.01	42 C-Suspension feeder: Motile	0.00	
43 P-Suspension feeder: Discrete	0.01	43 E-Surface deposit-detrital: Sessile	0.00	
44 O-Surface, suspension-deposit: Motile	0.01	44 E-Surface omnivore-deposit: Motile	0.00	
45 M-Surface deposit-detrital: Motile	0.00	45 M-Surface omnivore-deposit: Motile	0.00	
46 C-Suspension feeder: Discrete	0.00	46 O-Surface, suspension-deposit: Discrete	0.00	
47 E-Surface deposit-detrital: Sessile	0.00	47 O-Surface, suspension-deposit: Motile	0.00	
48 M-Surface omnivore-deposit	0.00	48 P-Suspension feeder: Discrete	0.00	

Table C.2-8. (cont.)

GROUP NO. 5	OBS SPECIES	GROUP NO. 6	OBS SPECIES
5	1 C-Surface omnivore-deposit: Motile 2 P-Surface carnivore-omnivore: Motile 3 P-Subsurface deposit feeder: Motile 4 O-Subsurface deposit feeder: Discrete 5 O-Surface carnivore-omnivore: Discrete 6 PPAR-Subsurface deposit feeder: Motile 7 M-Surface, suspension-deposit: Discrete 8 PCAP-Subsurface deposit feeder: Motile 9 O-Surface carnivore-omnivore: Motile 10 M-Suspension feeder: Sessile 11 P-Surface carnivore-omnivore: Discrete 12 M-Surface carnivore-omnivore: Motile 13 P-Surface, suspension-deposit: Discrete 14 C-Surface deposit-detrital: Motile 15 P-Surface deposit-detrital: Discrete 16 M-Surface carnivore-omnivore: Discrete 17 C-Surface, suspension-deposit: Sessile 18 O-Suspension feeder: Sessile 19 P-Suspension feeder: Motile 20 P-Surface deposit-detrital: Motile 21 C-Surface, suspension-deposit: Discrete 22 M-Surface deposit-detrital: Discrete 23 P-Surface deposit-detrital: Sessile 24 M-Subsurface deposit feeder: Discrete 25 M-Suspension feeder: Discrete 26 P-Subsurface deposit feeder: Sessile 27 E-Multi-feeding strategy: Discrete 28 C-Surface carnivore-omnivore: Discrete 29 C-Surface, suspension-deposit: Motile 30 P-Suspension feeder: Sessile 31 C-Surface omnivore-deposit: Discrete 32 P-Surface, suspension-deposit: Sessile 33 O-Surface deposit-detrital: Sessile 34 O-Surface carnivore-omnivore: Sessile 35 P-Suspension feeder: Discrete 36 C-Surface deposit-detrital: Discrete 37 E-Surface deposit-detrital: Motile 38 C-Surface carnivore-omnivore: Motile 39 M-Surface deposit-detrital: Motile 40 E-Surface deposit-detrital: Sessile 41 M-Surface omnivore-deposit: Motile 42 C-Suspension feeder: Discrete 43 C-Suspension feeder: Motile 44 E-Subsurface deposit feeder: Motile 45 E-Surface deposit-detrital: Motile 46 E-Surface omnivore-deposit: Motile 47 O-Surface, suspension-deposit: Discrete 48 O-Surface, suspension-deposit: Motile	5	1 C-Surface omnivore-deposit: Motile 2 C-Surface deposit-detrital: Motile 3 P-Surface Subsurface deposit: Discrete 4 PPAR-Subsurface deposit feeder: Motile 5 O-Suspension feeder: Sessile 6 P-Surface, suspension-deposit: Discrete 7 P-Suspension feeder: Sessile 8 C-Surface, suspension-deposit: Sessile 9 O-Surface carnivore-omnivore: Motile 10 P-Surface carnivore-omnivore: Discrete 11 C-Surface carnivore-omnivore: Motile 12 P-Surface carnivore-omnivore: Motile 13 M-Surface, suspension-deposit: Discrete 14 PCAP-Subsurface deposit feeder: Motile 15 P-Subsurface carnivore-deposit: Motile 16 C-Surface carnivore-omnivore: Discrete 17 P-Suspension feeder: Motile 18 C-Surface, suspension-deposit: Discrete 19 O-Surface carnivore-omnivore: Discrete 20 M-Surface carnivore-omnivore: Motile 21 P-Surface deposit-detrital: Motile 22 O-Subsurface deposit feeder: Discrete 23 P-Subsurface deposit feeder: Sessile 24 M-Surface carnivore-omnivore: Discrete 25 E-Surface deposit-detrital: Motile 26 P-Surface deposit-detrital: Sessile 27 C-Surface omnivore-deposit: Discrete 28 C-Surface, suspension-deposit: Motile 29 M-Surface deposit-detrital: Discrete 30 M-Suspension feeder: Sessile 31 E-Multi-feeding strategy: Discrete 32 C-Surface deposit-detrital: Discrete 33 O-Surface suspension feeder: Discrete 34 C-Suspension feeder: Motile 35 E-Subsurface deposit feeder: Motile 36 E-Surface carnivore-omnivore: Motile 37 E-Surface deposit-detrital: Sessile 38 E-Surface omnivore-deposit: Motile 39 M-Subsurface deposit feeder: Discrete 40 M-Surface deposit-detrital: Motile 41 M-Surface omnivore-deposit: Motile 42 M-Suspension feeder: Discrete 43 O-Surface carnivore-omnivore: Sessile 44 O-Surface deposit-detrital: Sessile 45 O-Surface, suspension-deposit: Discrete 46 O-Surface, suspension-deposit: Motile 47 P-Surface, suspension-deposit: Sessile 48 P-Suspension feeder: Discrete

Table C.2-9. Percent of the total abundance contributed by the trophic-motility groups and their subsets at 8 meters.
 B = Before period, A = After period.

DEPTH	TMGROUP	PHYLUM			PHYLUM			PHYLUM			
		B	A	700	B	A	700	B	A	700	
8	Subsurface deposit feeder: Discrete	All		0	0	0	0	0	0	6700	
	Molluscs	0	0	0	0	0	0	0	0	B	
	Others	0	0	0	0	0	0	0	0	A	
8	Subsurface deposit feeder: Motile	All	21	14	22	17	18	18	27	31	22
	Echinoderms	0	0	0	0	0	0	0	0	15	
	capitellid polychaetes	19	5	20	9	16	11	25	6	0	
	paraonid polychaetes	2	5	1	3	1	5	1	4	19	
								4	7	4	
8	Subsurface deposit feeder: Sessile	All	0	0	0	0	0	0	0	0	
	Polychaetes	0	0	0	0	0	0	0	0	0	
8	Subsurface carnivore-deposit: Motile	All	1	2	1	2	2	2	2	3	
	Polychaetes	1	2	1	2	2	2	2	3	2	
8	Surface deposit feeder: Discrete	All	1	4	1	4	2	4	2	5	
	Crustaceans	0	2	0	2	1	1	0	0	1	
	Molluscs	0	0	0	0	0	1	1	0	0	
	Polychaetes	0	2	0	2	1	2	0	1	3	
8	Surface deposit feeder: Motile	All	12	22	12	21	10	22	13	17	16
	Crustaceans	12	22	12	21	10	22	13	17	17	15
	Echinoderms	0	0	0	0	0	0	0	0	0	14
	Molluscs	0	0	0	0	0	0	0	0	0	0
	Polychaetes	0	0	0	0	0	0	0	0	0	0
8	Surface deposit feeder: Sessile	All	0	0	0	0	0	0	0	0	4
	Others	0	0	0	0	0	0	0	0	0	0
	Polychaetes	0	0	0	0	0	0	0	0	0	4
8	Surface omnivore-deposit: Discrete	All	0	3	0	2	1	2	0	3	2
	Crustaceans	0	0	0	0	0	0	0	0	0	2
	Echinoderms	0	2	0	2	0	1	0	0	0	2
8	Surface omnivore-deposit: Motile	All	4	8	8	13	6	12	7	15	6
	Crustaceans	4	8	8	13	6	12	7	15	10	11
	Molluscs	0	0	0	0	0	0	0	0	0	0
8	Surface suspension-deposit: Discrete	All	49	25	46	24	52	20	34	18	21
	Crustaceans	1	3	1	3	1	1	2	2	4	1
	Molluscs	2	2	2	1	3	2	5	1	1	5
	Others	0	0	0	0	0	0	0	0	0	2
	Polychaetes	46	20	44	20	48	16	27	15	11	31
8	Surface suspension-deposit: Motile	All	1	1	1	2	1	1	0	4	1
	Crustaceans	1	1	1	2	1	1	0	4	1	2
	Others	0	0	0	0	0	0	0	0	0	0

Table C.2-9. (cont.)

DEPTH	TMGROUP	PHYLUM	700	1100	1900	3350	6700	9400
			B	A	B	A	B	A
8	Surface suspension-deposit:	Sessile	All					
			Crustaceans	1	4	1	0	1
			Polychaetes	1	3	3	6	0
				0	0	0	0	1
						0	0	0
8	Suspension feeder:	Discrete	All					
			Crustaceans	0	5	0	1	13
			Molluscs	0	0	0	0	0
				0	4	0	1	0
						3	0	0
						0	6	0
						0	6	13
8	Suspension feeder:	Motile	All					
			Crustaceans	0	0	0	0	0
			Polychaetes	0	0	0	0	0
				0	0	0	0	0
8	Suspension feeder:	Sessile	All					
			Crustaceans	1	2	1	1	3
			Molluscs	1	1	0	0	2
			Others	0	1	0	1	0
			Polychaetes	0	0	0	0	0
				0	0	0	0	0
8	Surface carnivore-omnivore:	Discrete	All					
			Crustaceans	4	3	3	3	4
			Molluscs	3	1	2	1	1
			Others	0	0	0	0	1
			Polychaetes	0	0	0	0	0
				1	1	1	1	0
						1	1	0
8	Surface carnivore-omnivore:	Motile	All					
			Crustaceans	4	6	4	6	10
			Molluscs	0	1	0	2	2
			Others	2	2	1	2	3
			Polychaetes	1	2	1	1	2
						2	2	2
8	Surface carnivore-omnivore:	Sessile	All					
			Others	0	0	0	0	0
8	Multi-feeding strategy:	Discrete	All					
			Echinoderms	0	0	0	0	0
				0	0	0	0	0

Table C.2-10. Mean abundance and number of species in the trophic-motility groups at 8 meters. B = Before period, A = After period.

DEPTH TM GROUP	MEASURE	700	$\frac{B}{A}$	1100	$\frac{B}{A}$	1900	$\frac{B}{A}$	3350	$\frac{B}{A}$	6700	$\frac{B}{A}$	9400	$\frac{B}{A}$
8 Subsurface deposit feeder:	Discrete NUMBER OF SPECIES	1.0	1.1	0	0	0	1.2	1.0	1.3	0	1.0	1.0	1.0
8 Subsurface deposit feeder:	Motile NUMBER OF SPECIES	50	15	42	16	35	23	48	14	35	16	39	15
8 Subsurface deposit feeder:	Sessile NUMBER OF SPECIES	4.0	5.0	3.2	4.5	3.5	5.7	3.3	4.2	3.4	4.3	3.7	3.9
8 Subsurface carnivore-deposit:	Motile ABUND NUMBER OF SPECIES	2.7	3.3	2.7	2.1	4.2	2.7	4.1	3.2	3.5	3.1	3.9	2.6
8 Surface deposit-detrital:	Discrete NUMBER OF SPECIES	1.8	1.3	1.5	1.3	1.9	1.6	1.4	1.4	1.6	1.7	1.7	1.5
8 Surface deposit-detrital:	Motile ABUND NUMBER OF SPECIES	2.3	6.0	2.7	4.4	4.1	5.7	3.9	4.6	2.6	6.6	2.0	4.2
8 Surface deposit-detrital:	Sessile NUMBER OF SPECIES	1.8	2.0	1.6	2.0	1.7	1.9	1.6	1.7	1.7	1.5	1.2	1.7
8 Surface deposit-detrital:	Motile ABUND NUMBER OF SPECIES	28	24	23	20	20	28	23	20	21	18	27	16
8 Surface deposit-detrital:	Sessile NUMBER OF SPECIES	3.8	3.8	3.4	3.5	2.4	3.5	3.3	3.4	3.2	4.2	3.8	3.7
8 Surface omnivore-deposit:	Discrete NUMBER OF SPECIES	1.0	1.2	0	1.4	1.0	1.0	1.0	1.7	1.0	1.3	1.0	8.7
8 Surface omnivore-deposit:	Motile ABUND NUMBER OF SPECIES	2.0	3.3	1.5	2.4	1.8	3.1	1.7	3.8	1.1	3.3	1.8	3.3
8 Surface omnivore-deposit:	Sessile NUMBER OF SPECIES	1.0	1.5	1.0	1.2	1.2	1.2	1.1	1.1	1.1	1.3	1.2	1.1
8 Surface suspension-deposit:	Motile ABUND NUMBER OF SPECIES	10	9.0	15	13	11	15	13	17	6.4	10	7.0	11
8 Surface, suspension-deposit:	Discrete ABUND NUMBER OF SPECIES	3.8	3.9	3.6	4.5	3.2	4.4	3.8	4.8	3.3	4.2	3.4	3.9
8 Surface, suspension-deposit:	Motile ABUND NUMBER OF SPECIES	115	27	88	22	99	25	60	21	24	17	64	16
8 Surface, suspension-deposit:	Sessile NUMBER OF SPECIES	4.1	4.9	4.3	4.7	4.9	4.9	5.1	5.0	4.8	5.1	4.1	4.6
8 Surface, suspension-deposit:	Motile ABUND NUMBER OF SPECIES	2.8	2.2	2.3	2.1	3.3	2.0	1.7	4.9	1.9	1.9	4.4	1.8
8 Suspension feeder: Discrete NUMBER OF SPECIES	Sessile ABUND NUMBER OF SPECIES	3.3	6.8	5.5	4.6	1.7	9.3	0	14	0	4.4	1.0	2.9
8 Suspension feeder: Motile NUMBER OF SPECIES	ABUND NUMBER OF SPECIES	1.0	1.2	1.0	1.2	1.0	1.2	0	1.1	0	1.2	1.0	1.1
8 Suspension feeder: Sessile NUMBER OF SPECIES	ABUND NUMBER OF SPECIES	2.9	3.2	2.1	2.8	2.3	3.5	6.3	3.9	2.3	2.5	5.9	3.6
8 Surface carnivore-omnivore:	Discrete ABUND NUMBER OF SPECIES	9.8	3.2	5.9	2.9	6.8	4.1	8.4	3.5	6.5	3.9	11	4.6
8 Surface carnivore-omnivore:	Motile ABUND NUMBER OF SPECIES	3.4	2.6	3.2	2.4	2.8	3.0	3.1	2.5	3.1	3.0	3.5	3.2
8 Surface carnivore-omnivore:	Sessile ABUND NUMBER OF SPECIES	0	0	1.0	0	0	0	1.0	4.2	4.2	4.6	5.6	5.4
8 Multi-feeding strategy: Discrete NUMBER OF SPECIES	ABUND NUMBER OF SPECIES	1.0	1.0	0	1.0	1.0	1.0	1.5	1.3	1.2	1.0	1.0	1.0

Table C.2-11. Percent of the total abundance contributed by the trophic-motility groups and their subsets at 18 meters.
 B = Before period, A = After period.

DEPTH TMGROUP		PHYLUM			PHYLUM			PHYLUM			
		B	A	700	B	A	1100	B	A	1900	B
18 Subsurface deposit feeder:	Discrete	All		1	0	1	0	1	0	1	0
		Molluscs		0	0	0	0	0	0	0	0
		Others		1	0	1	0	1	0	1	0
18 Subsurface deposit feeder:	Motile	All		30	39	37	32	34	23	29	14
		Echinoderms		0	0	0	0	0	0	0	0
		capitellid polychaetes		22	17	22	13	23	13	19	7
		paraonid polychaetes		8	21	15	17	10	10	10	6
18 Subsurface deposit feeder:	Sessile	All		0	1	1	1	0	1	0	0
		Polychaetes		0	1	1	1	0	1	0	0
18 Subsurface carnivore-deposit:	Motile	All		10	4	8	4	8	3	9	2
		Polychaetes		10	4	8	4	8	3	9	2
18 Surface deposit feeder:	Discrete	All		3	2	3	2	4	3	3	2
		Crustaceans		1	1	1	1	1	2	1	1
		Molluscs		0	0	0	0	0	0	0	0
		Polychaetes		1	1	1	1	2	1	1	1
18 Surface deposit feeder:	Motile	All		4	6	3	5	4	6	4	4
		Crustaceans		3	4	2	4	2	5	3	4
		Echinoderms		0	0	0	0	0	0	0	0
		Molluscs		0	0	0	0	0	0	0	0
		Polychaetes		1	1	1	1	1	1	1	1
18 Surface deposit feeder:	Sessile	All		1	1	1	1	1	2	1	1
		Echinoderms		0	0	0	0	0	0	0	0
		Others		0	0	0	0	0	0	0	0
		Polychaetes		1	1	1	1	2	1	1	1
18 Surface omnivore-deposit:	Discrete	All		4	4	3	3	3	8	6	8
		Crustaceans		4	4	3	3	3	8	6	8
18 Surface omnivore-deposit:	Motile	All		7	7	6	8	8	10	6	8
		Crustaceans		7	7	6	8	8	10	6	8
		Echinoderms		0	0	0	0	0	0	0	0
		Molluscs		0	0	0	0	0	0	0	0
18 Surface suspension-deposit:	Discrete	All		19	17	16	18	14	23	17	19
		Crustaceans		7	7	5	8	6	12	7	8
		Molluscs		4	3	3	4	4	4	5	5
		Others		0	0	0	0	0	0	0	0
		Polychaetes		8	7	8	7	4	7	5	6
18 Surface suspension-deposit:	Motile	All		1	1	1	1	1	1	1	1
		Crustaceans		1	1	1	1	1	1	1	1
		Others		0	0	0	0	0	0	0	0

Table C.2-11. (cont.)

DEPTH TMGROUP	PHYLUM	700		1100		1900		3200		6700		9400	
		B	A	B	A	B	A	B	A	B	A	B	A
18 Surface suspension-deposit:	Sessile												
All		3	4	3	3	2	3	3	3	3	4	3	2
Crustaceans		3	4	2	3	2	3	3	3	2	4	3	2
Polychaetes		0	0	0	0	0	0	0	0	0	0	0	0
All		1	1	1	0	3	1	1	1	2	1	1	0
Molluscs		1	1	1	0	3	1	1	1	2	1	1	0
Polychaetes		0	0	0	0	0	0	0	0	0	0	0	0
18 Suspension feeder: Discrete													
All		1	1	0	1	1	1	0	1	1	0	1	1
Polychaetes		1	1	0	1	1	1	0	1	1	0	1	1
All		2	4	2	3	2	4	3	3	3	4	3	4
Molluscs		2	1	1	0	1	1	2	1	2	1	1	1
Others		0	1	0	0	0	1	0	0	0	1	0	0
Polychaetes		1	3	1	2	1	3	1	2	1	3	1	2
18 Suspension feeder: Motile													
All		5	4	7	4	6	3	6	2	5	3	4	2
Molluscs		0	0	0	0	0	0	0	0	0	0	0	0
Others		1	1	1	1	1	0	0	0	0	0	0	0
Polychaetes		3	1	3	1	2	1	2	1	2	1	2	1
18 Surface carnivore-omnivore: Discrete													
All		2	2	3	2	4	2	4	1	2	1	2	1
Crustaceans		7	6	7	14	7	7	7	29	7	12	7	14
Echinoderms		1	1	1	8	1	1	0	25	1	6	1	8
Molluscs		0	0	0	0	0	0	0	0	0	0	0	0
Others		2	2	2	2	2	2	2	2	2	2	2	2
Polychaetes		2	2	2	2	4	2	3	2	3	1	4	2
18 Surface carnivore-omnivore: Motile													
All		7	6	7	14	7	7	7	29	7	12	7	14
Crustaceans		1	1	1	8	1	1	0	25	1	6	1	8
Echinoderms		0	0	0	0	0	0	0	0	0	0	0	0
Molluscs		2	2	2	2	2	2	2	2	2	2	2	2
Others		2	2	2	2	2	2	2	2	2	1	2	1
Polychaetes		3	2	2	2	4	2	3	2	3	1	4	2
18 Surface carnivore-omnivore: Sessile													
All		0	0	0	0	0	0	0	0	0	0	0	0
Others		0	0	0	0	0	0	0	0	0	0	0	0
18 Multi-feeding strategy: Discrete													
All		1	1	1	1	2	0	2	0	2	0	2	0
Echinoderms		1	1	1	1	2	0	2	0	2	0	2	0

Table C.2-12. Mean abundance and number of species in the trophic-motility groups at 18 meters. B= Before period, A= After period.

DEPTH	TMGROUP	MEASURE	700 ABUND	700 NUMBER OF SPECIES	1100 ABUND	1100 NUMBER OF SPECIES	1900 ABUND	1900 NUMBER OF SPECIES	3200 ABUND	3200 NUMBER OF SPECIES	6700 ABUND	6700 NUMBER OF SPECIES	9400 ABUND	9400 NUMBER OF SPECIES
18	Subsurface	deposit feeder:	Discrete	3.1 1.3	2.7 1.3	2.9 1.0	2.4 1.4	2.1 1.3	2.1 1.4	2.1 1.3	2.1 1.3	2.0 2.0	2.0 2.0	
18	Subsurface	deposit feeder:	Motile	68 123	78 88	87 61	61 44	55 38	55 38	6.7 6.6	6.7 6.6	6.1 6.3	6.1 6.3	
18	Subsurface	deposit feeder:	Sessile	5.3 7.7	6.3 7.3	7.6 7.9	6.4 7.6	6.1 7.6	6.1 7.6	1.1 1.0	1.1 1.0	1.1 1.0	1.1 1.0	
18	Subsurface	carnivore-deposit:	Motile	1.4 2.8	1.7 2.4	1.4 2.6	1.1 1.9	1.0 1.7	1.0 1.7	1.0 1.2	1.0 1.2	1.0 1.1	1.0 1.1	
18	Surface	deposit-detrital:	Discrete	2.5 3.6	2.8 3.0	2.8 3.2	2.7 3.0	2.4 2.9	2.4 2.9	2.4 2.9	2.4 2.9	2.5 2.7	2.5 2.7	
18	Surface	deposit-detrital:	Motile	6.9 6.8	6.1 6.0	11 3.4	6.3 5.6	7.9 5.1	7.9 5.1	2.3 2.2	2.3 2.2	2.6 2.0	2.6 2.0	
18	Surface	deposit-detrital:	ABUND	2.8 2.6	2.3 2.3	3.0 2.3	2.4 2.3	2.4 2.2	2.4 2.2	2.4 2.2	2.4 2.2	2.4 2.2	2.4 2.2	
18	Surface	deposit-detrital:	ABUND	8.4 1.8	7.0 1.3	9.4 15	7.7 13	8.4 14	8.4 14	4.1 6.3	4.1 6.3	4.1 5.8	4.1 5.8	
18	Surface	deposit-detrital:	Sessile	3.7 6.8	3.4 6.3	4.3 6.0	3.8 5.5	4.1 6.3	4.1 6.3	4.1 6.3	4.1 6.3	4.1 6.3	4.1 6.3	
18	Surface	omnivore-deposit:	Discrete	2.0 5.9	2.0 4.9	2.7 7.4	2.3 5.1	1.5 8.8	1.5 8.8	1.6 1.6	1.6 1.6	1.3 1.7	1.3 1.7	
18	Surface	omnivore-deposit:	Motile	1.4 2.3	1.6 1.7	1.9 2.0	1.6 1.6	1.3 1.7	1.3 1.7	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	
18	Surface	suspension-deposit:	Discrete	15 14	9.4 9.8	10 21	17 28	21 32	21 32	1.0 1.2	1.1 1.1	1.1 1.1	1.1 1.1	
18	Surface	suspension-deposit:	Motile	1.2 1.2	1.1 1.1	1.1 1.1	1.0 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	1.1 1.1	
18	Surface	suspension-deposit:	ABUND	5.9 7.7	5.7 7.2	5.9 8.2	5.8 7.8	5.9 7.7	5.9 7.7	7.1 7.7	7.1 7.7	7.1 7.7	7.1 7.7	
18	Surface,	suspension-deposit:	ABUND	42 53	34 50	36 61	35 58	54 52	54 52	6.1 8.6	7.1 7.9	6.4 8.2	6.4 8.2	
18	Surface,	suspension-deposit:	ABUND	2.3 3.6	2.3 4.0	2.3 2.7	1.6 2.2	2.1 1.9	2.1 1.9	1.0 1.2	1.0 1.0	1.1 1.0	1.1 1.0	
18	Surface,	suspension-deposit:	Sessile	7.6 11	6.2 7.7	5.5 9.1	6.8 10	6.2 8.4	6.2 8.4	2.0 3.0	2.0 3.0	2.2 2.8	2.3 2.7	
18	Suspension	feeder:	Discrete	2.0 3.1	1.8 2.8	2.2 3.0	2.0 3.0	2.0 3.0	2.0 3.0	2.0 3.0	2.0 3.0	2.2 2.8	2.3 2.7	
18	Suspension	feeder:	Motile	4.0 3.2	2.4 2.9	9.8 2.5	3.6 2.8	6.8 2.9	6.8 2.9	1.0 1.2	1.0 1.2	1.0 1.0	1.0 1.0	
18	Suspension	feeder:	ABUND	1.5 1.5	1.6 1.7	1.5 1.7	1.8 1.6	1.8 1.7	1.8 1.7	1.1 1.1	1.1 1.1	1.5 1.7	1.5 1.7	
18	Suspension	feeder:	Sessile	4.8 12	3.6 7.9	6.6 9.7	7.2 11	6.9 10	6.9 10	3.8 3.6	3.8 3.7	3.6 3.6	3.4 3.8	
18	Surface	carnivore-omnivore:	Discrete	12 12	14 9.8	17 7.8	13 6.6	11 6.3	11 6.3	6.9 4.6	6.1 4.3	5.1 3.9	5.2 3.8	
18	Surface	carnivore-omnivore:	Motile	15 18	14 39	18 19	15 89	17 28	17 28	7.9 8.9	8.2 7.9	8.6 7.0	8.1 9.2	
18	Surface	carnivore-omnivore:	ABUND	8.8 9.6	7.9 9.2	8.6 8.9	8.2 7.9	8.6 7.0	8.6 7.0	1.0 1.0	1.0 1.0	1.0 1.0	1.0 1.0	
18	Multi-feeding strategy:	Discrete	4.9 2.8	4.6 2.4	7.6 2.1	8.8 2.1	6.1 1.4	6.1 1.4	1.1 1.1	1.1 1.1	1.0 1.0	1.0 1.0	1.0 1.0	

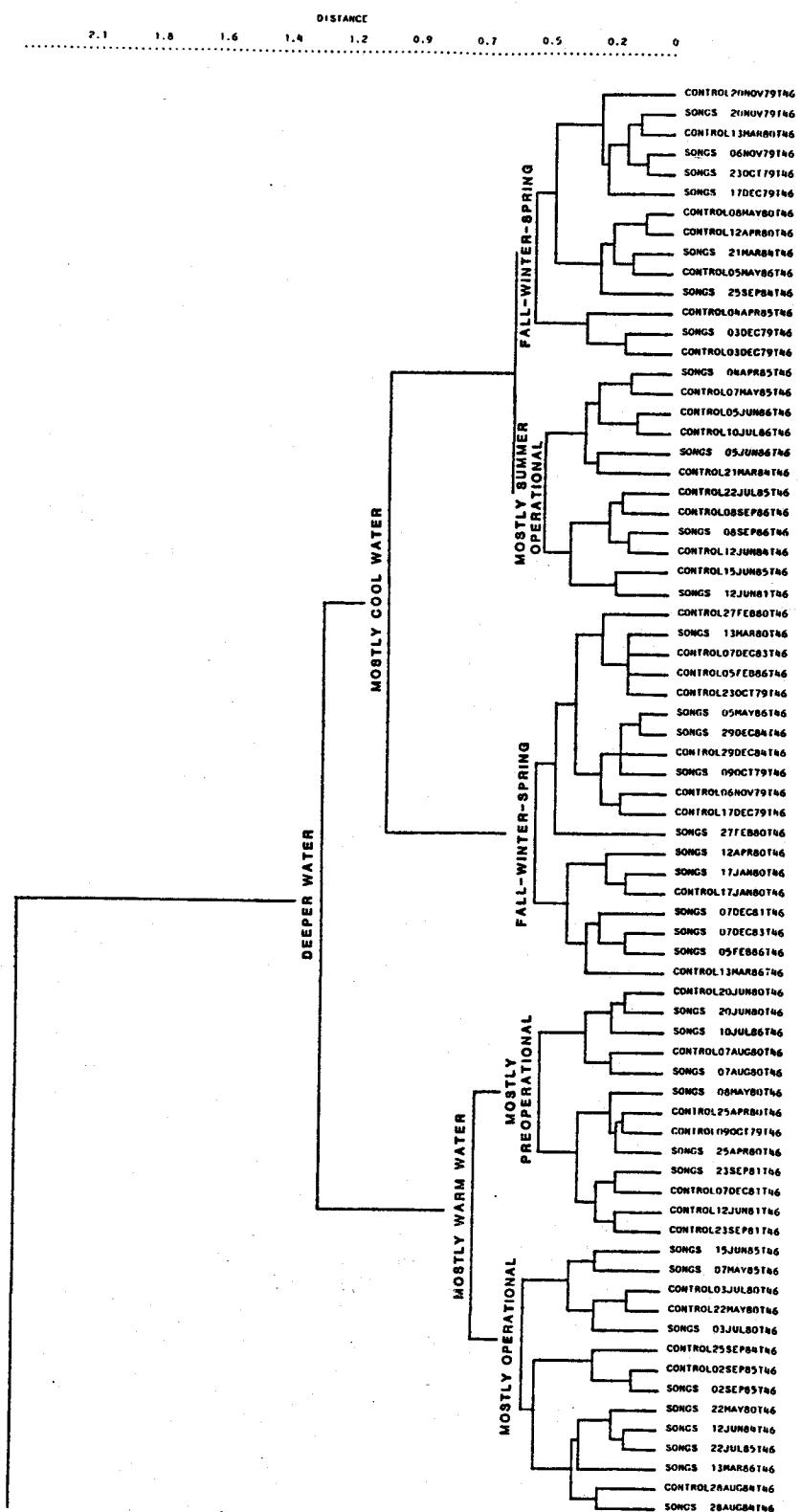
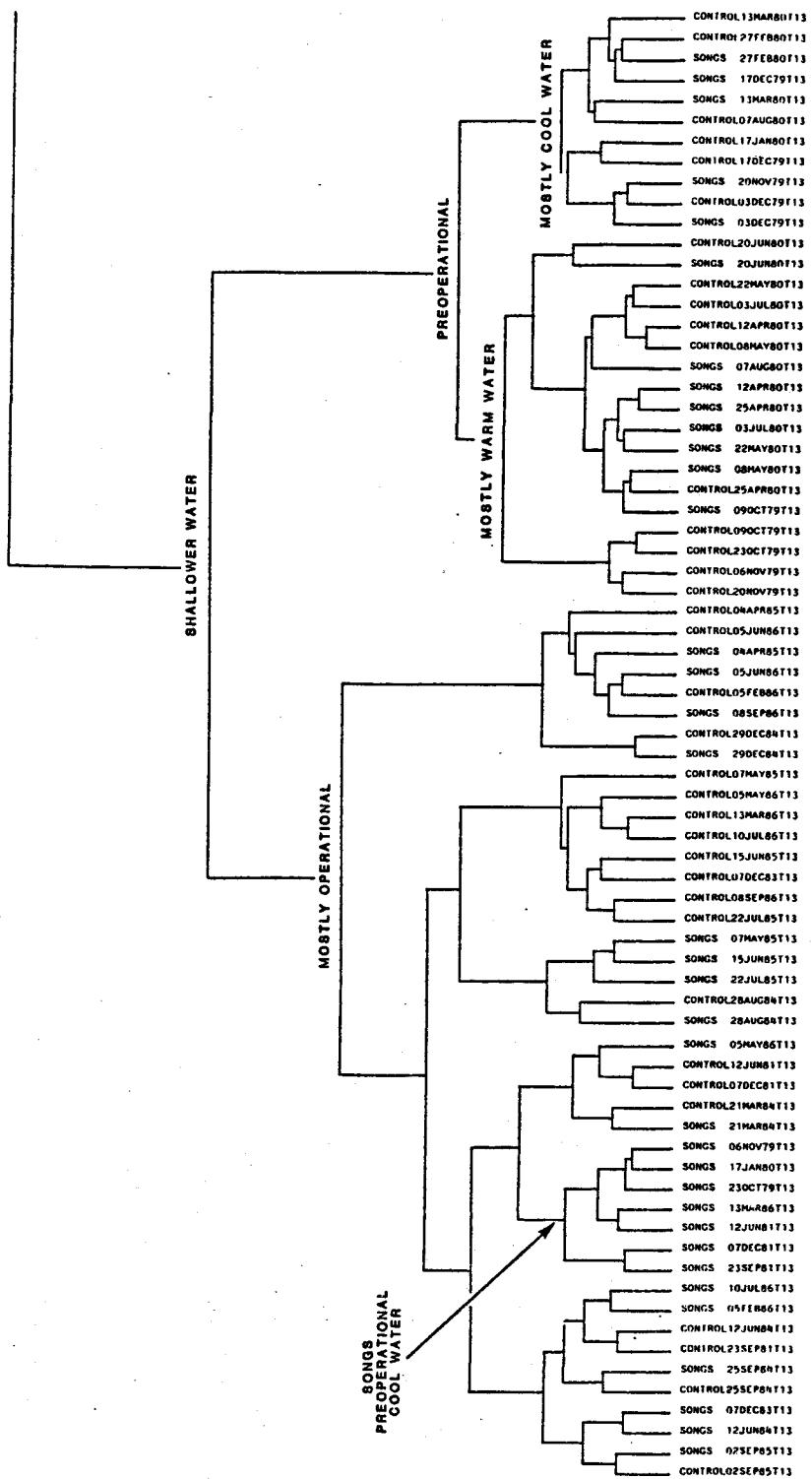


Figure C.2-1. Dendrogram of mysid preoperational and operational surveys identified by location (SONGS and Control) and depth (T13 = 6-15 m, T46 = 15-37 m). Survey groupings used in the text are indicated. Higher distance values indicate higher dissimilarity.



NOTE: BRAY-CURTIS DISTANCES CALCULATED.
 NOTE: STEP-ACROSS THRESHOLD VALUE = .08000 / ESTIMATES = 567.
 NOTE: IN FINAL STEP-ACROSS, 26 ESTIMATES < ORIGINAL VALUE WERE NOT USED.
 NOTE: ** FLEXIBLE SORTING + B = -0.250 * A = 0.625.

Figure C.2-1. (cont.)

APPENDIX D

BACI Results and Supporting Figures
(the continuation of Appendix D, containing the
benthos results, forms a separate volume)

APPENDIX D
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Taxon: Inshore
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
Untransformed	19	17	Deleted for Additivity
$\log(x+0)$	19	17	20 June 80
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity	Serial Correlation	Trends	α	Power % at α	Delta Variance
See Key		Before/	Before/			
Note:		Before/	After			
none	ns	ns/ns	ns/ns	.10	61.8	62.9/6.9
$\log(x+0)$	D	sig/sig	sig/ns			
$\log(x+.1)$	D	sig/sig	sig/ns			
$\log(x+1)$	D	sig/ns	sig/ns			

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):

Two straight lines, nonzero common intercept

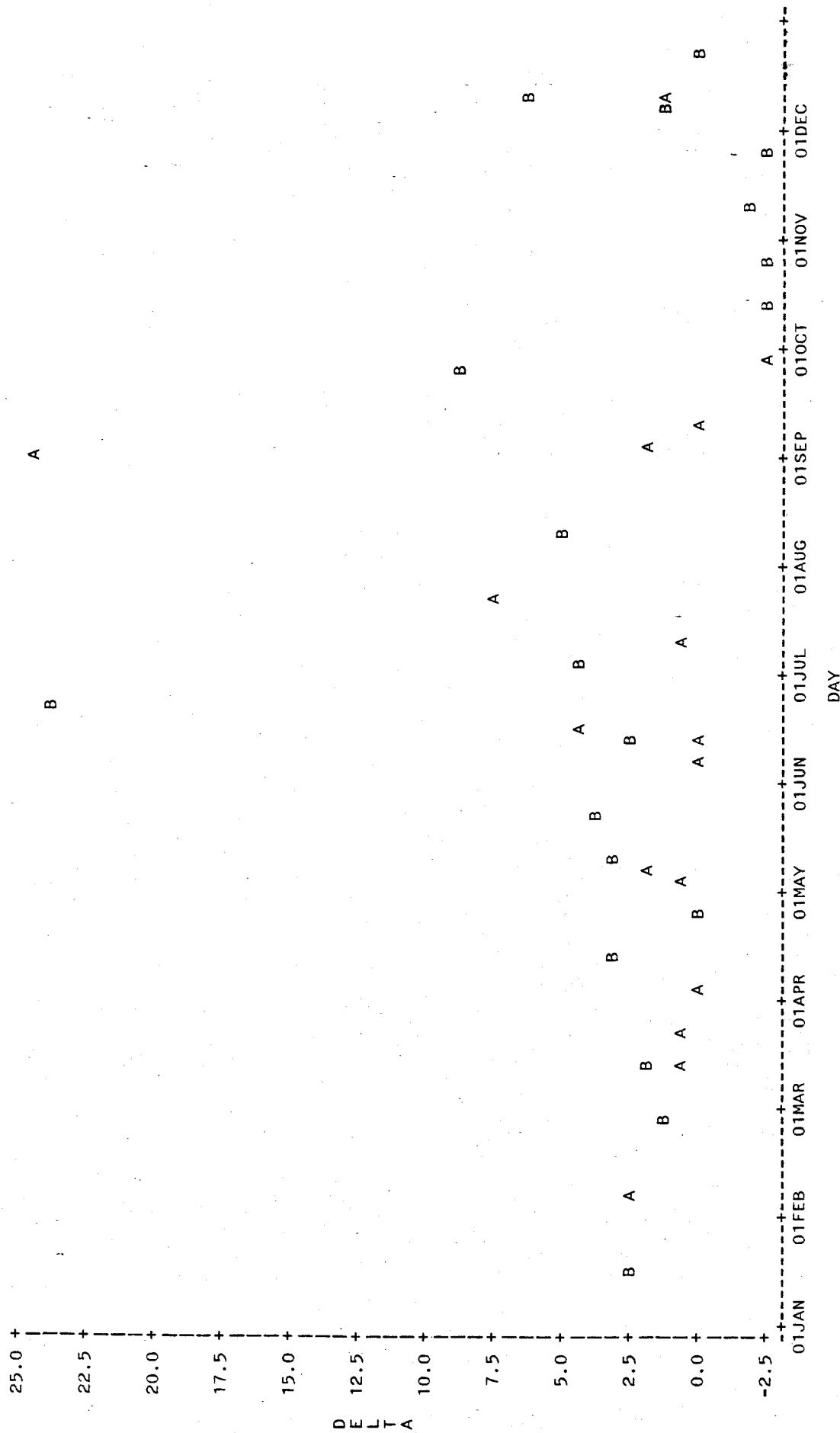
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 1. Summary of Test Results for Inshore,
All Stages Combined.

SPCODE=Inshore summary group STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-2. Plot of preoperational (B) and operational (A) Delta values for Inshore summary group all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-5

SPCODE=Inshore summary group STAGE=ALL

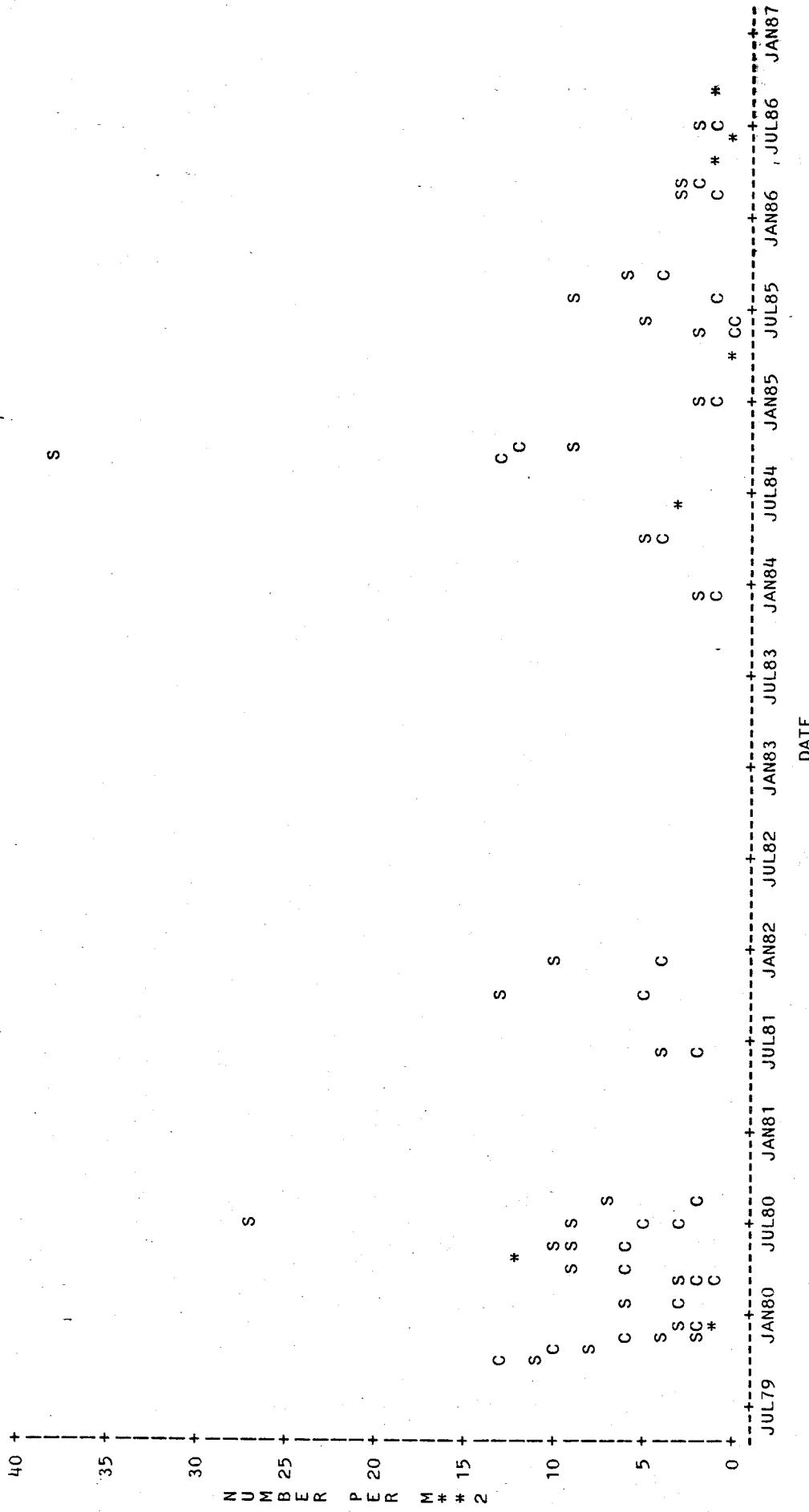


Figure D-3. Abundance values at SONGS (S) and Control (C) plotted through time for Inshore summary group all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE	DEPTH STRATA (m)					
	6-8	8-12	12-15	15-23	23-30	30-37
All Stages B or C Combined	6.4	6.2	4.9	3.2	2.5	2.4
	A-S	6.7	6.1	4.3	3.1	2.5
Adults	B or C	4.4	4.2	2.9	1.9	
	A-S	4.8	4.2	2.8	1.7	
Immatures	B or C	6.0	5.9	4.4	2.9	2.4
	A-S	5.4	5.2	3.6	2.3	2.3
Juveniles	B or C	6.1	5.9	4.7	3.1	2.6
	A-S	6.4	5.6	3.5	2.9	2.6

Figure D-4. Cross-shelf distributional patterns for Inshore Summary Group. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Inshore
Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	16	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	A,D	sig	ns/ns	sig/ns			
$\log(x+0)$	B	ns	ns/sig	ns/ns	.10	77.8	.12/.07
$\log(x+.1)$	B	ns	ns/sig	ns/ns	.10	80.0	.08/.04
$\log(x+1)$	A	sig	ns/sig	ns/ns	.10	83.7	.02/.01

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: $\log(x)$: ns, first order model
* Transformation 2: $\log(x+.1)$: ns, first order model

Binomial: ns

Regression (SONGS vs Control Abundances):
One Straight line, intercept = 0

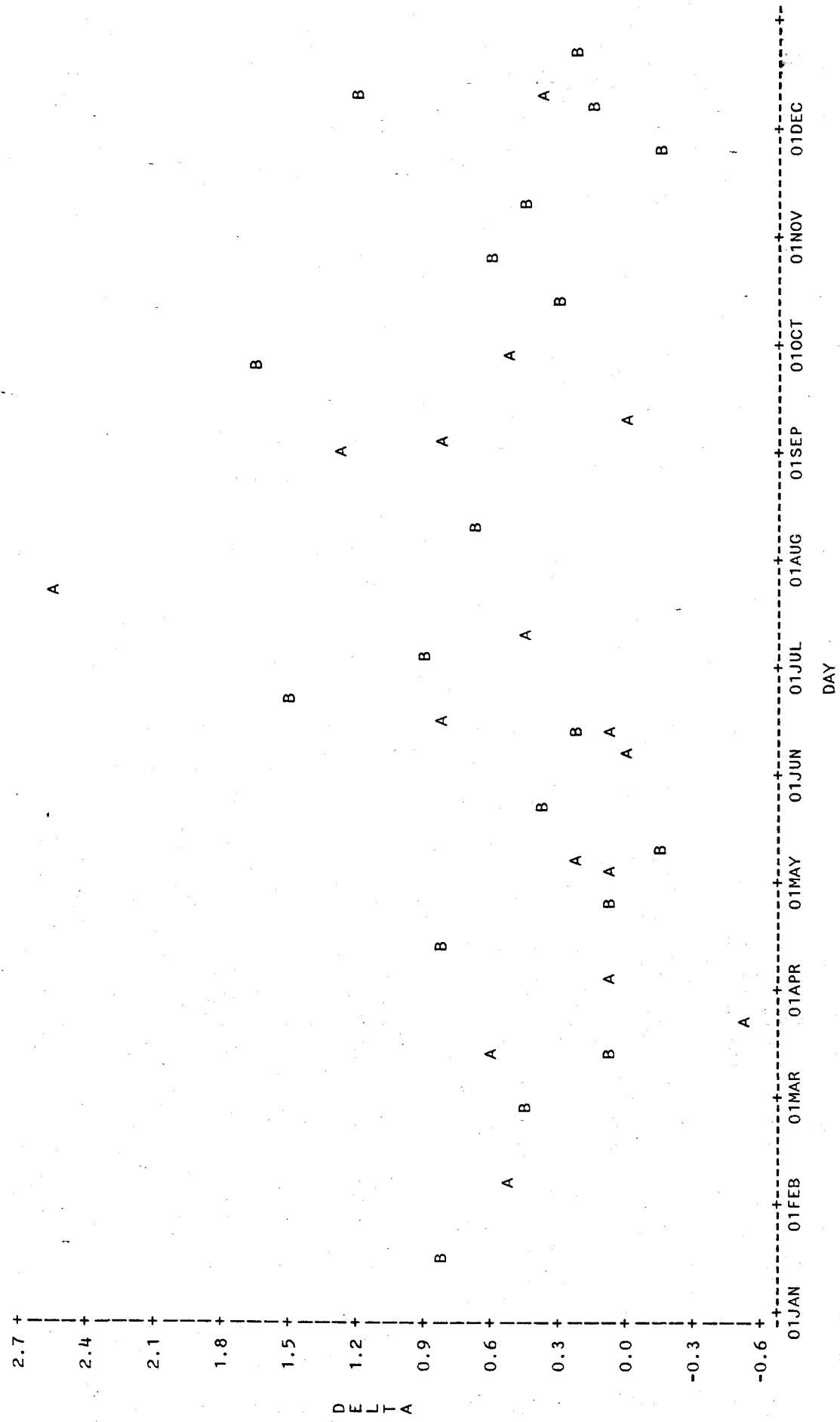
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 5. Summary of Test Results for Inshore,
Adult.

SPCODE=Inshore summary group STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-6. Plot of preoperational (A) and operational (B) Delta values for Inshore summary group adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Inshore summary group STAGE=ADULT

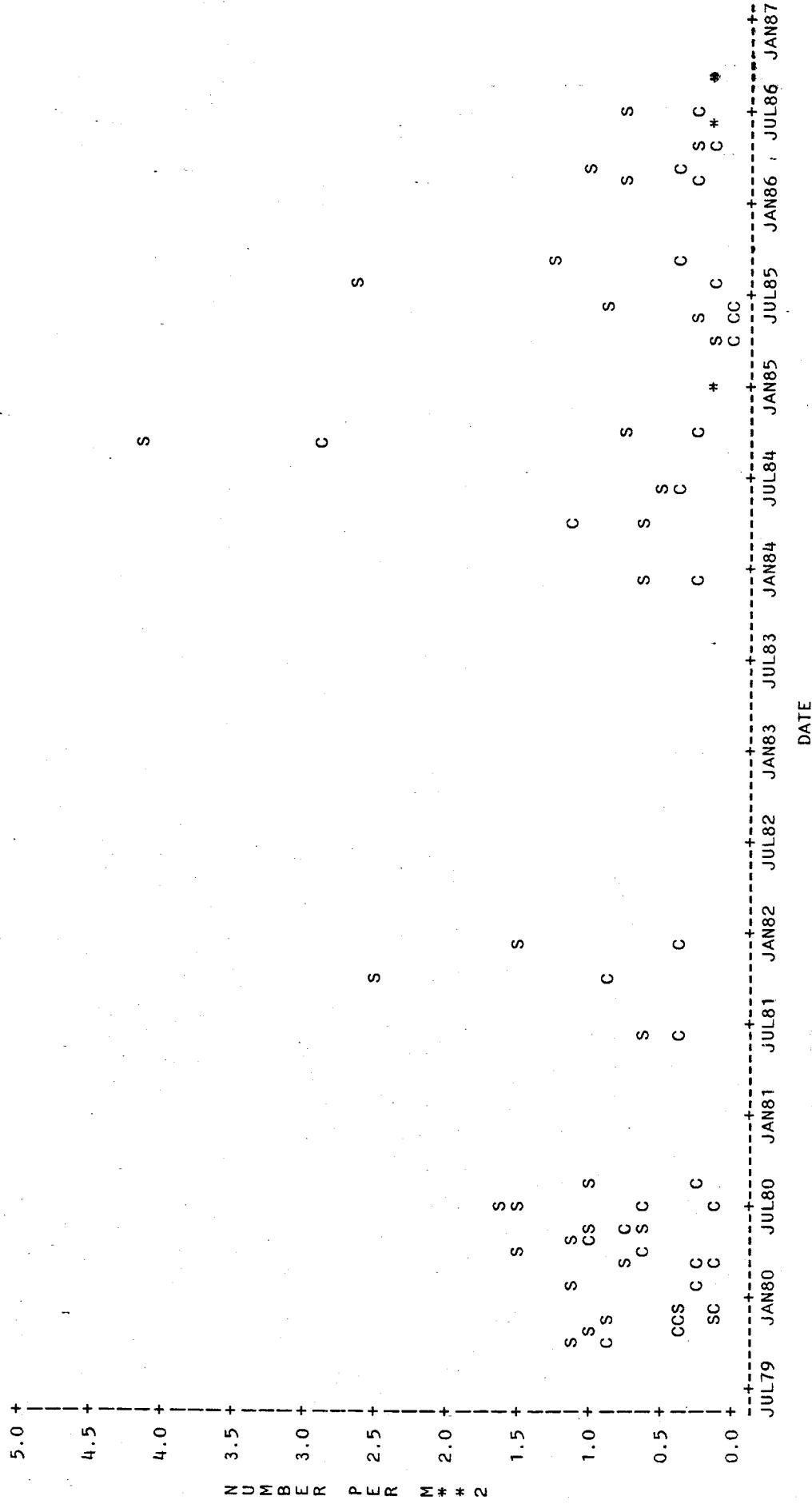


Figure D-7. Abundance values at SONGS (S) and Control (C) plotted through time for inshore summary group adults. Similar abundances at both locations are designated by asterisks.

Taxon: Inshore
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	16	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Abun/Sprse
none	A	sig	ns/ns	ns/ns			
$\log(x+0)$	B	ns	ns/sig	ns/ns	.05	82.3	.10/.05
$\log(x+.1)$	B	ns	ns/sig	ns/ns	.10	84.9	.10/.03
$\log(x+1)$	N/A						

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A

* Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A

Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

** Transformation 1: $\log(x)$: ns, first order model

Transformation 2: $\log(x+.1)$: ns first order model

C

Binomial: ns

Regression (SONGS vs Control Abundances):

Two different curves

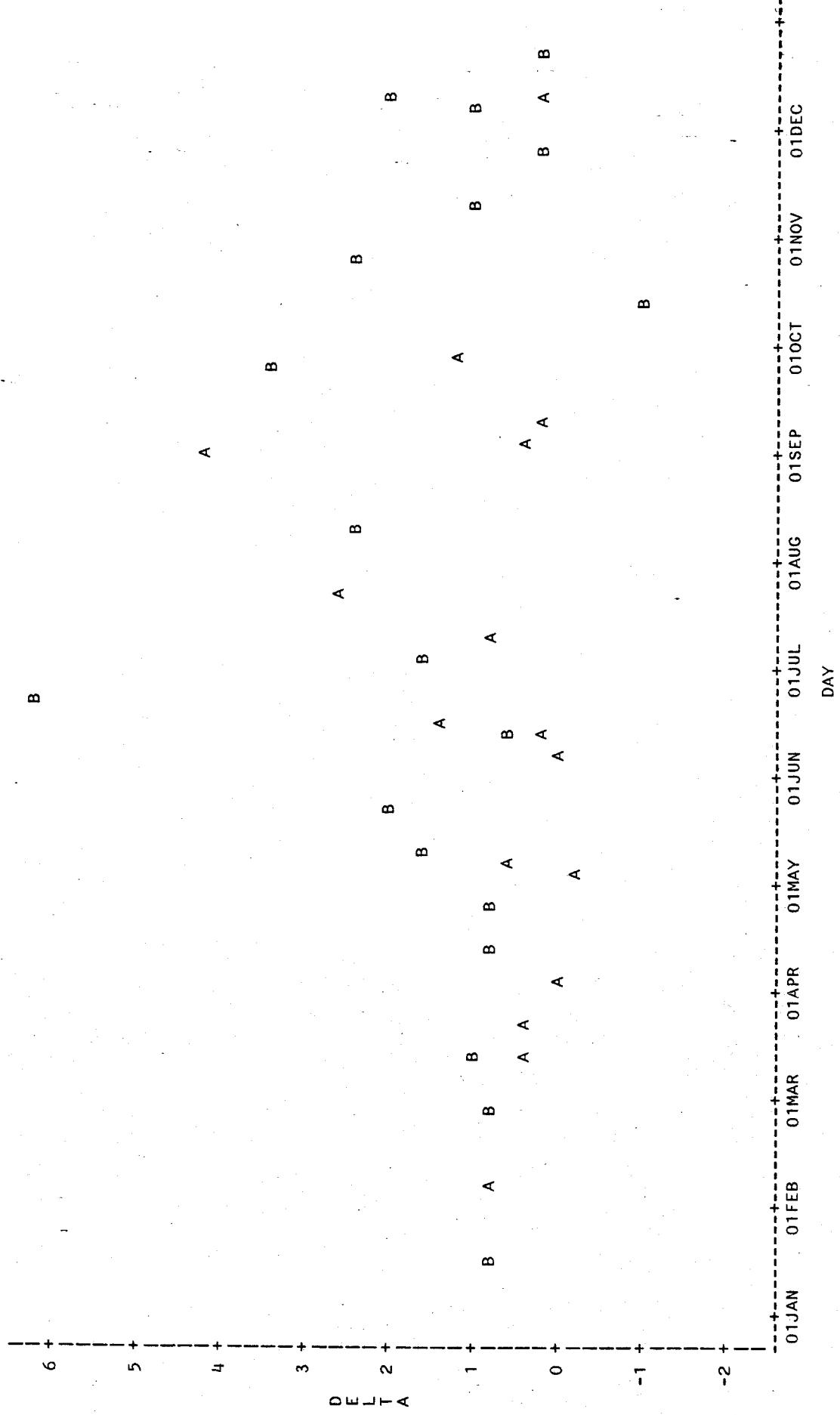
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 8. Summary of Test Results for Inshore,
Immature.

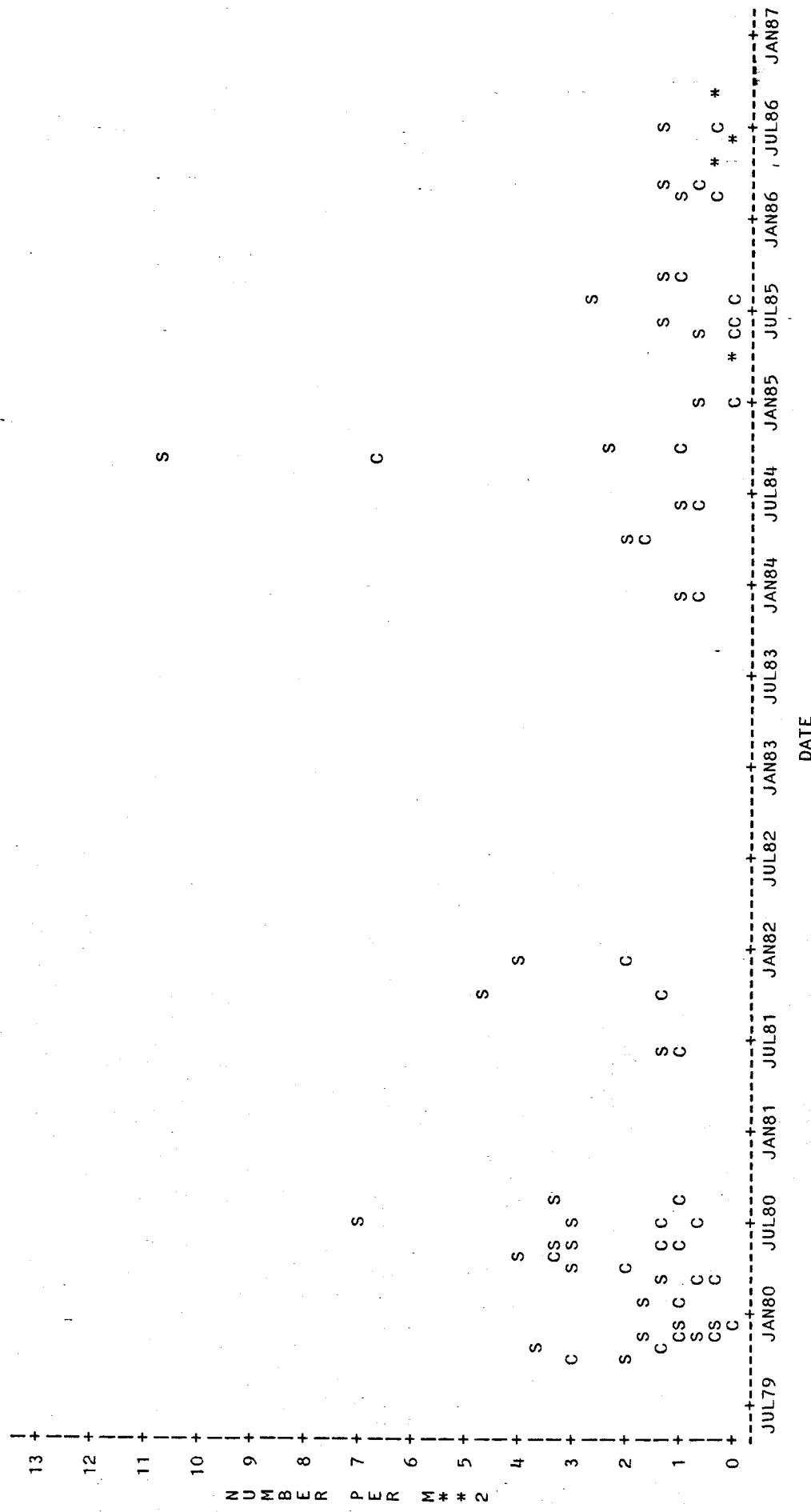
SPCODE=Inshore summary group STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-9. Plot of preoperational (B) and operational (A) Delta values for Inshore summary group immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Inshore summary group STAGE=IMMATURE



NOTE: 6 OBS HIDDEN

Figure D-10. Abundance values at SONGS (S) and Control (C) plotted through time for Inshore summary group immatures. Similar abundances at both locations are designated by asterisks.

D-13

Taxon: Inshore
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none		ns	ns/ns	ns/ns	.10	39.6
$\log(x+0)$	D	ns	sig/ns	sig/ns		34.3/3.4
$\log(x+.1)$	D	ns	sig/ns	sig/ns		
$\log(x+1)$	D	ns	sig/ns	sig/ns		

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

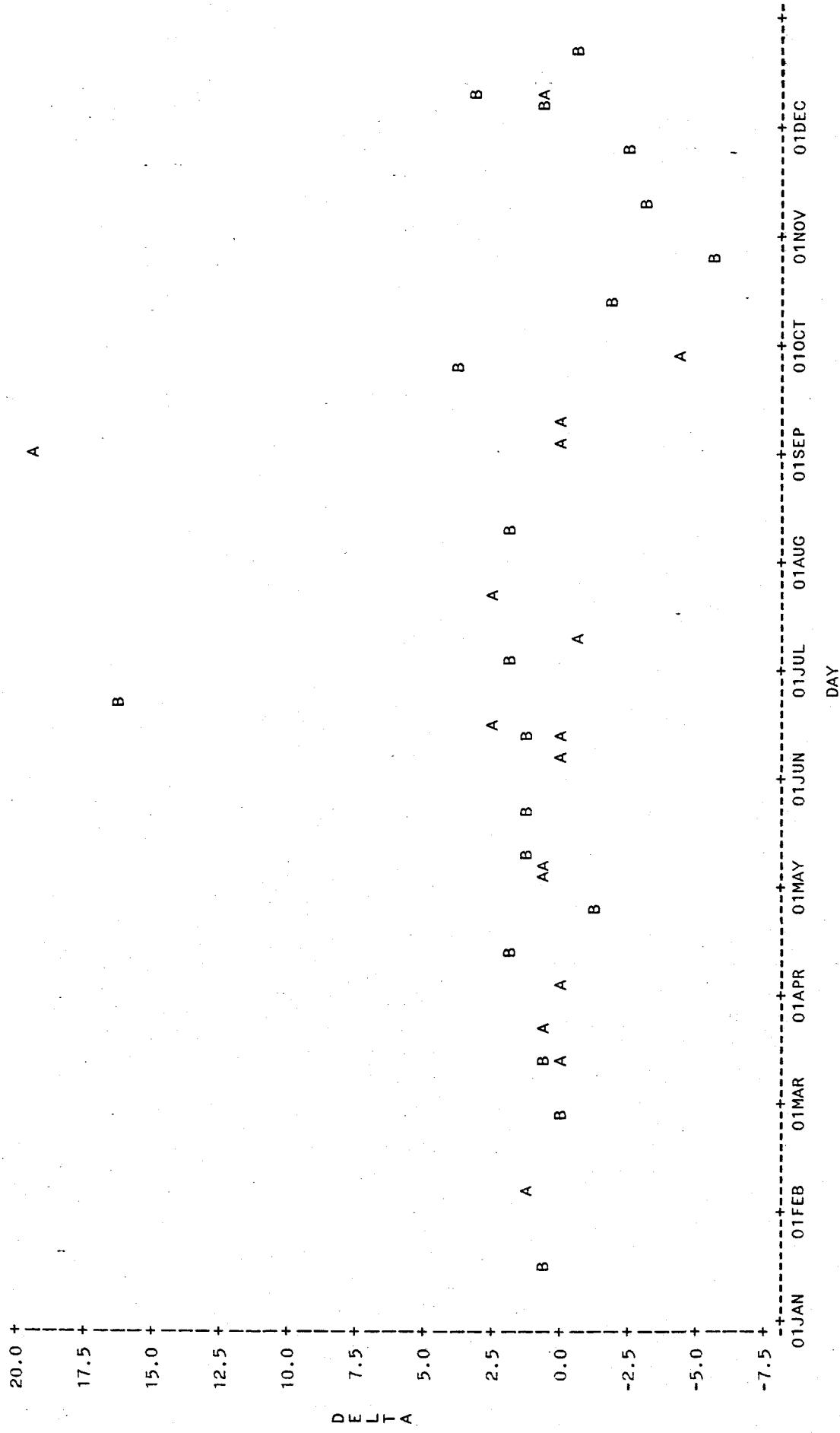
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 11. Summary of Test Results for Inshore,
Juvenile.

SPCODE=Inshore summary group STAGE=JUVENILE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-12. Plot of preoperational (B) and operational (A) Delta values for Inshore summary group juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Inshore summary group STAGE=JUVENILE

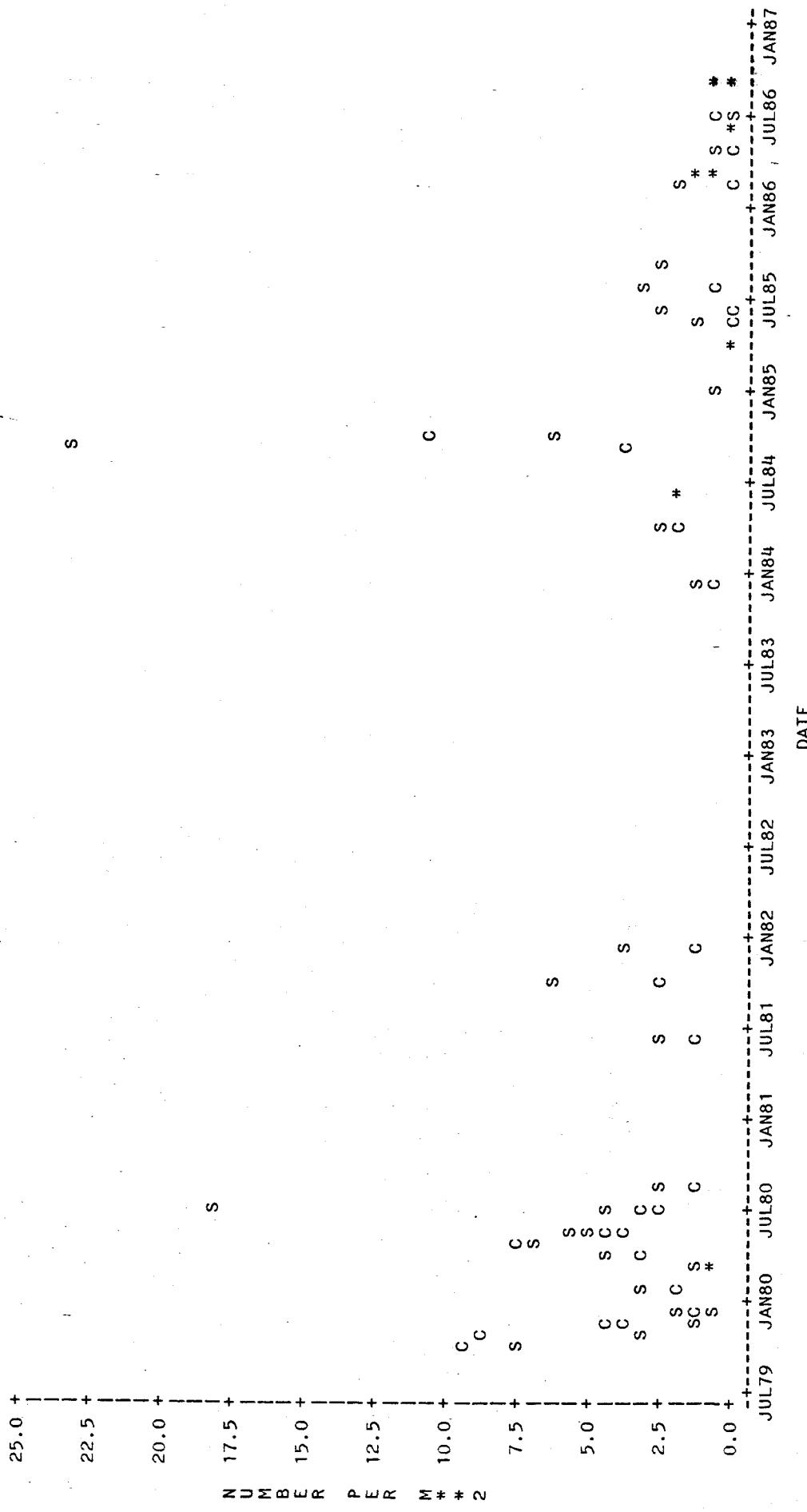


Figure D-13. Abundance values at SONGS (S) and Control (C) plotted through time for Inshore summary group juveniles. Similar abundances at both locations are designated by asterisks.

Taxon: Mysidopsis cathengelae
Stage: All

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	16	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/ Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	A,D	sig	sig/ns	sig/ns		
$\log(x+0)$		ns	ns/ns	ns/ns	.10	.72.6 .08/.27
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	.67.4 .06/.08
$\log(x+1)$	A,D	sig	ns/ns	sig/ns		

Chi Square; Ho:even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$. ns
Transformation 2: N/A

F

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: ns
Transformation 2: N/A

F

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

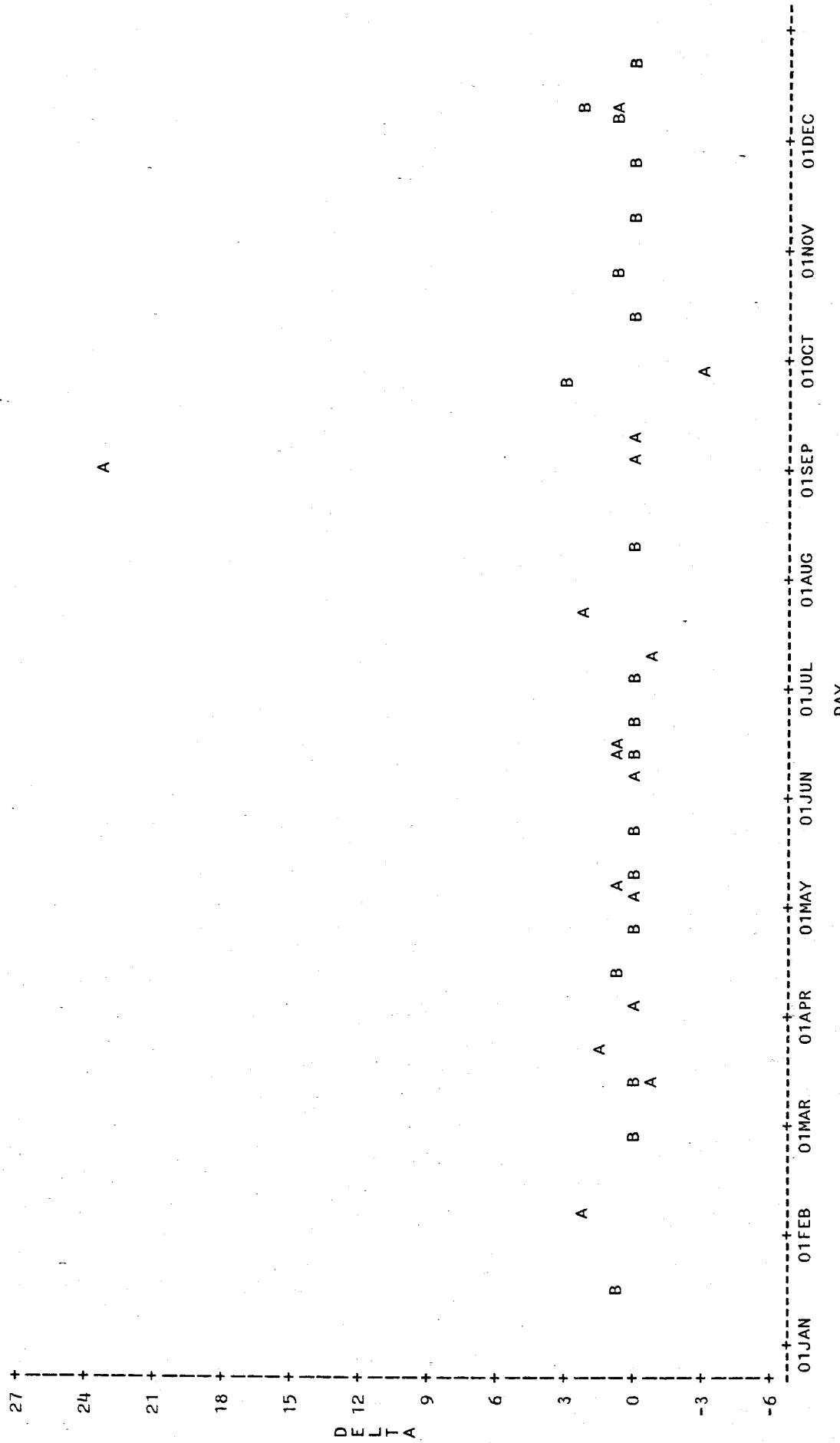
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 14. Summary of Test Results for Mysidopsis cathengelae,
All Stages Combined.

SPCODE=Mysidopsis cathegatae STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-15. Plot of preoperational (B) and operational (A) Delta values for *Mysidopsis cathegatae* all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Mysidopsis cathengelae STAGE=ALL

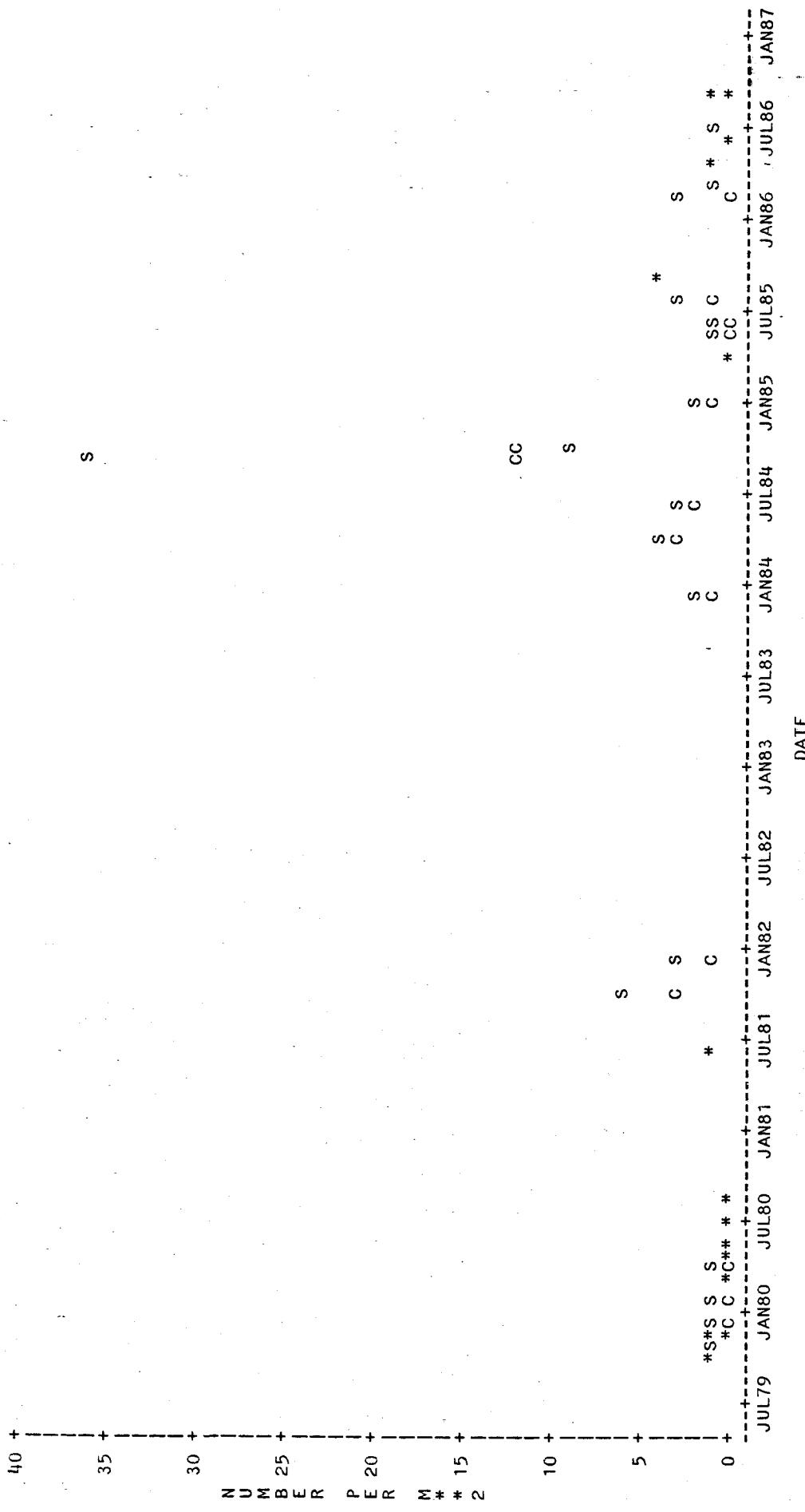


Figure D-16. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis cathengelae* all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages Combined	B or C	4.7	3.9	2.5	2.0		
	A-S	4.8	4.2	2.5	1.9		
Adults	B or C	3.8	4.1			2.8	2.2
p=.01	A-S	4.6	3.8			2.9	1.9
Immatures	B or C	4.4	3.8			2.6	2.2
p=.02	A-S	4.5	4.4			2.6	1.8
Juveniles	B or C	4.6	3.8			2.3	2.1
p=.05	A-S	4.7	4.2			2.4	1.9

Figure D-17. Cross-shelf distributional patterns for *Mysidopsis cathengelae*. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Mysidopsis cathengelae

Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	17	17	
$\log(x+0)$	13	15	
$\log(x+\text{constant})$	17	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none		ns	ns/ns	ns/ns	.10	18.9
$\log(x+0)$	N/A					.01/.002
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	42.0
$\log(x+1)$	N/A					.02/.05

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: sig($p=.043$)
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):

Two different straight lines, same intercept(= 0)

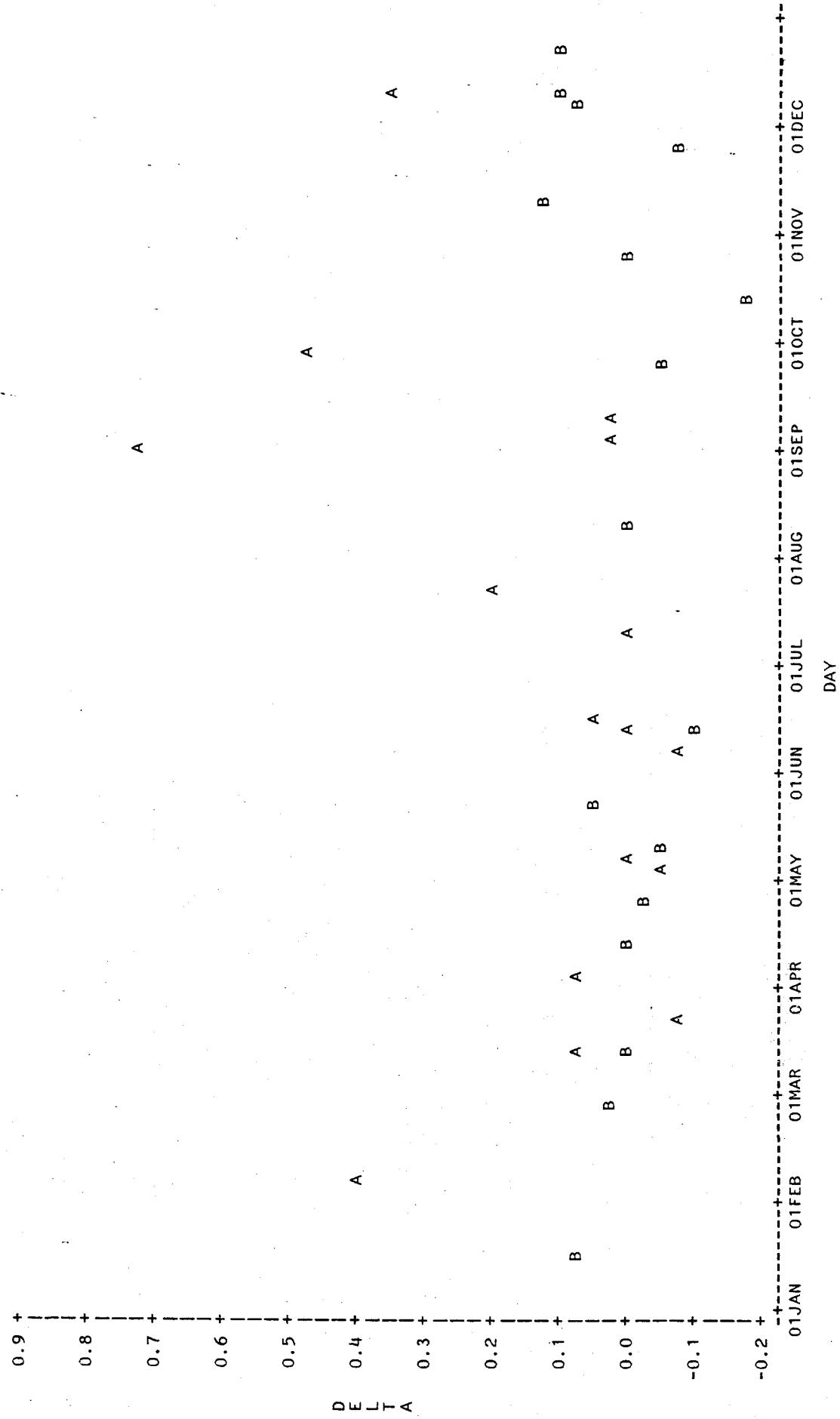
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-18 . Summary of Test Results for Mysidopsis cathengelae,
Adult.

SPCODE=Mysidopsis cathengelae STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-19. Plot of preoperational (B) and operational (A) Delta values for *Mysidopsis cathengelae* adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Mysidopsis cathegatae STAGE=ADULT

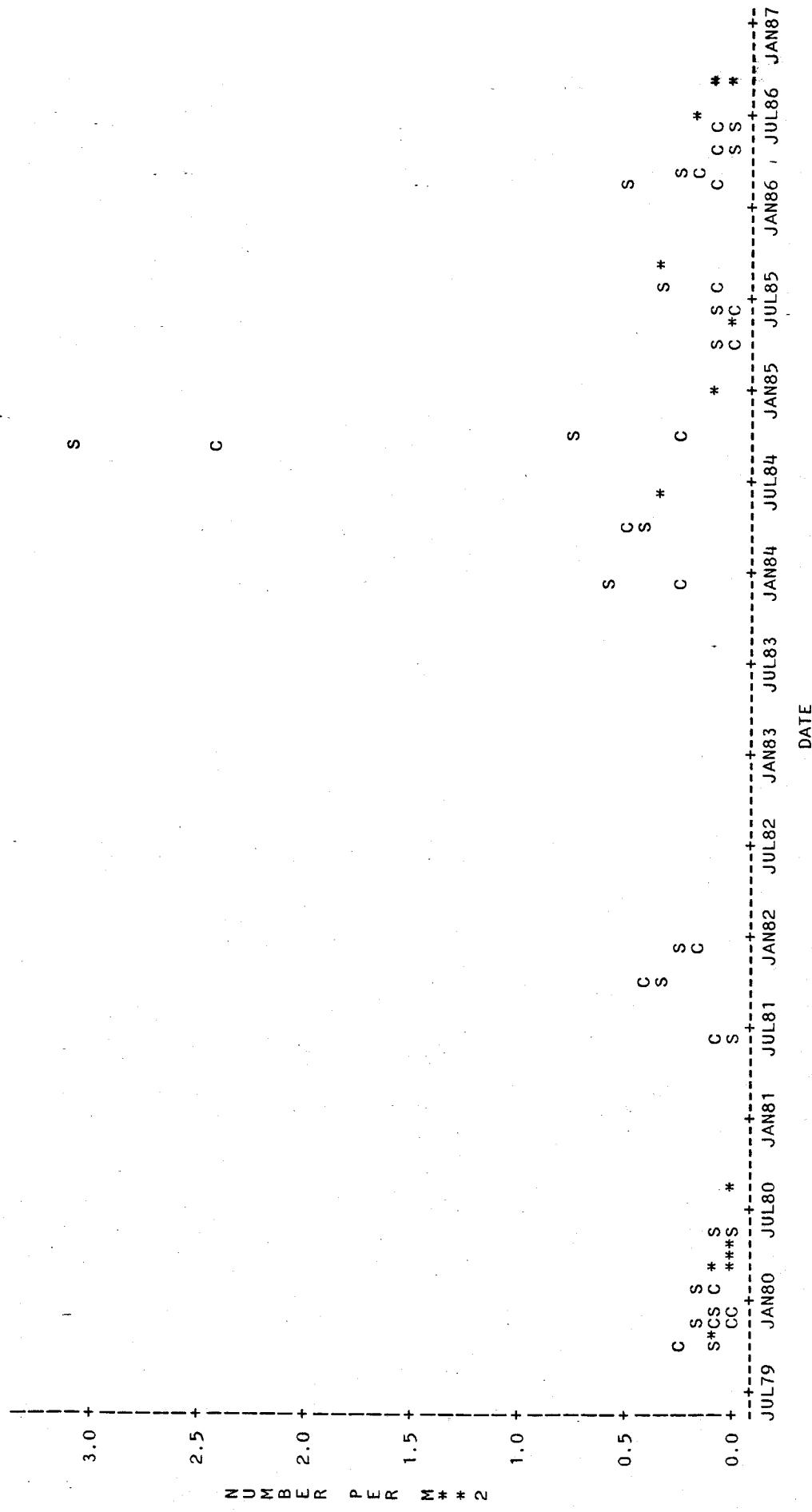


Figure D-20. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis cathegatae* adults. Similar abundances at both locations are designated by asterisks.

D-23

Taxon: Mysidopsis cathengelae
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	17	17	
$\log(x+0)$	14	16	
$\log(x+\text{constant})$	17	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends	α	Power % at α	Delta Variance
	Note:	Before/After	Before/ After			Abun/Sprse
none	A,D	sig	sig/ns			
$\log(x+0)$	N/A					
$\log(x+.1)$		ns+	ns/ns			
$\log(x+1)$	A	sig+	sig/ns			
				ns/ns	.10	51.0
					ns/ns	.01/.05

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x+.1)$: ns
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x+.1)$: ns
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):

Two different straight lines, same intercept (= 0)

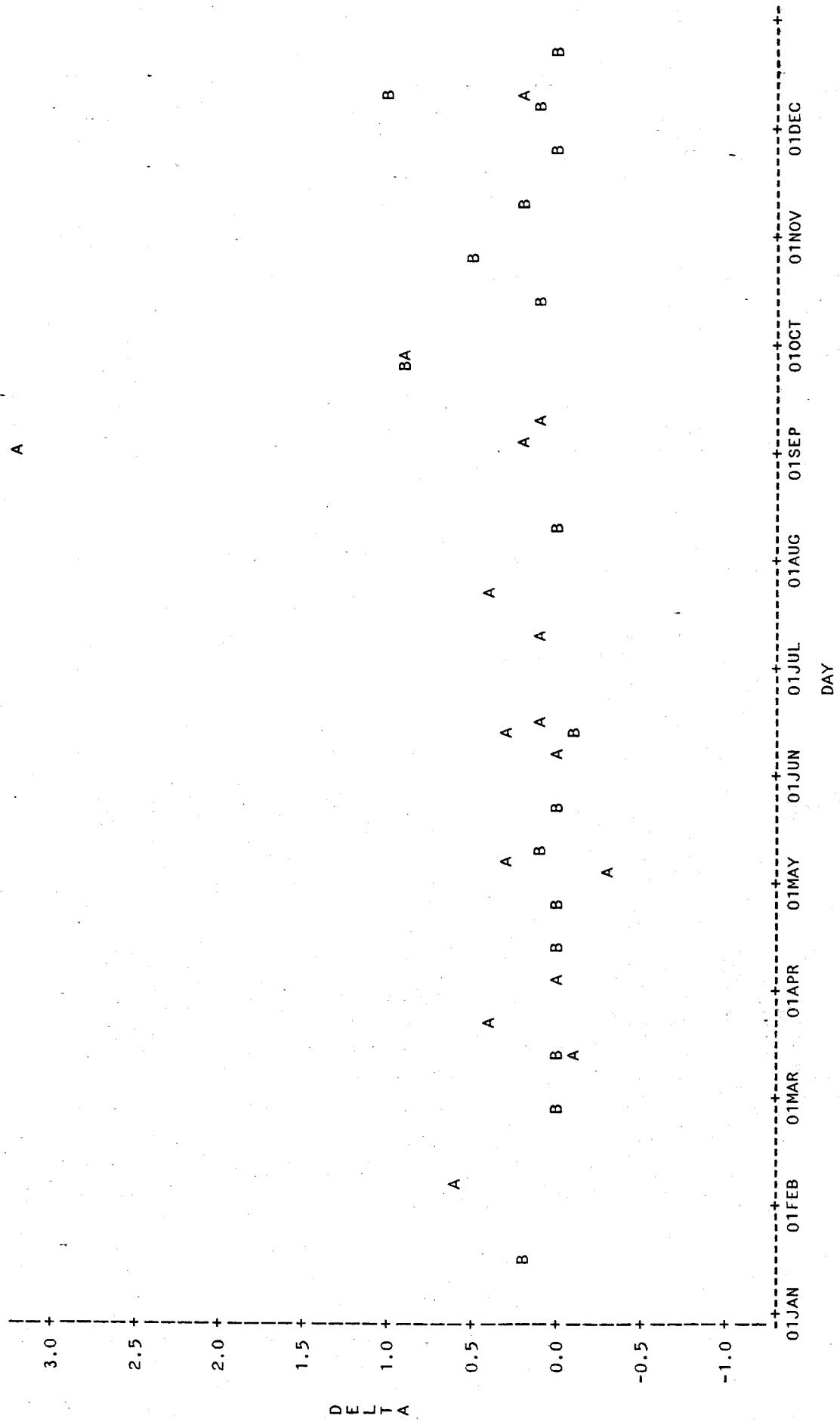
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 21. Summary of Test Results for Mysidopsis cathengelae,
Immature.

SPCODE=Mysidopsis cathengelae STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-22. Plot of preoperational (B) and operational (A) Delta values for *Mysidopsis cathengelae* immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Mysidopsis cathengelae STAGE=IMMATURE

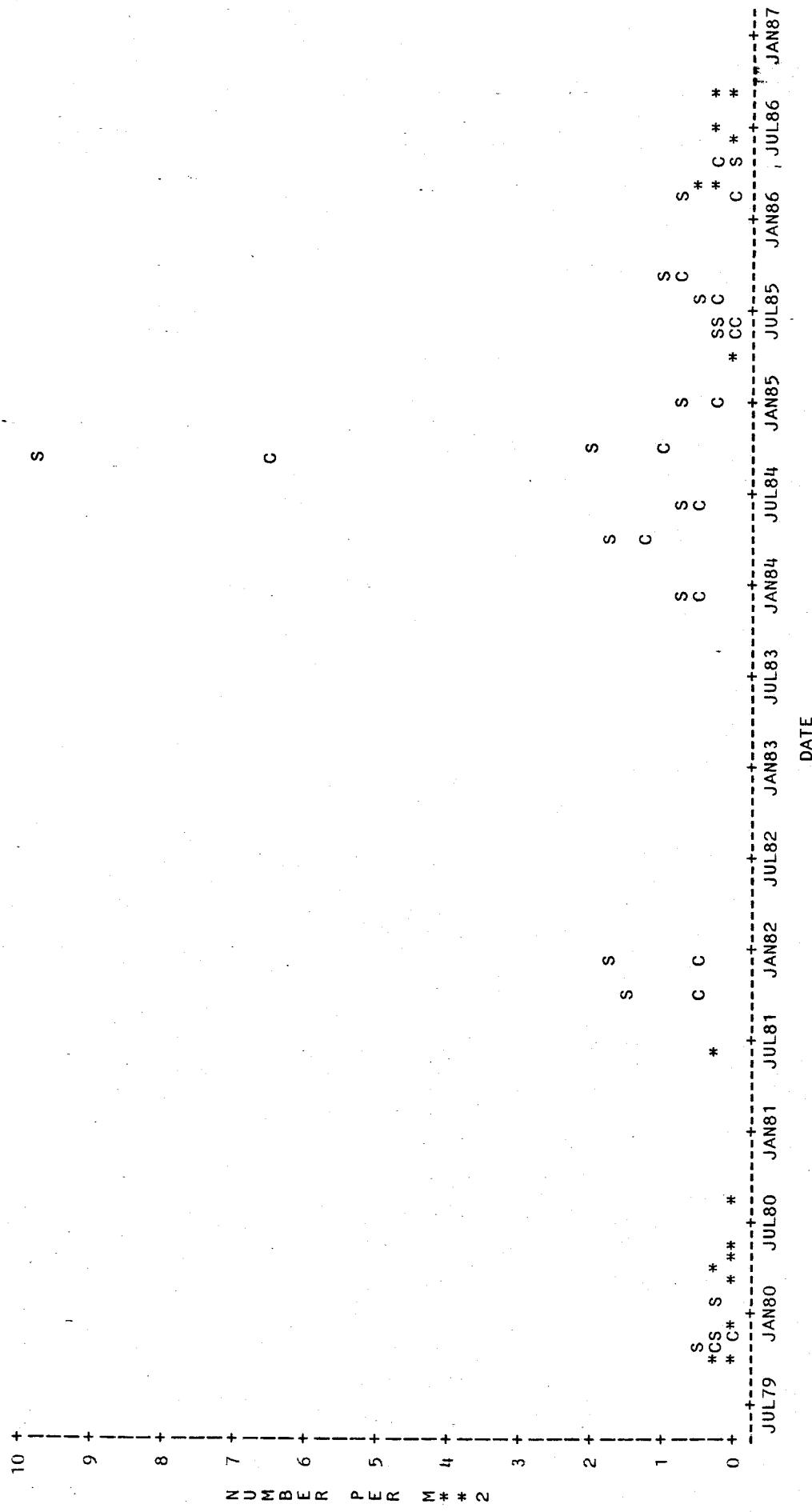


Figure D-23. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis cathengelae* immatures. Similar abundances at both locations are designated by asterisks.

Taxon: Mysidopsis cathengelae
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	14	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note: Before/After	Trends Before/ After	α	Power % at α	Delta Variance
none	A,D	sig	sig/ns	sig/ns		
$\log(x+0)$	N/A					
$\log(x+.1)$		ns	ns/ns	ns/ns		
$\log(x+1)$	A,D	sig	ns/ns	sig/ns		

Chi Square; H_0 : even distribution of zeroes in BACI cells: sig

TEST RESULTS

BACI t-test See Key Note:
Transformation 1: $\log(x+.1)$: N/A F
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)
Transformation 1: $\log(x+.1)$: N/A F
Transformation 2: N/A

Autoregressive Errors t-test
Transformation 1: N/A
Transformation 2: N/A

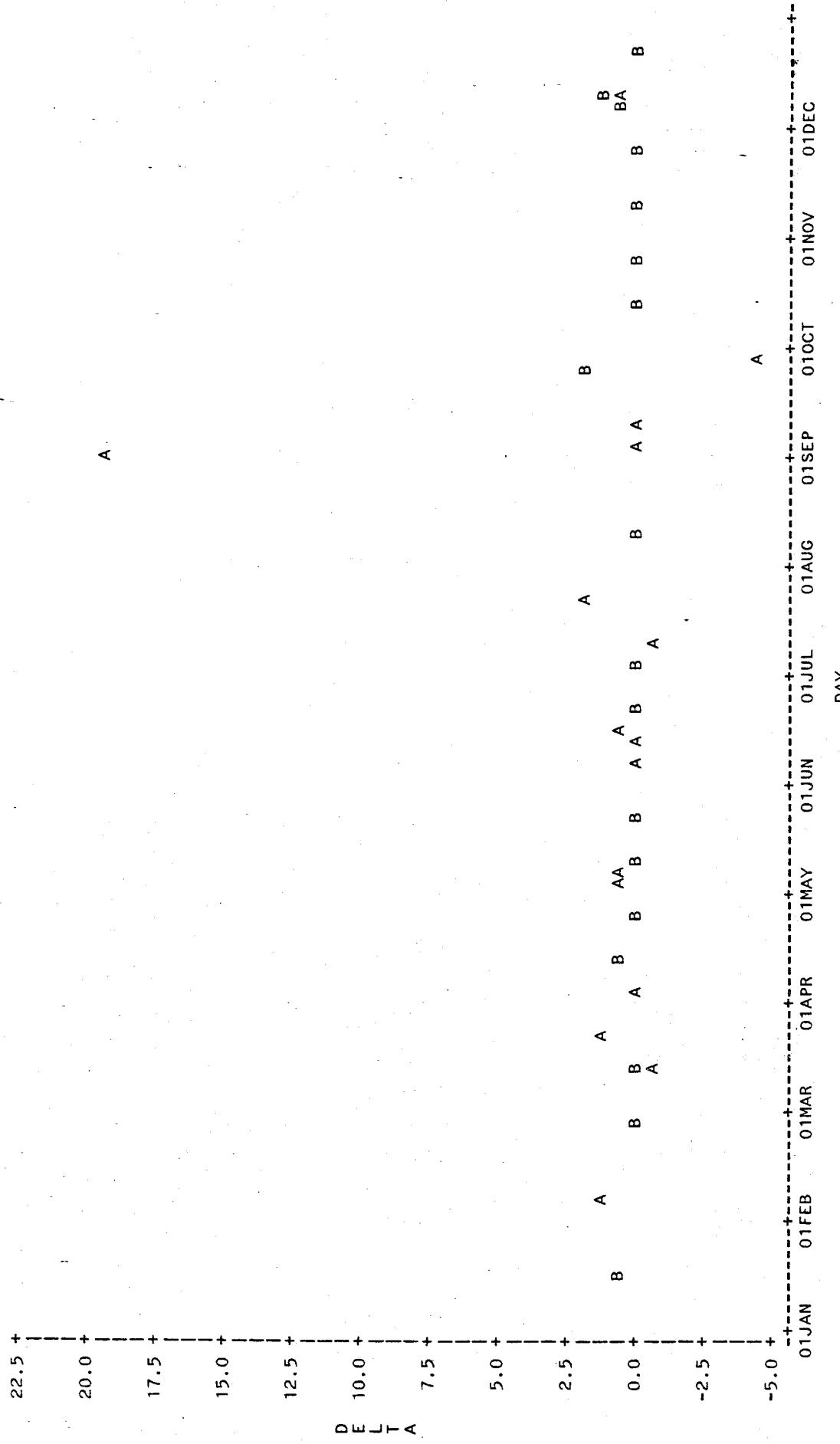
Binomial: ns **

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0 *

**Primary test results
* Corroborative results
+ Indicates deletion of abundance=0 to attain additivity

Figure D- 24. Summary of Test Results for Mysidopsis cathengelae, Juvenile.

SPCODE=Mysidopsis cathengelae STAGE=JUVENILE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE 1 OBS HIDDEN

Figure D-25. Plot of preoperational (B) and operational (A) Delta values for *Mysidopsis cathengelae* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Mysidopsis catheguae STAGE=JUVENILE

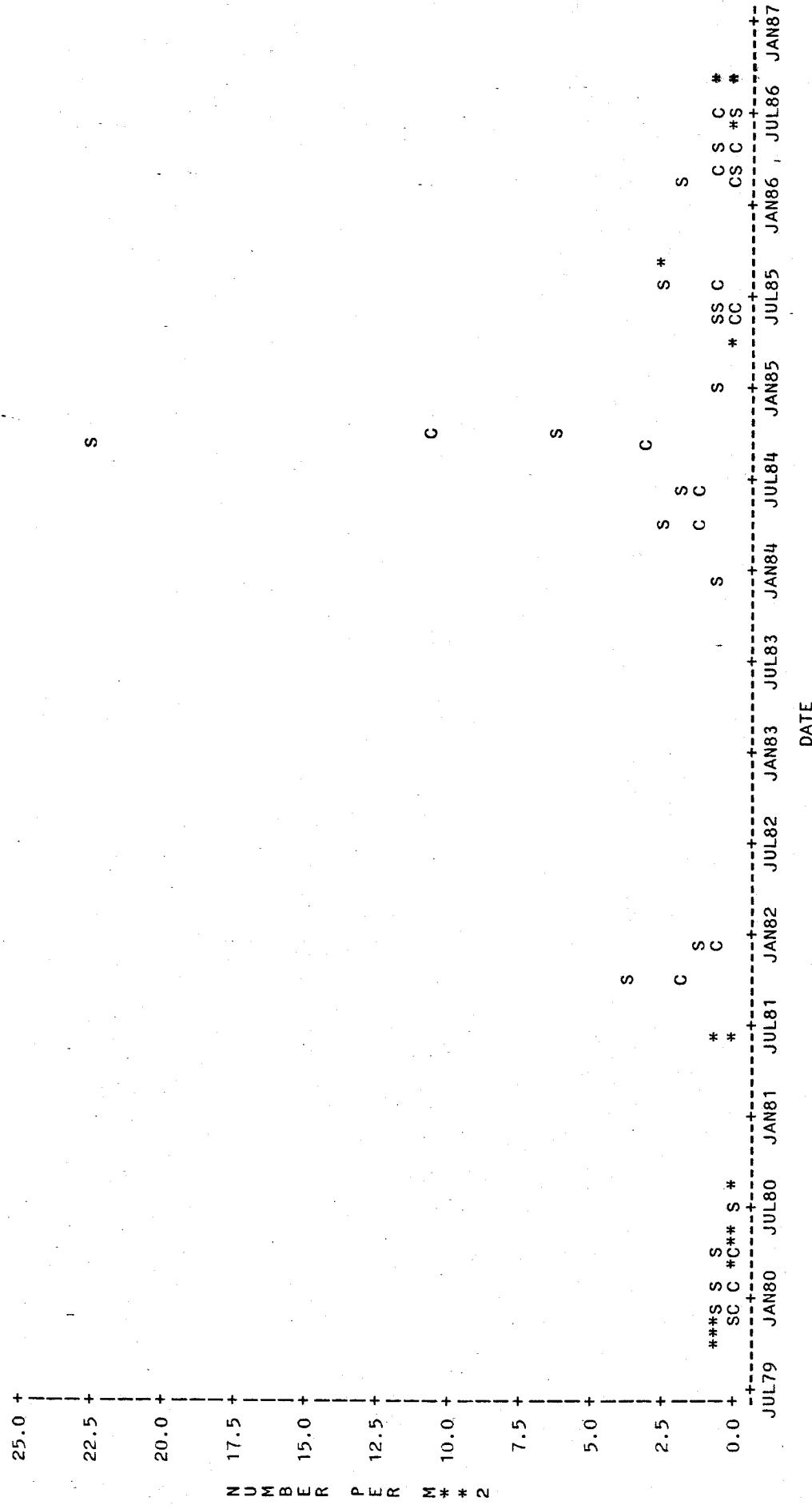


Figure D-26. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis catheguae* juveniles. Similar abundances at both locations are designated by asterisks.

D-29

TAXON: Holmesimysis costata
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	16	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
	Note:	Before/After	After				
none	A	sig+	ns/sig	ns/ns			
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	45.5	.19/.16
$\log(x+.1)$	B	ns	ns/sig	ns/ns	.10	62.0	.17/.10
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: $\log(x)$: ns: second order model
* Transformation 2: $\log(x+.1)$: ns: second order model

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

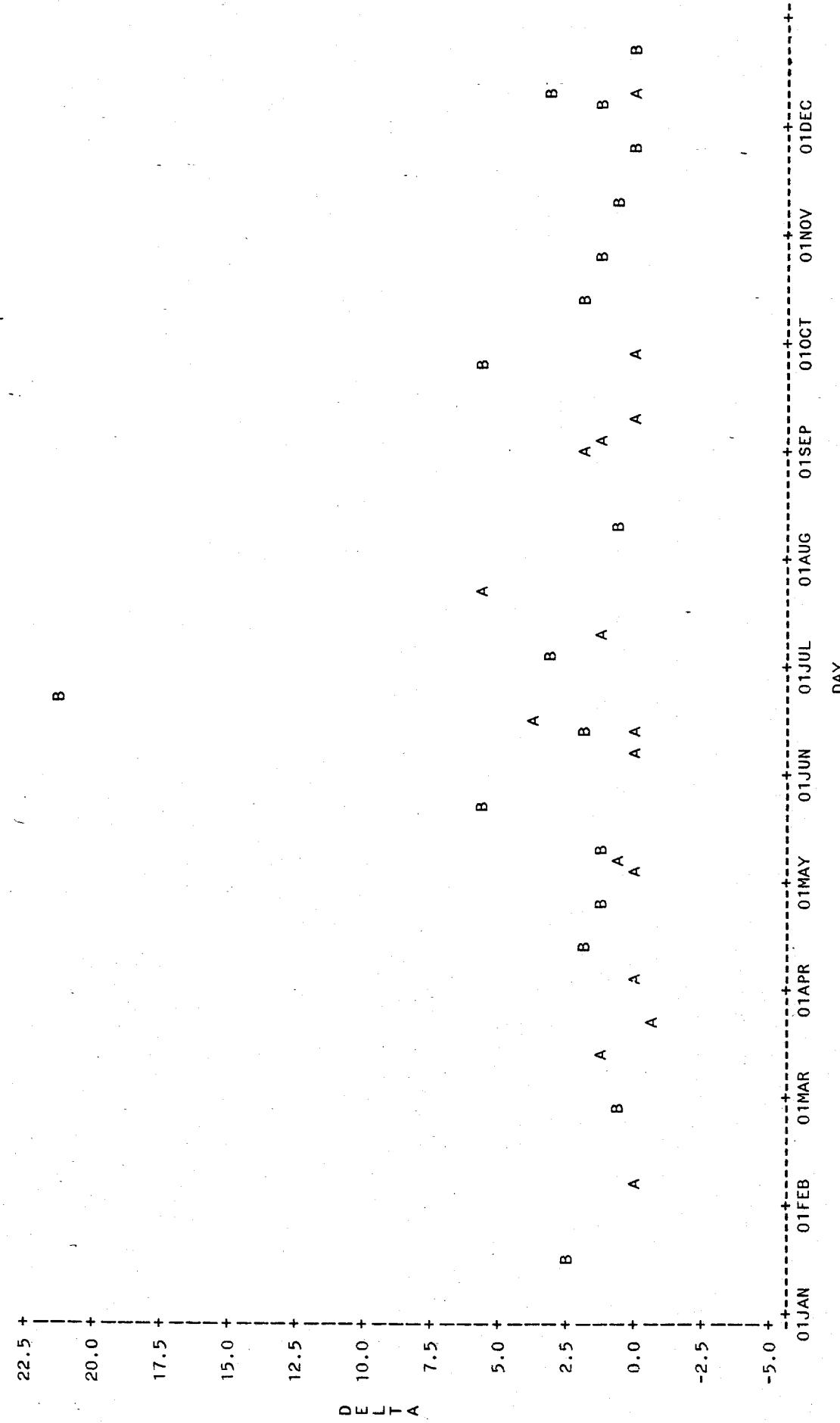
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 27. Summary of Test Results for Holmesimysis costata,
All Stages Combined.

SPCODE=Holmesimysis costata STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE 1 OBS HIDDEN

Figure D-28. Plot of preoperational (B) and operational (A) Delta values for Holmesimysis costata all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-31

SPCODE=Holmesimyssis costata STAGE=ALL

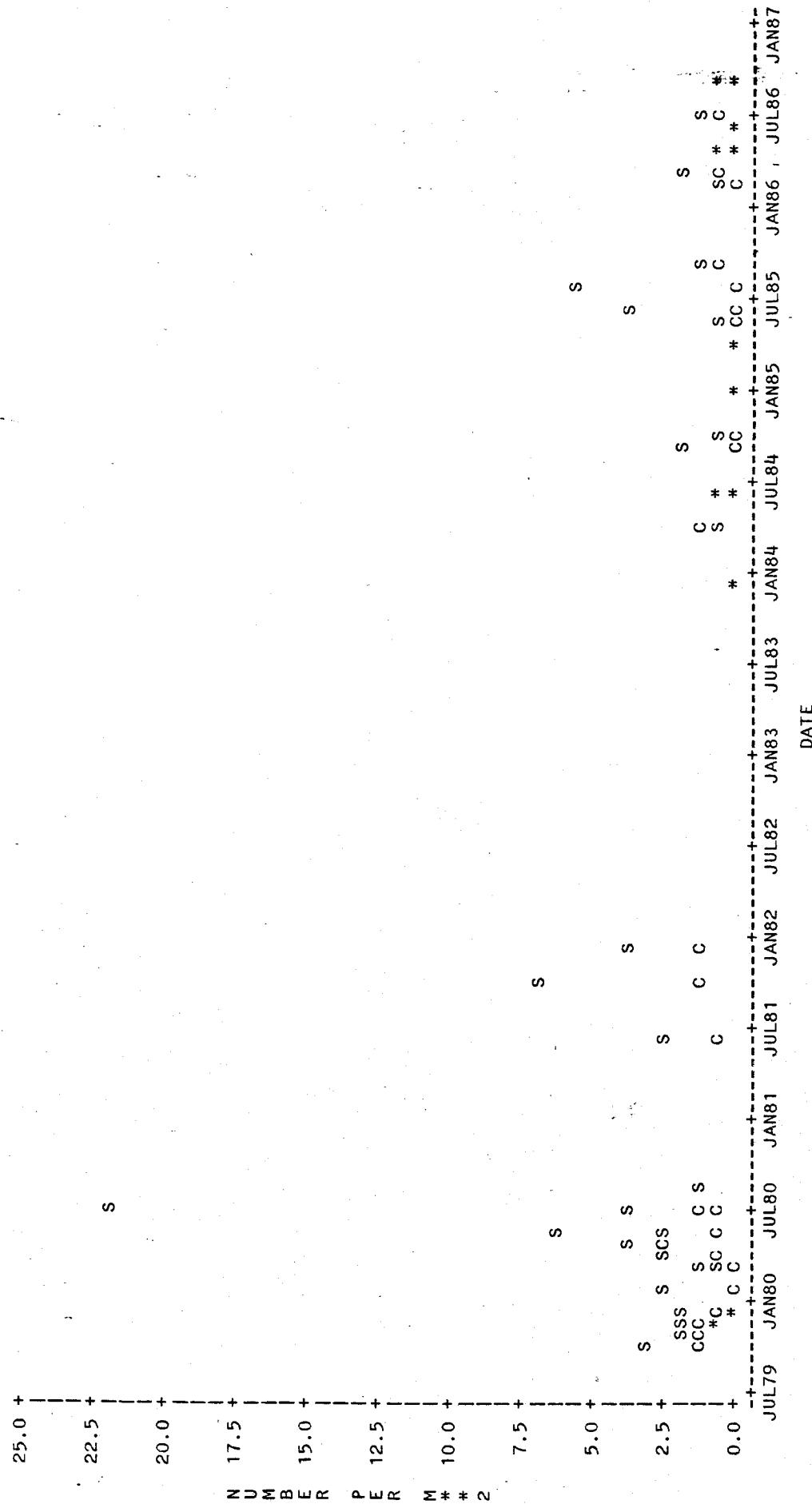


Figure D-29. Abundance values at SONGS (S) and Control (C) plotted through time for *Holmesimyssis costata* all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages Combined	B or C	4.4	4.2	2.5	2.0		
	A-S	4.8	3.9	2.6	1.9		
Adults	B or C	4.2	3.9	2.5	2.2		
	A-S	4.9	3.9	2.4	1.9		
Immatures	B or C	4.2	4.1	2.4	2.1		
	A-S	4.6	4.0	2.6	1.9		
Juveniles	B or C	3.3	3.2	2.0			
	A-S	3.3	3.0	1.8			

Figure D-30. Cross-shelf distributional patterns for Holmesimysis costata. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Holmesimysis costata
Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u> <u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	15	13	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note: Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	A,D	sig	sig/ns	sig/ns		
$\log(x+0)$	N/A					
$\log(x+.1)$	B	ns	sig/sig	ns/ns		
$\log(x+1)$	A	sig+	sig/sig	ns/ns		

Chi Square; Ho: even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: $\log(x+.1)$: N/A
Transformation 2: N/A

F

Binomial: ns**

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0*

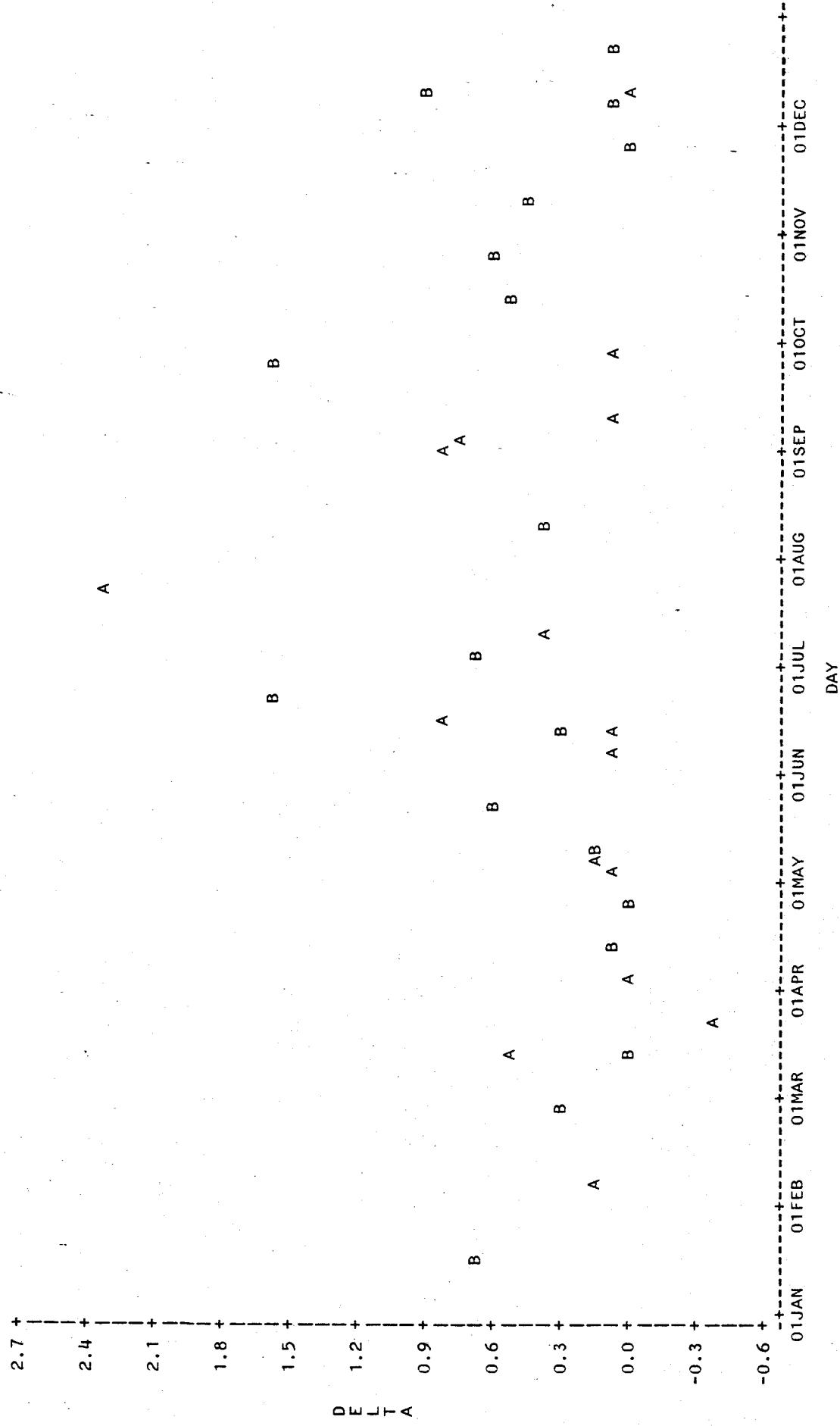
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 31. Summary of Test Results for Holmesimysis costata,
Adult.

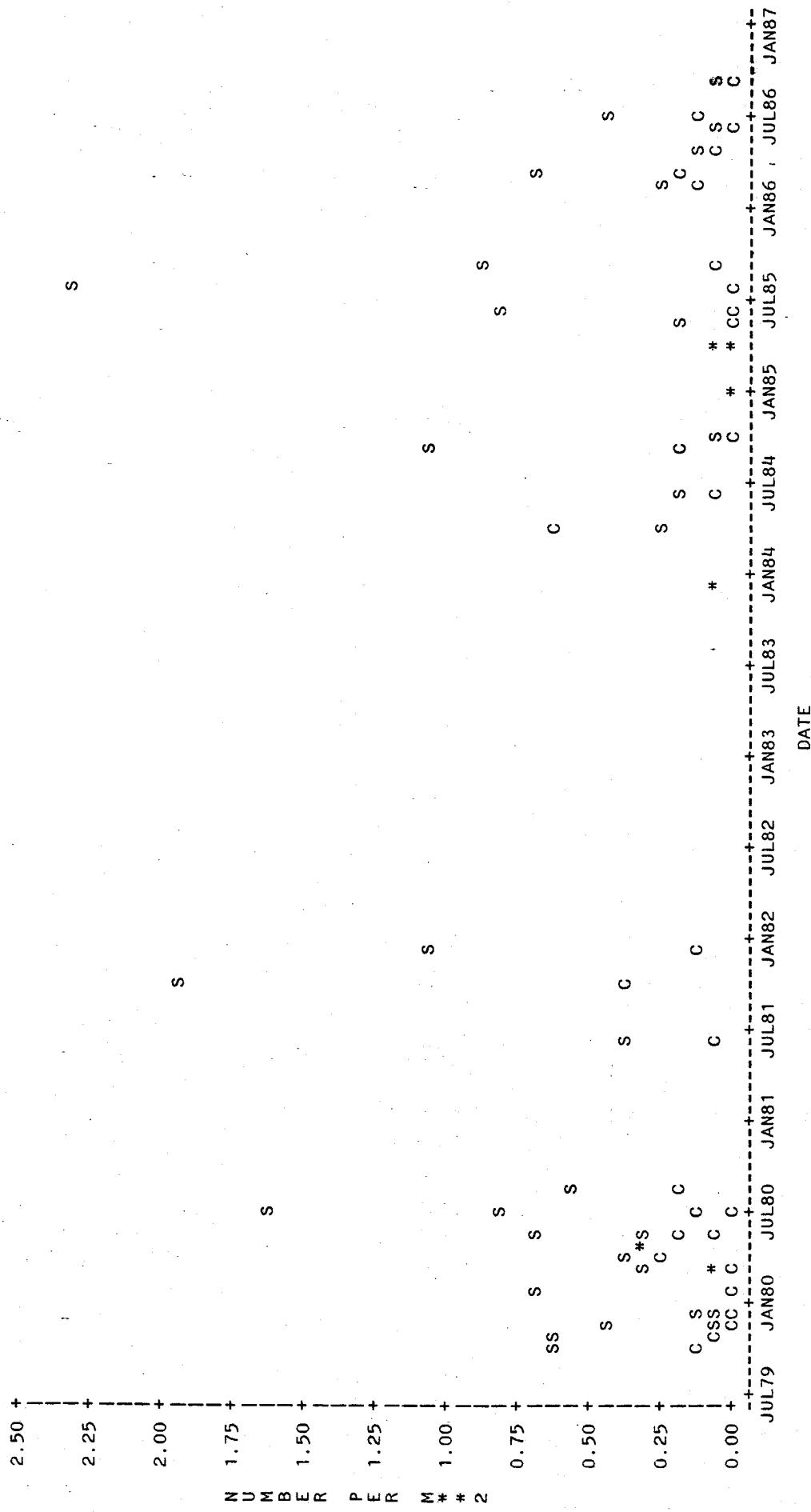
SPCODE=Holmesimyss costata STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-32. Plot of preoperational (B) and operational (A) Delta values for *Holmesimyss costata* adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Holmesimyss costata STAGE=ADULT



NOTE: 6 OBS HIDDEN

Figure D-33. Abundance values at SONGS (S) and Control (C) plotted through time for Holmesimyss costata adults. Similar abundances at both locations are designated by asterisks.

Taxon: Holmesimysis costata
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	16	
$\log(x+0)$	19	11	
$\log(x+\text{constant})$	19	16	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/ Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	A	sig+	ns/ns	ns/ns		
$\log(x+0)$	N/A					
$\log(x+.1)$		ns	ns/ns	ns/ns		
$\log(x+1)$	A	sig+	ns/ns	ns/ns		

Chi Square; Ho:even distribution of zeroes in BACI cells: sig

TEST RESULTS

BACI t-test

See Key Note:

Transformation 1: $\log(x+.1)$: N/A
Transformation 2: N/A

F

Nonparametric (Wilcoxon Rank Sums test)

F

Transformation 1: $\log(x+.1)$: N/A
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns**

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0*

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 34. Summary of Test Results for Holmesimysis costata,
Immature.

SPCODE=Holmesimyssis costata STAGE=IMMATURE

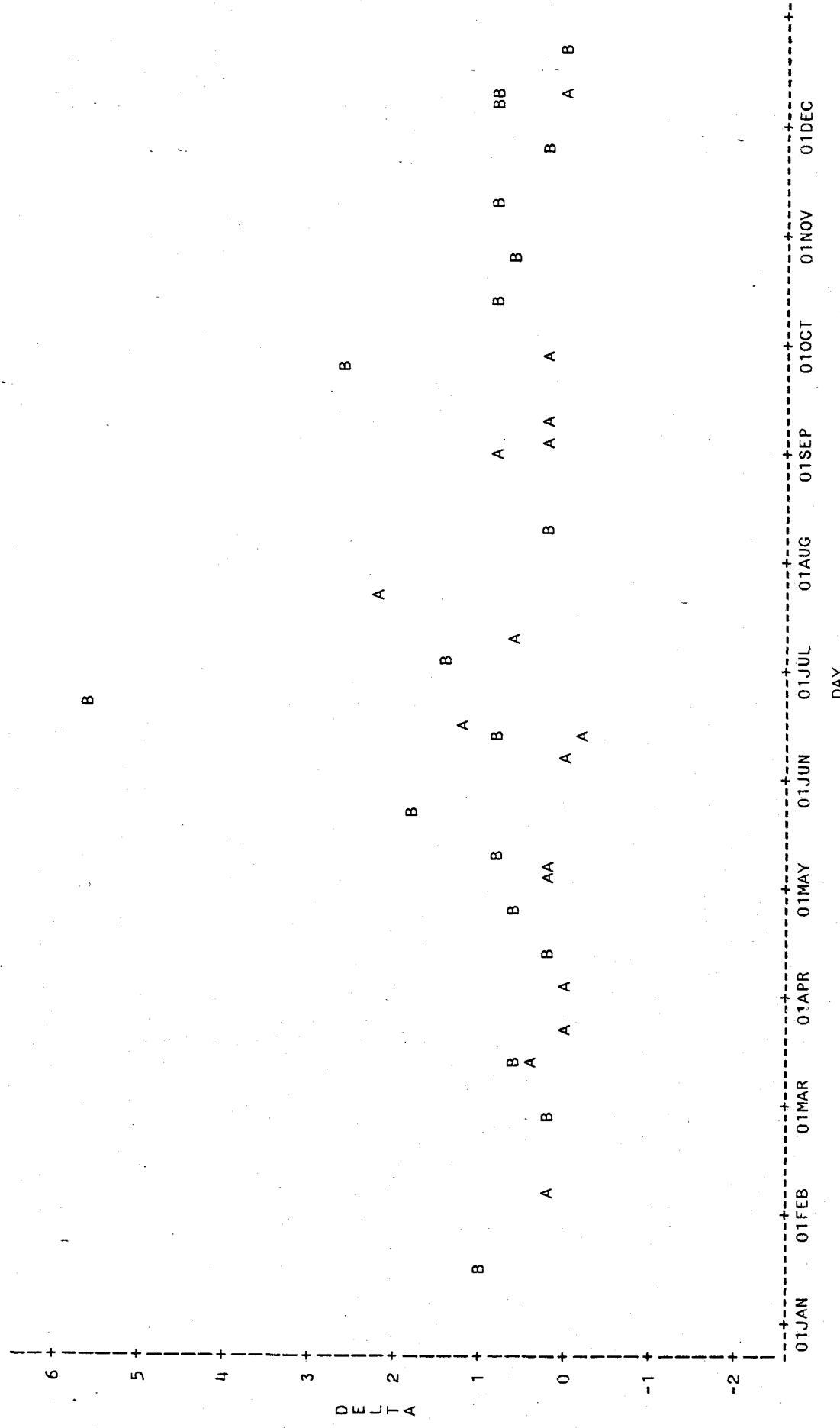


Figure D-35. Plot of preoperational (B) and operational (A) Delta values for *Holmesimyssis costata* immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Holmesimyss costata STAGE=IMMATURE

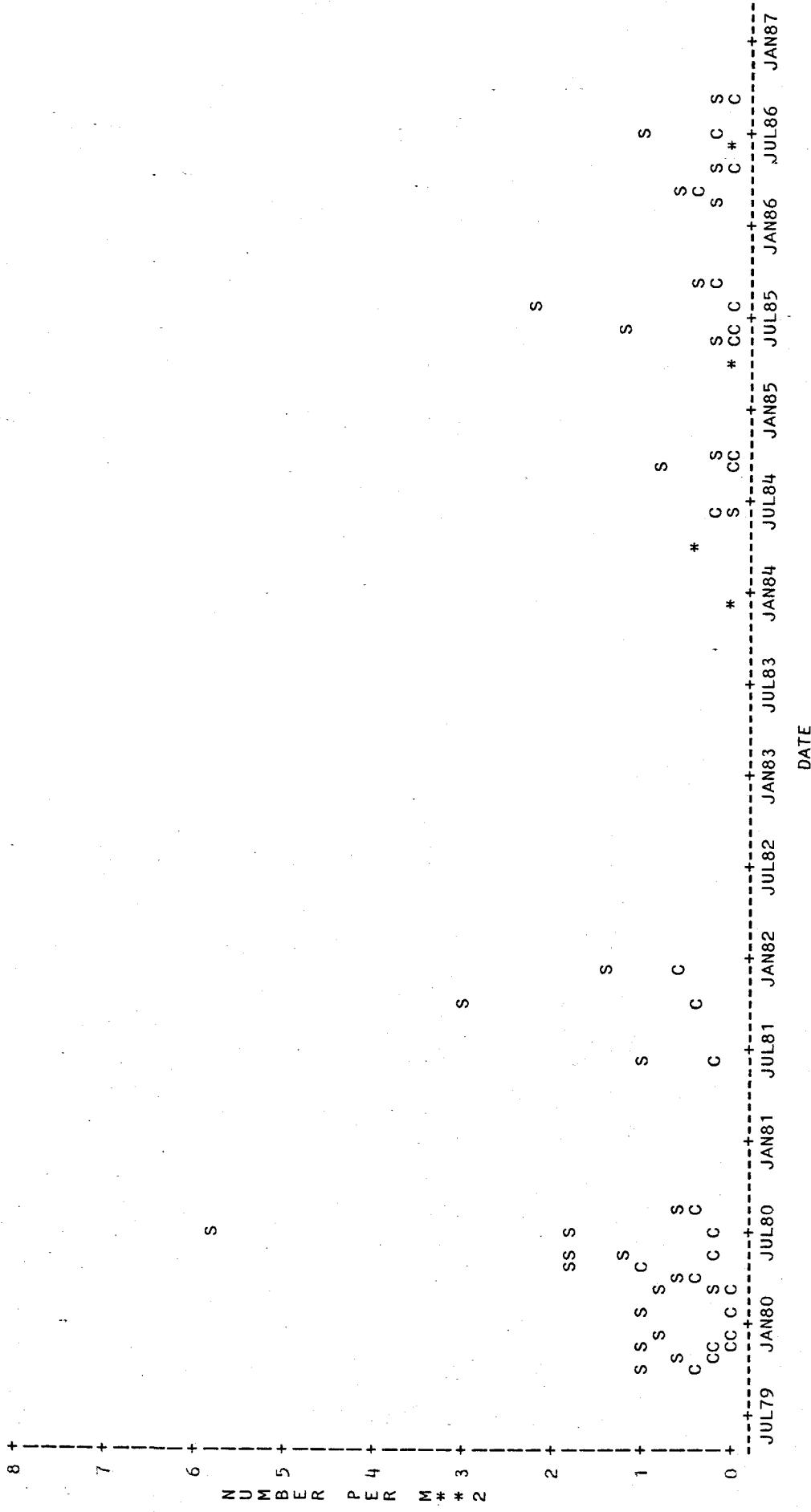


Figure D-36. Abundance values at SONGS (S) and Control (C) plotted through time for *Holmesimyss costata* immatures. Similar abundances at both locations are designated by asterisks.

Taxon: Holmesimysis costata
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	15	
$\log(x+0)$	19	12	
$\log(x+\text{constant})$	19	15	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Abun/Sprse
none	A	sig+	ns/ns		ns/ns		
$\log(x+0)$	N/A						
$\log(x+.1)$		ns	ns/ns		sig/ns		
$\log(x+1)$	A	sig+	ns/ns		ns/ns		

Chi Square; Ho:even distribution of zeroes in BACI cells: sig

TEST RESULTS

BACI t-test

See Key Note:

Transformation 1: $\log(x+.1)$: N/A F
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

F

Transformation 1: $\log(x+.1)$: N/A
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns**

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0*

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 37. Summary of Test Results for Holmesimysis costata, Juvenile.

SPCODE=Holmesimyssis costata STAGE=JUVENILE

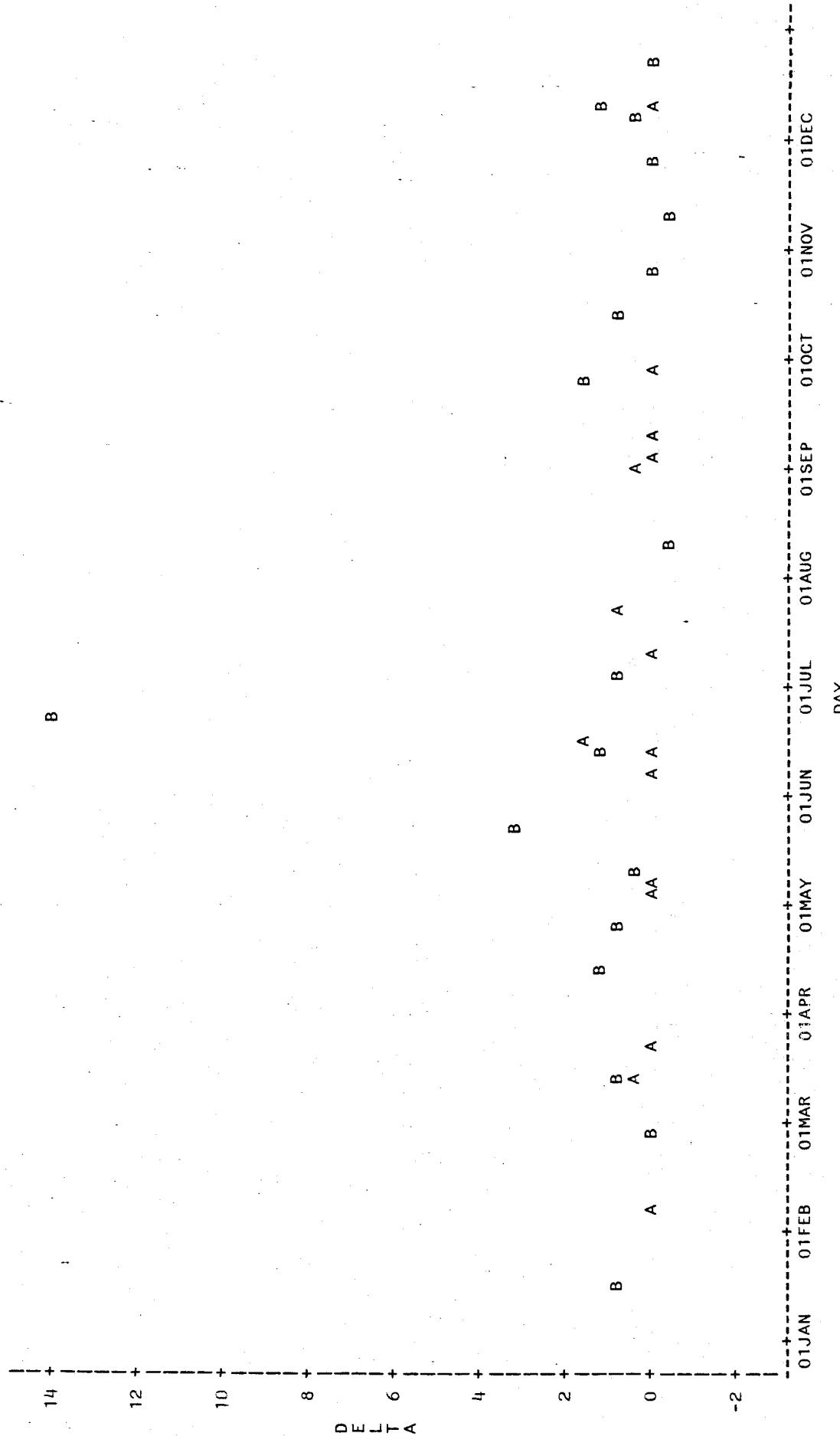


Figure D-38. Plot of preoperational (B) and operational (A) Delta values for *Holmesimyssis costata* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-41

SPCODE=Holmesimyss costata STAGE=JUVENILE

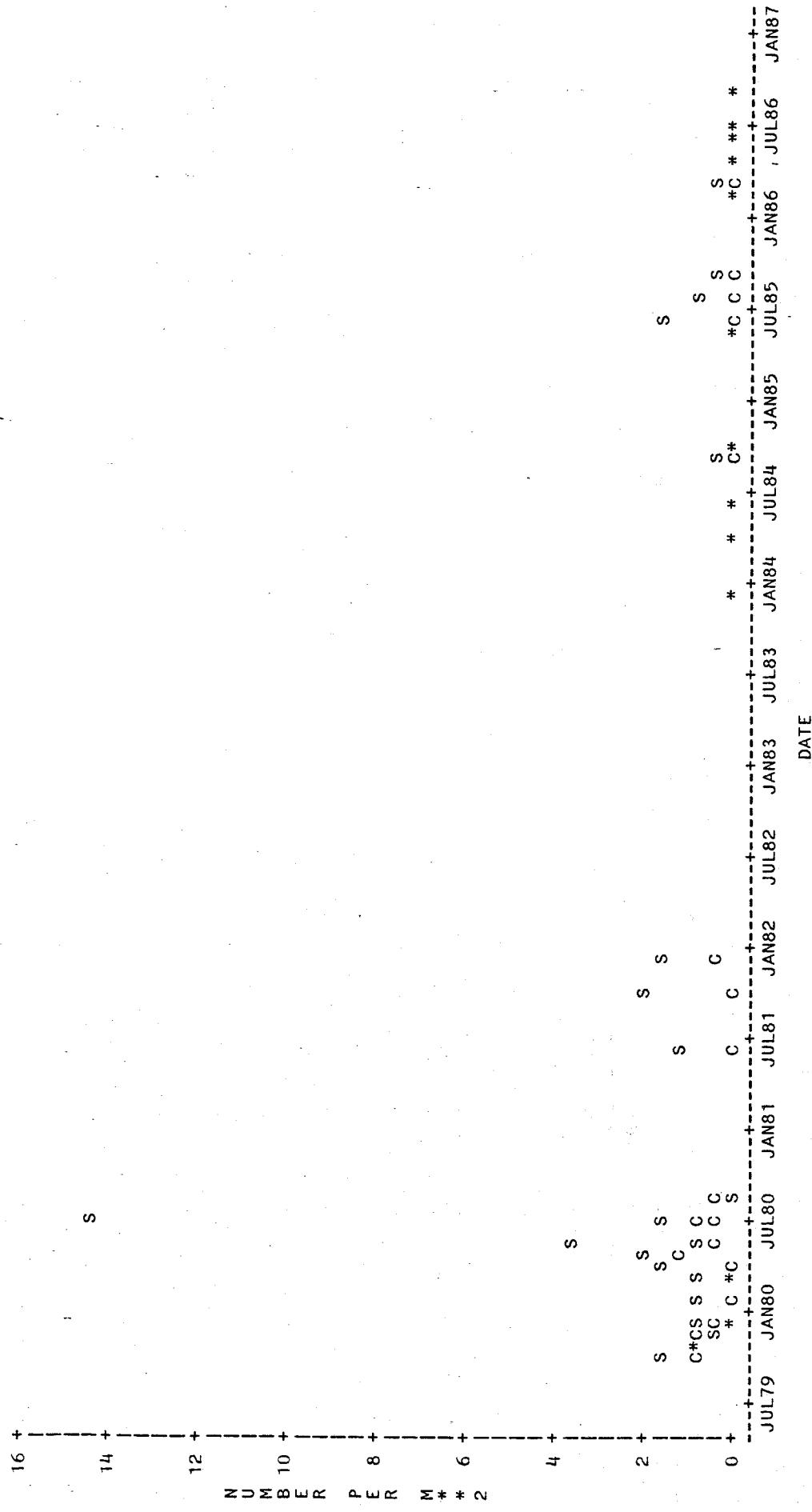


Figure D-39. Abundance values at SONGS (S) and Control (C) plotted through time for *Holmesimyss costata* juveniles. Similar abundances at both locations are designated by asterisks.

D-42

TAXON: Acanthomysis davisii

Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	15	
$\log(x+0)$	19	9	
$\log(x+\text{constant})$	19	15	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	81.8
$\log(x+0)$	N/A					7.8/.3
$\log(x+.1)$	B	ns	sig/sig	ns/ns	.10	84.5
$\log(x+1)$	B	ns	sig/sig	ns/ns	.10	94.1

Chi Square; Ho:even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: none: ns, second order model

* Transformation 2: $\log(x+.1)$ & $\log(x+1)$:ns, first order model

E

Binomial: ns

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 40. Summary of Test Results for Acanthomysis davisii,
All stages Combined.

SPCODE=Acanthomysis davisii STAGE=ALL

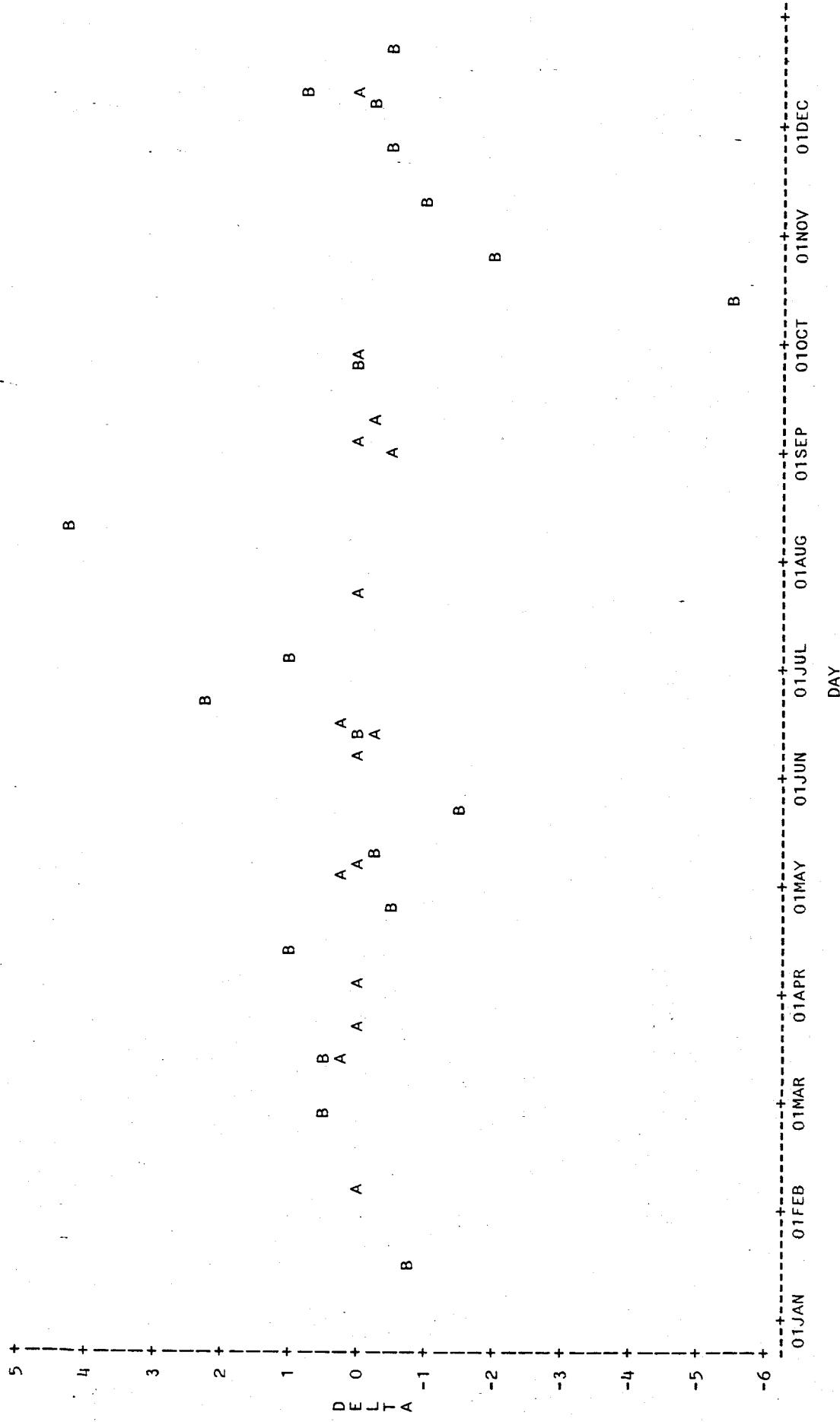
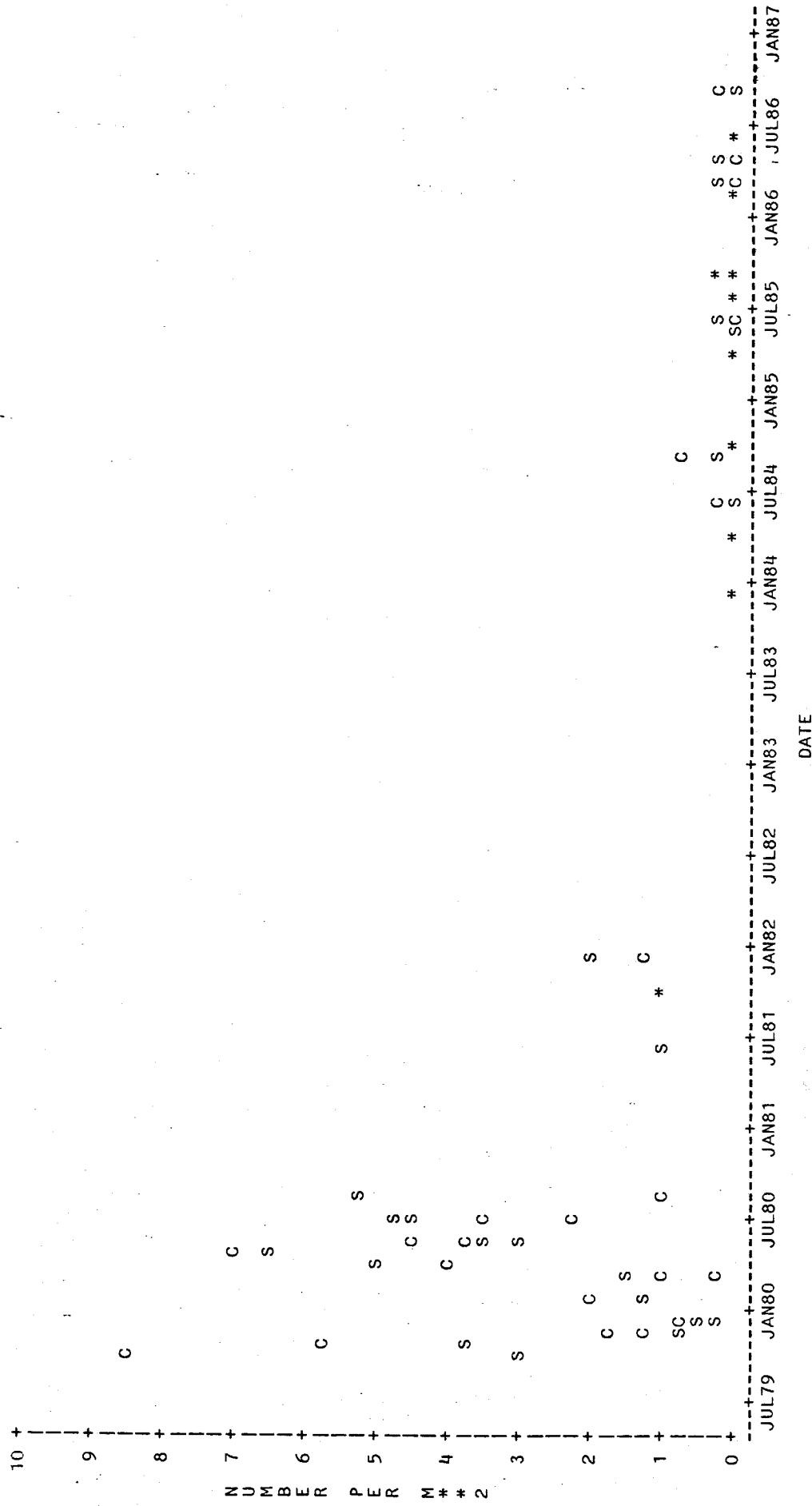


Figure D-41. Plot of preoperational (B) and operational (A) Delta values for Acanthomysis davisii all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Acanthomysis davisii STAGE=ALL



NOTE: 13 OBS HIDDEN

Figure D-42. Abundance values at SONGS (S) and Control (C) plotted through time for Acanthomysis davisii at all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages	B or C	5.0	6.0	5.2	3.5	2.8	2.7
Combined		3.7	5.4	5.6	3.5	3.3	3.3
p=.01	A-S						
Adults	B or C	3.6	3.9	3.3	2.2		
p=.006	A-S	2.7	3.7	3.5	2.5		
Immatures	B or C	4.0	5.1	4.3	2.8	2.4	
	A-S	3.0	4.7	4.8	2.8	2.8	
Juveniles	B or C	4.7	6.0	5.2	3.4	2.9	2.9
p=.03	A-S	3.8	5.0	5.0	3.9	3.5	3.5

Figure D-43. Cross-shelf distributional patterns for Acanthomysis davisii. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Acanthomysis davisii
Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>	<u>Deleted for Additivity</u>
Untransformed	19	12		
$\log(x+0)$	19	5		
$\log(x+\text{constant})$	19	12		

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends Before/ After	α	Power % at α	Delta Variance
	Note:	Before/After	After			Abun/Sprse
none	ns	ns/ns	ns/ns	.10	62.9	.10/.010
$\log(x+0)$	H					
$\log(x+.1)$	B	ns	sig/ns	ns/ns	.10	70.7
$\log(x+1)$	B	ns	sig/ns	ns/ns	.10	68.7

Chi Square; H_0 : even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns first order model E

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 44. Summary of Test Results for Acanthomysis davisii,
Adult.

SPCODE=Acanthomysis davisii STAGE=ADULT

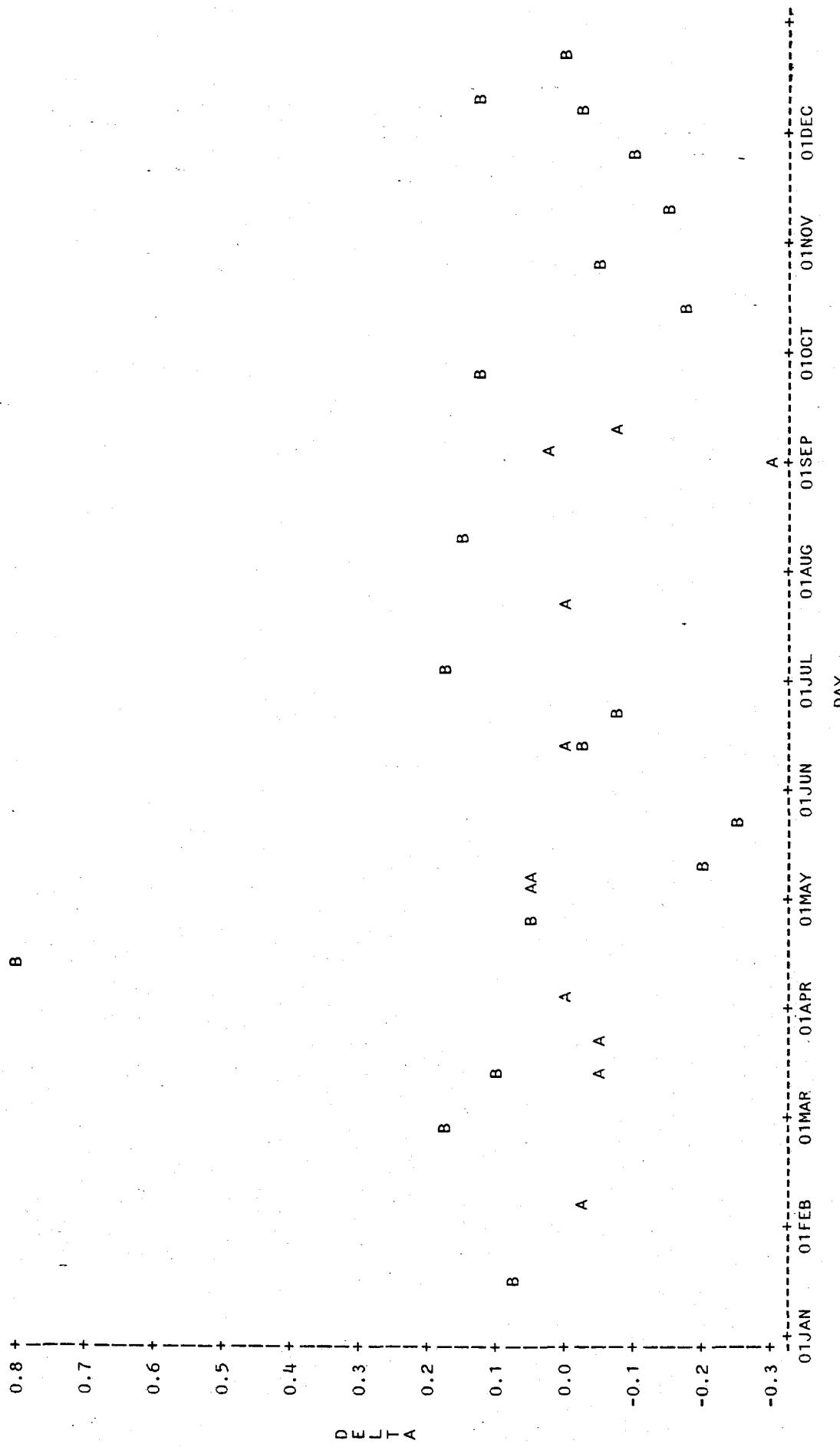


Figure D-45. Plot of preoperational (B) and operational (A) Delta values for *Acanthomysis davisii* adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Acanthomysis davisii STAGE=ADULT

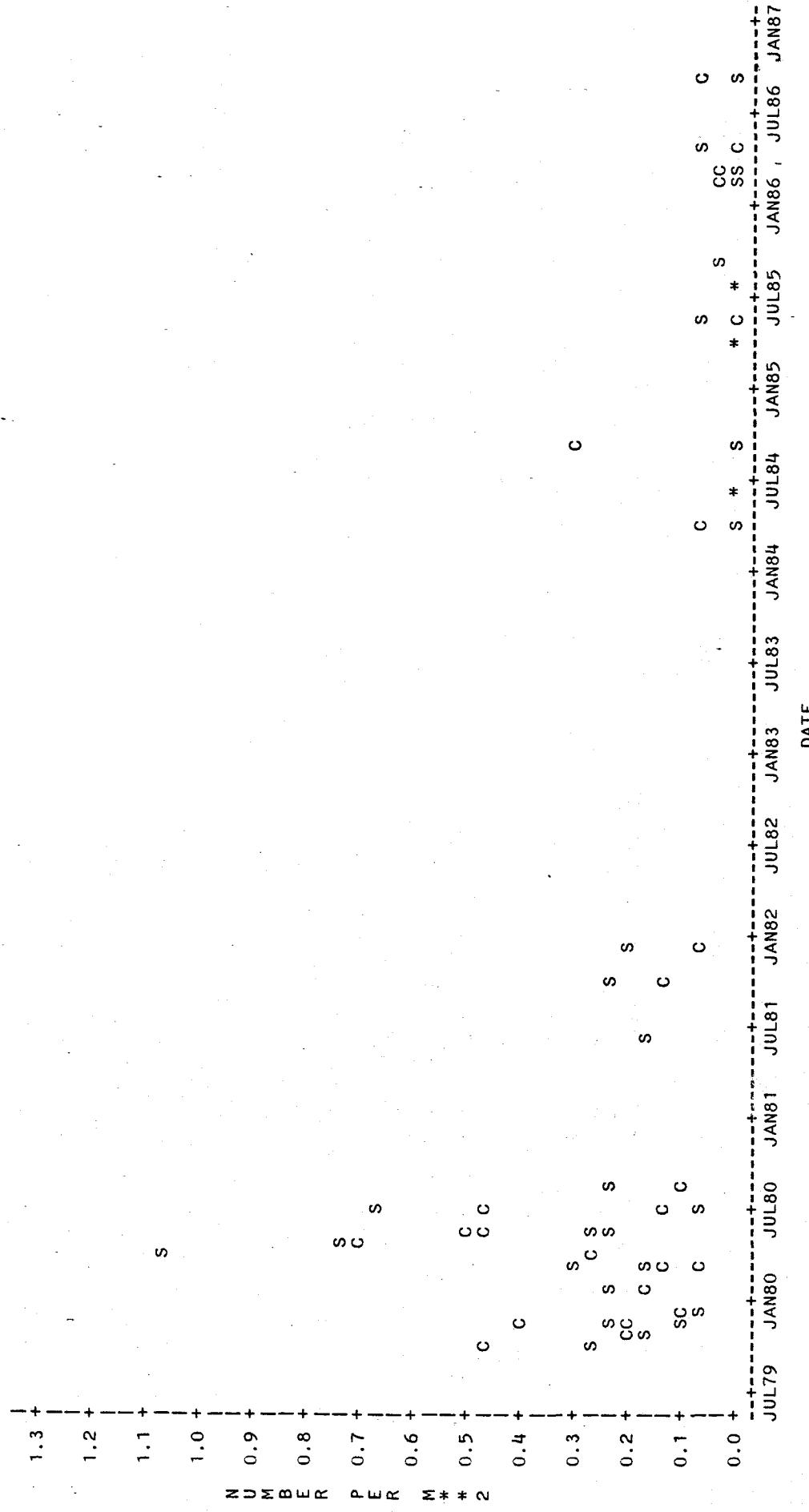


Figure D-46. Abundance values at SONGS (S) and Control (C) plotted through time for *Acanthomysis davisii* adults. Similar abundances at both locations are designated by asterisks.

D-49

TAXON: Acanthomysis davisii
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u> <u>Deleted for Additivity</u>
Untransformed	19	12	
$\log(x+0)$	19	6	
$\log(x+\text{constant})$	19	12	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.10	70.4	1.2/.080
$\log(x+0)$	N/A					
$\log(x+.1)$	ns	ns/ns	ns/ns	.10	83.2	.12/.040
$\log(x+1)$	ns	ns/ns	ns/ns	.10	78.8	.04/.010

Chi Square; Ho:even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$

E

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 47. Summary of Test Results for Acanthomysis davisii,
Immature

SPCODE=Acanthomysis davisii STAGE=IMMATURE

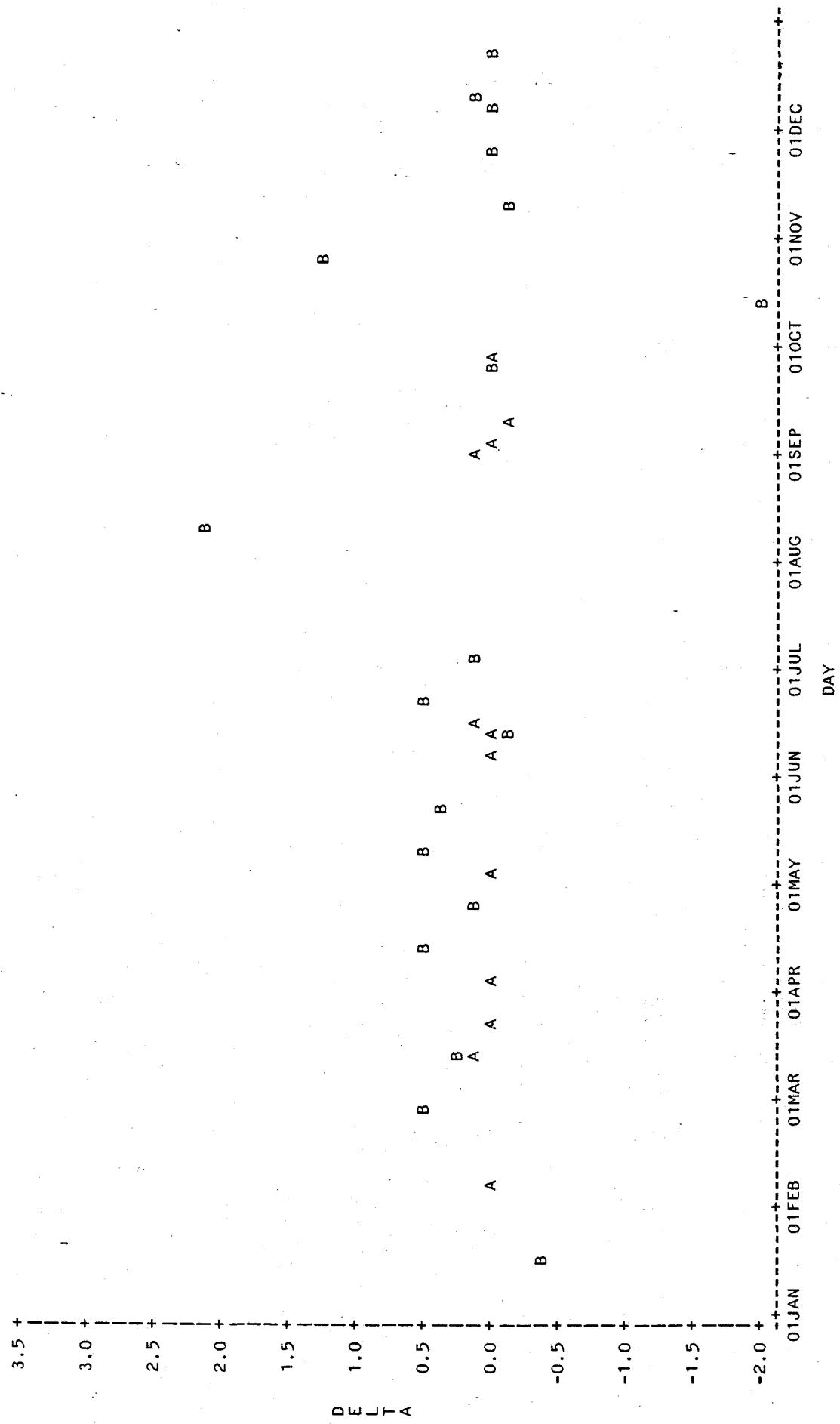


Figure D-48. Plot of preoperational (B) and operational (A) Delta values for *Acanthomysis davisii* immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

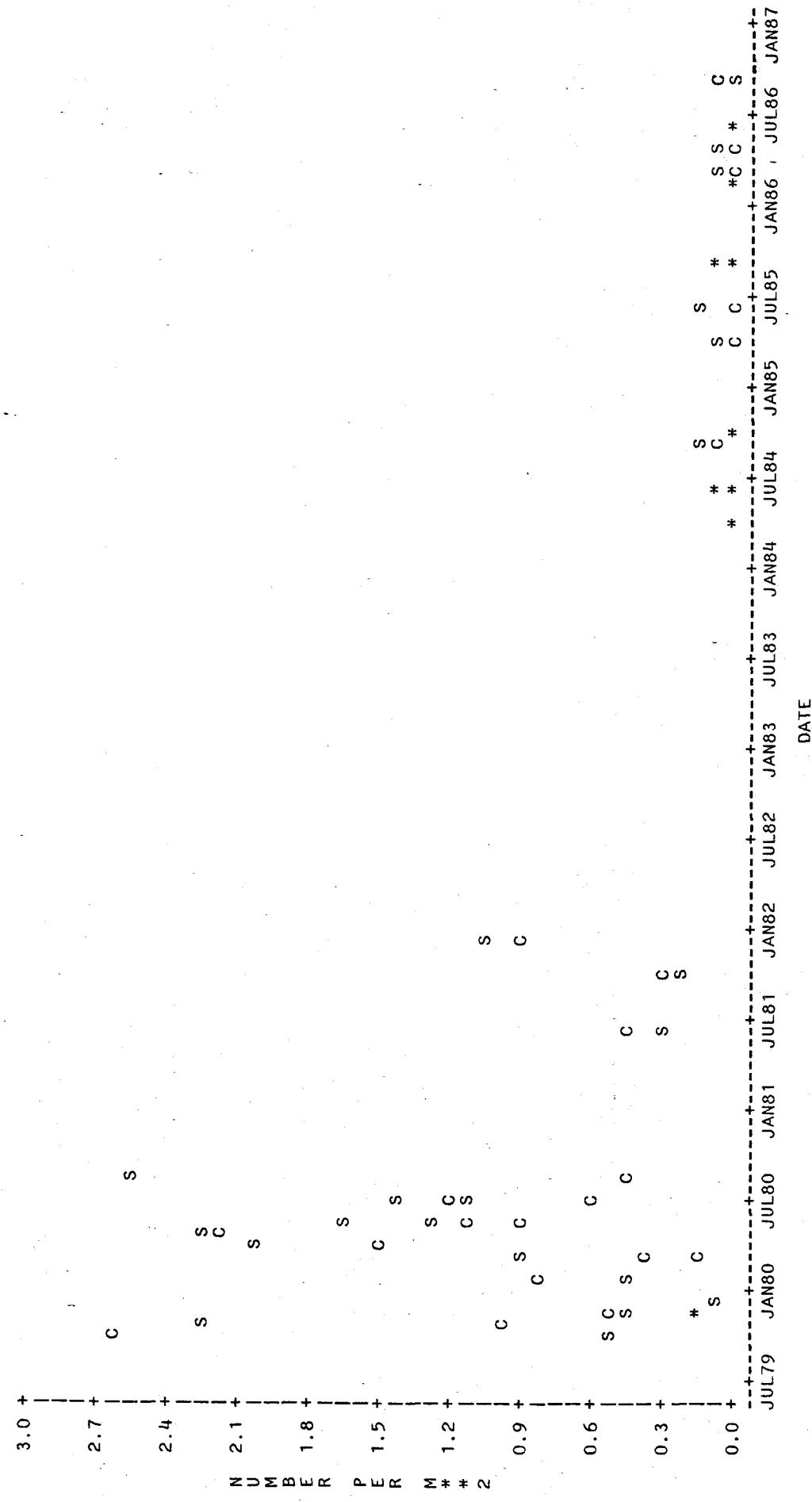


Figure D-49. Abundance values at SONGS (S) and Control (C) plotted through time for *Acanthomysis davisi* immatures. Similar abundances at both locations are designated by asterisks.

TAXON: Acanthomysis davisii
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	11	
$\log(x+0)$	19	5	
$\log(x+\text{constant})$	19	11	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends Before/ After	α	Power % at α	Delta Variance
	Note:	Before/After	After			Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	46.6
$\log(x+0)$	H					3.8/.150
$\log(x+.1)$	D	ns	sig/ns	sig/sig	.10	
$\log(x+1)$	D	ns	sig/ns	sig/ns		

Chi Square; H_0 : even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: none: ns, first order model
Transformation 2: N/A

Binomial: ns*

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

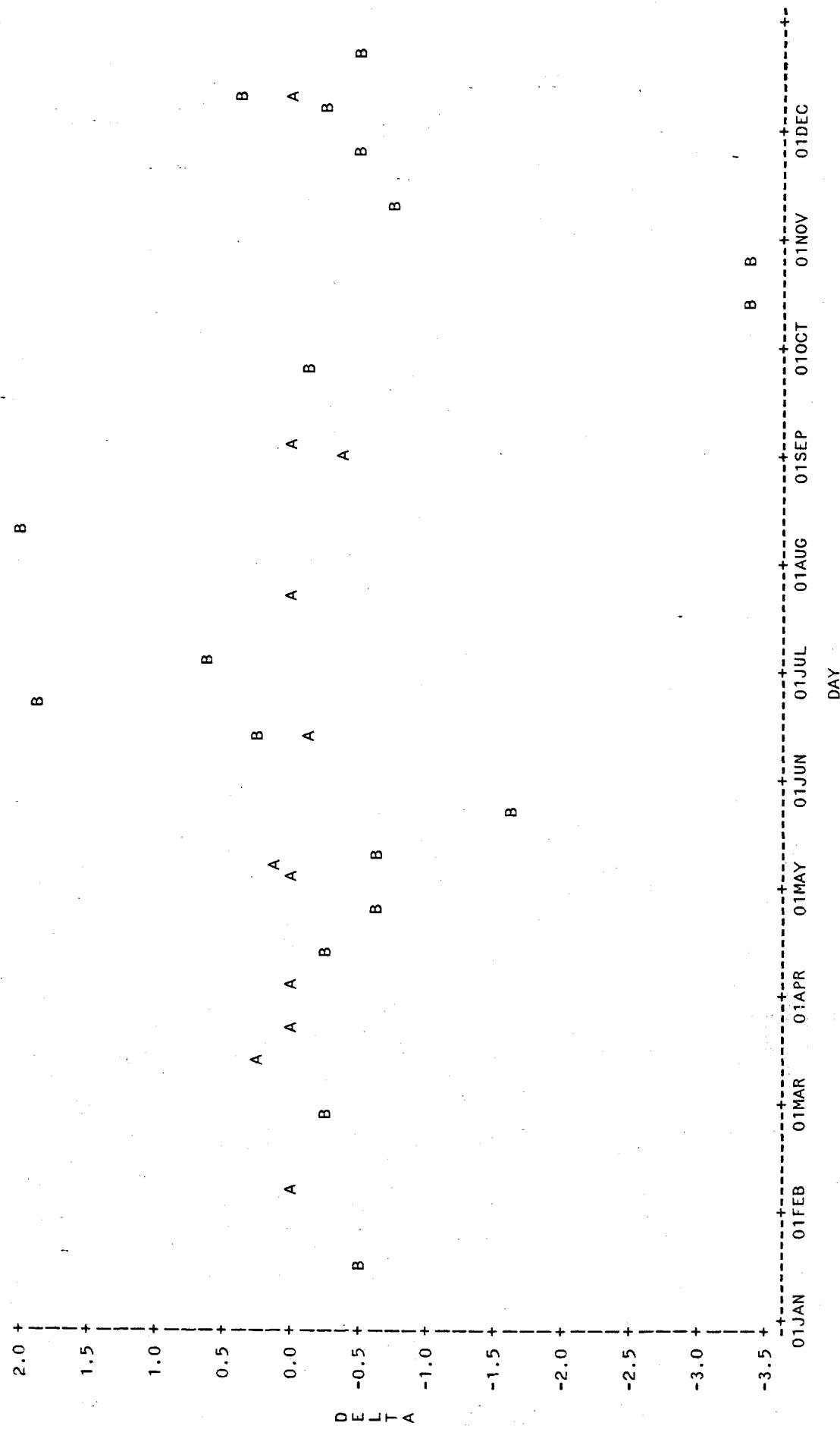
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 50. Summary of Test Results for Acanthomysis davisii, Juvenile.

SPCODE=Acanthomysis davisii STAGE=JUVENILE

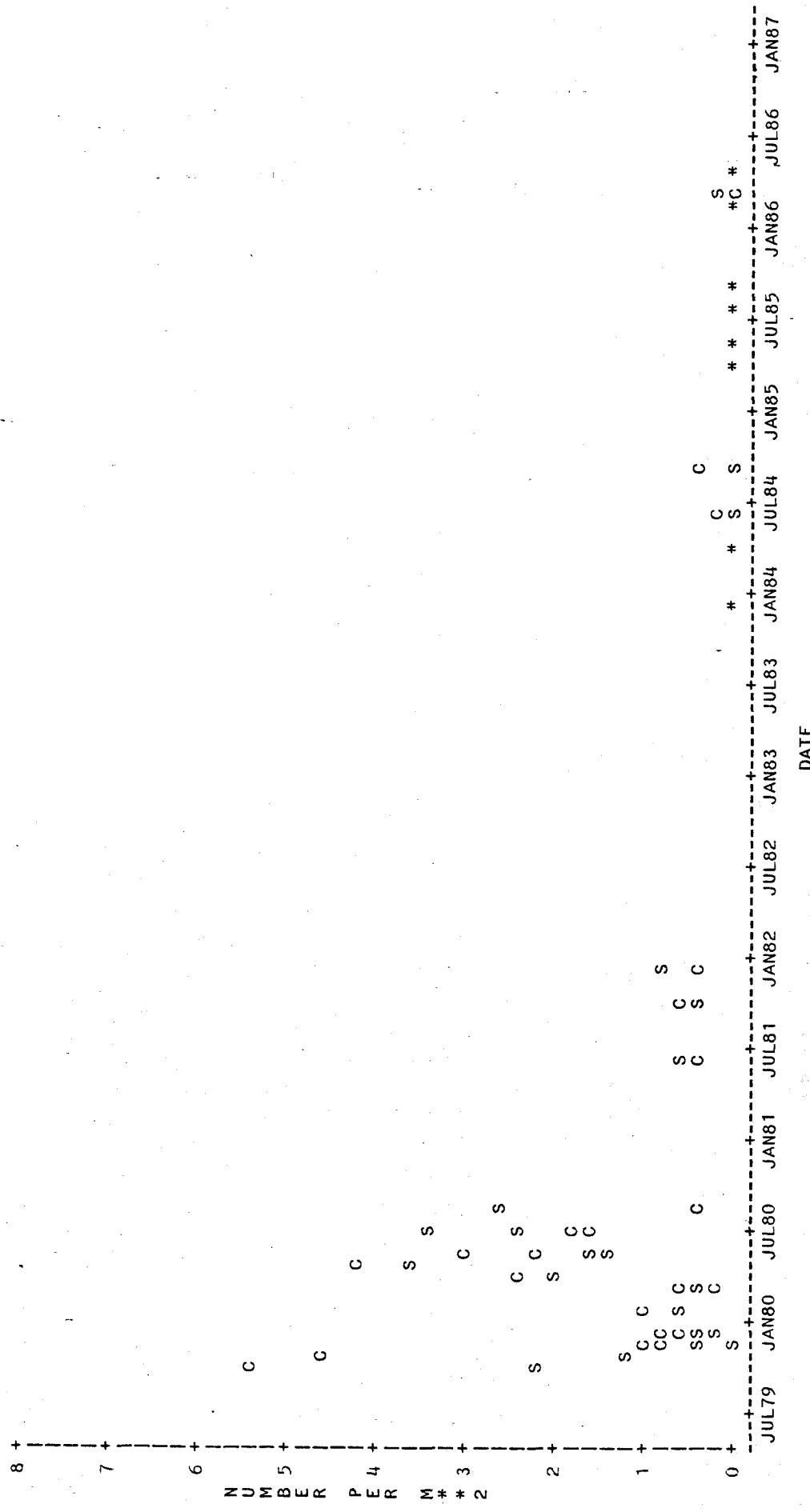


NOTE: 1 OBS HIDDEN

Figure D-51. Plot of preoperational (B) and operational (A) Delta values for *Acanthomysis davisii* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-54

SPCODE=Acanthomysis davisii STAGE=JUVENILE



NOTE: 9 OBS HIDDEN

Figure D-52. Abundance values at SONGS (S) and Control (C) plotted through time for Acanthomysis davisii juveniles. Similar abundances at both locations are designated by asterisks.

TAXON: Neomysis rayii
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u> <u>Deleted for Additivity</u>
Untransformed	19	13	
$\log(x+0)$	18	3	
$\log(x+\text{constant})$	19	13	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.10	43.3	1.6/.010
$\log(x+0)$	H					
$\log(x+.1)$	ns	ns/ns	ns/ns	.10	69.9	.14/.040
$\log(x+1)$	ns	ns/ns	ns/ns	.10	57.6	.05/.002

Chi Square; Ho:even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

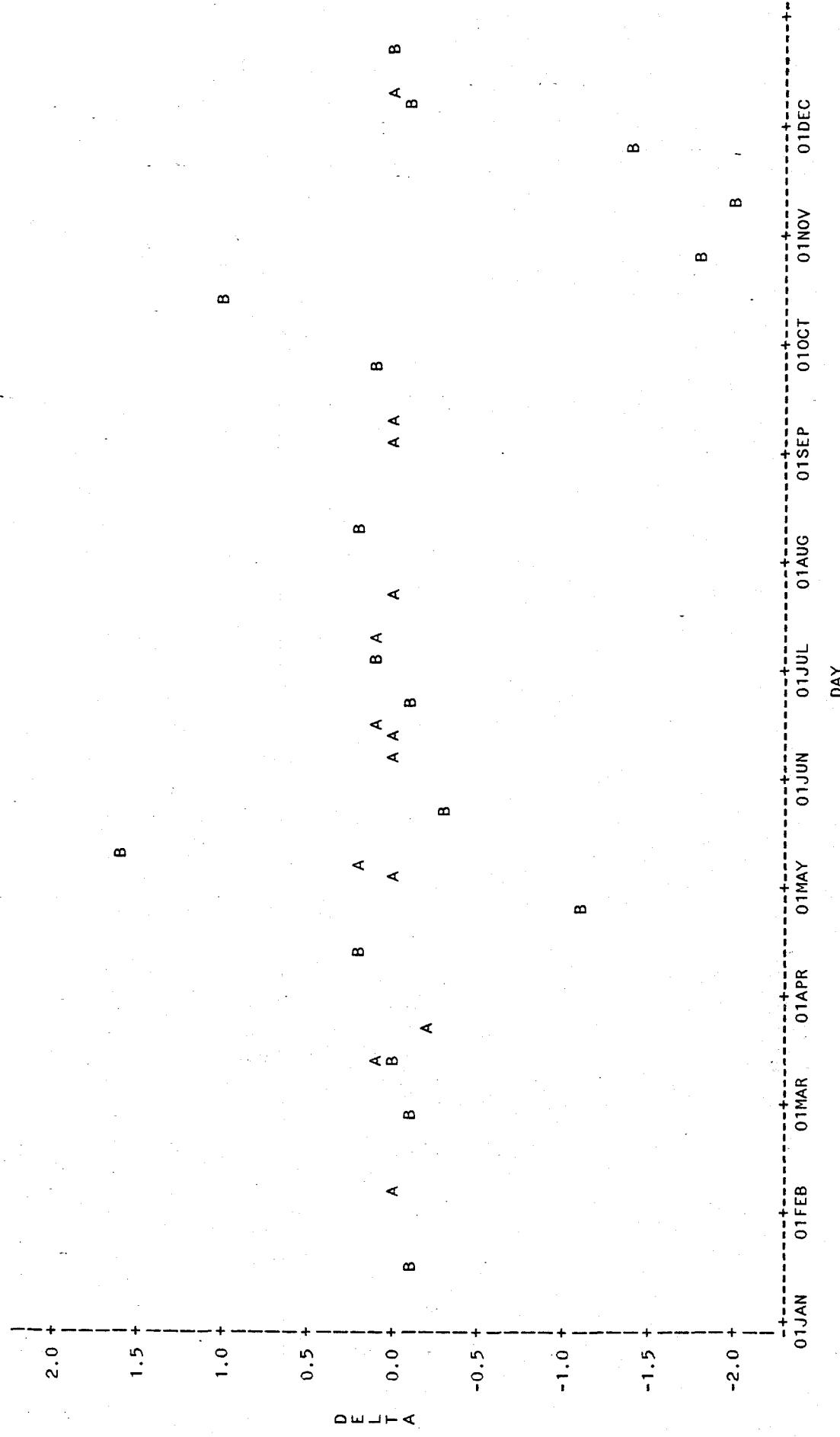
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 53. Summary of Test Results for Neomysis rayii,
All Stages Combined.

SPCODE=Neomysis rayii STAGE=ALL



NOTE:

2 OBS HIDDEN

Figure D-54. Plot of preoperational (B) and operational (A) Delta values for *Neomysis rayii* at all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Neomysis rayii STAGE=ALL

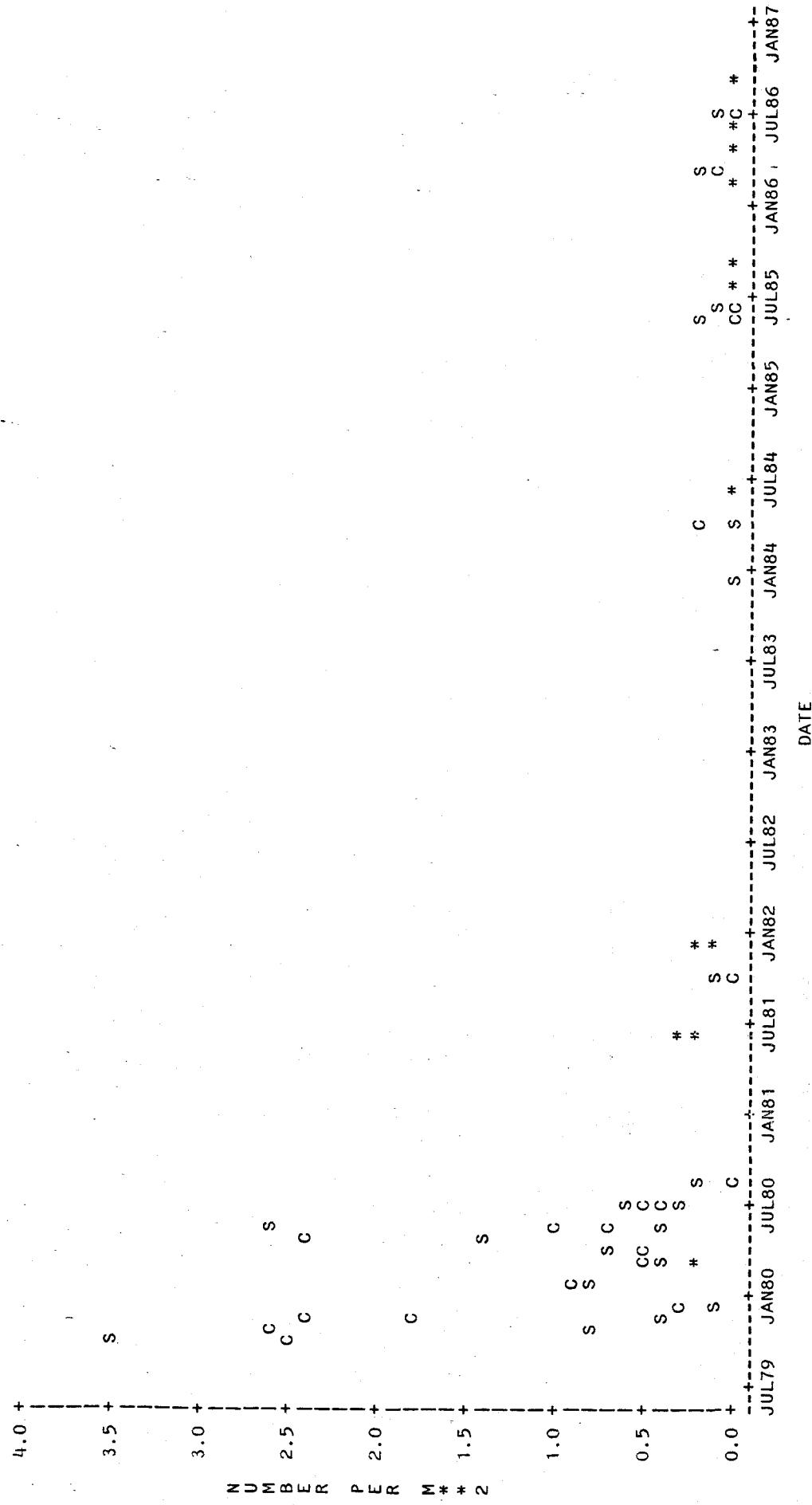


Figure D-55. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis rayii* all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE	B or C	DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages	B or C	4.7	5.8	5.2	3.5	3.0	2.9
	A-S	4.8	5.1	4.1	4.0	3.3	3.3
Adults	B or C	3.1	3.8	3.1	2.5		
	A-S	3.5	3.6	3.1	2.4		
Immatures	B or C	4.2	4.9	4.9	3.5	3.5	3.5
	A-S	4.7	4.5	5.5	3.3	3.3	3.3
Juveniles	B or C	4.0	4.9	4.3	2.9	2.5	
	A-S	3.8	4.4	3.3	3.8	2.9	

Figure D-56. Cross-shelf distributional patterns for Neomysis rayii. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Neomysis rayii
Stage: Adult

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	17	8	
$\log(x+0)$	8	2	
$\log(x+\text{constant})$	17	8	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	28.9 .005/.001
$\log(x+0)$	H					
$\log(x+.1)$	B	ns	sig/ns	ns/ns	.10	27.4 .04/.010
$\log(x+1)$	B	ns	sig/ns	ns/ns	.10	28.7 .001/.00

Chi Square; H_0 : even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Autoregressive Errors t-test

Transformation 1: none: ns first order model
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns first order model C, E

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 57. Summary of Test Results for Neomysis rayii,
Adult.

SPCODE=Neomysis rayii STAGE=ADULT

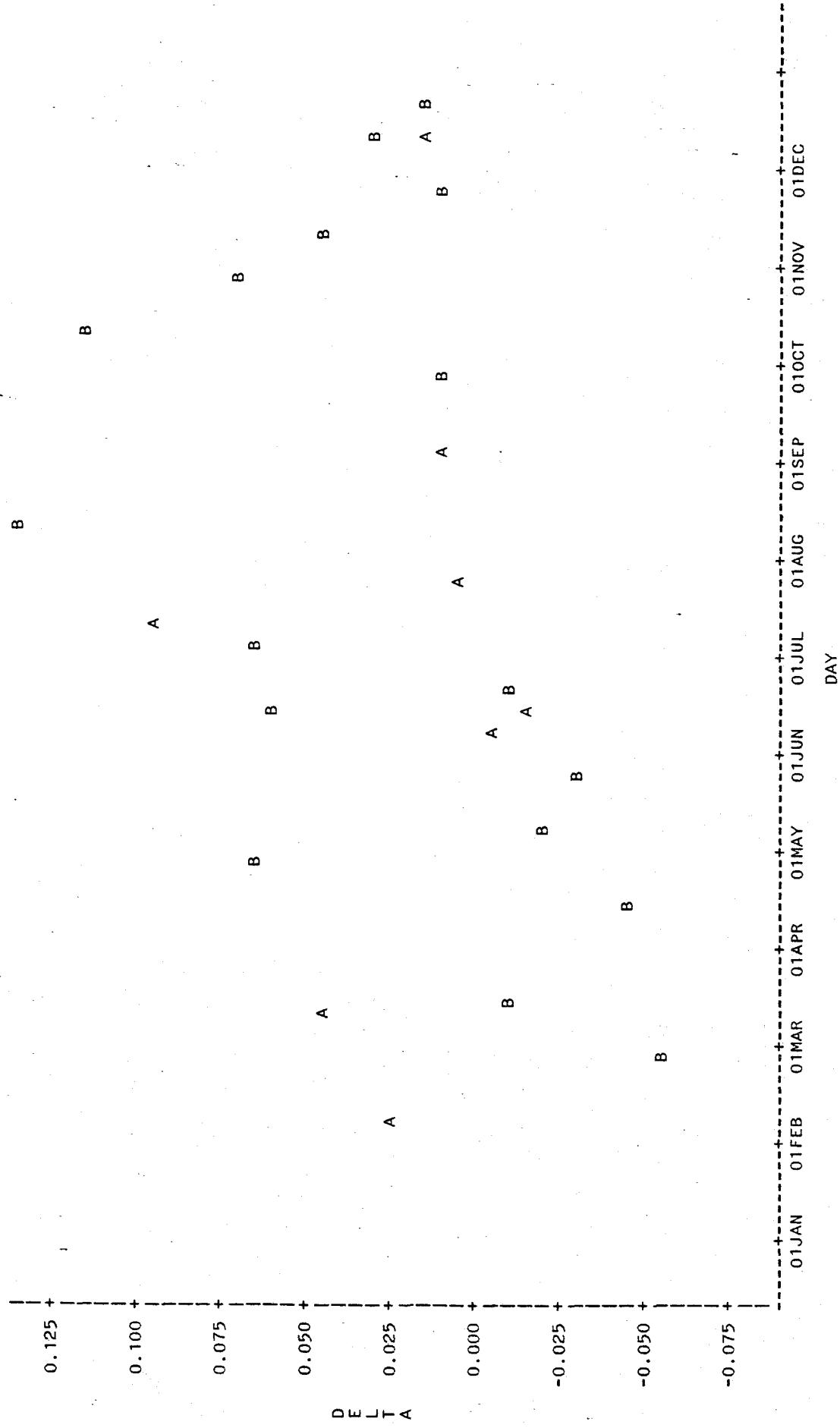
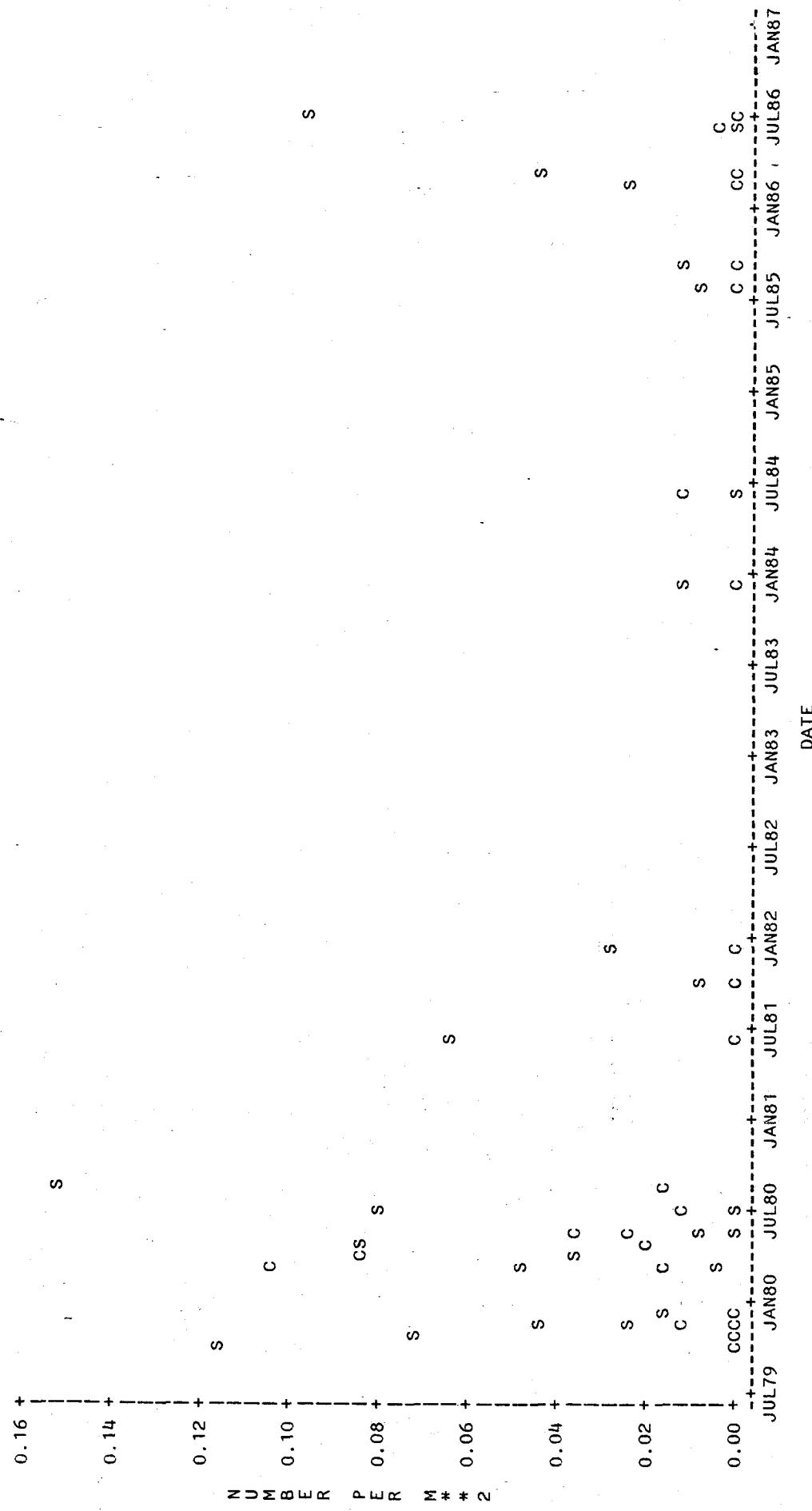


Figure D-58. Plot of preoperational (B) and operational (A) Delta values for *Neomysis rayii* adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Neomysis rayii STAGE=ADULT



NOTE: 1 OBS HIDDEN

Figure D-59. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis rayii* adults. Similar abundances at both locations are designated by asterisks.

D-62

Taxon: Neomysis rayii
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates Deleted for Additivity</u>
Untransformed	18	3	
$\log(x+0)$	9	0	
$\log(x+\text{constant})$	18	3	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns+	sig/	ns/ns	.10	26.8 .004/.001
$\log(x+0)$	H					
$\log(x+.1)$		ns+	sig/	ns/ns	.10	28.4 .02/.010
$\log(x+1)$	B	ns+	sig/	ns/ns	.10	27.3 .001/.000

Chi Square; H_0 : even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Autoregressive Errors t-test

Transformation 1: none: ns first order model

C

Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns first order model

C, E

Binomial: ns

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 60. Summary of Test Results for Neomysis rayii,
Immature.

SPCODE=Neomysis rayii STAGE=IMMATURE

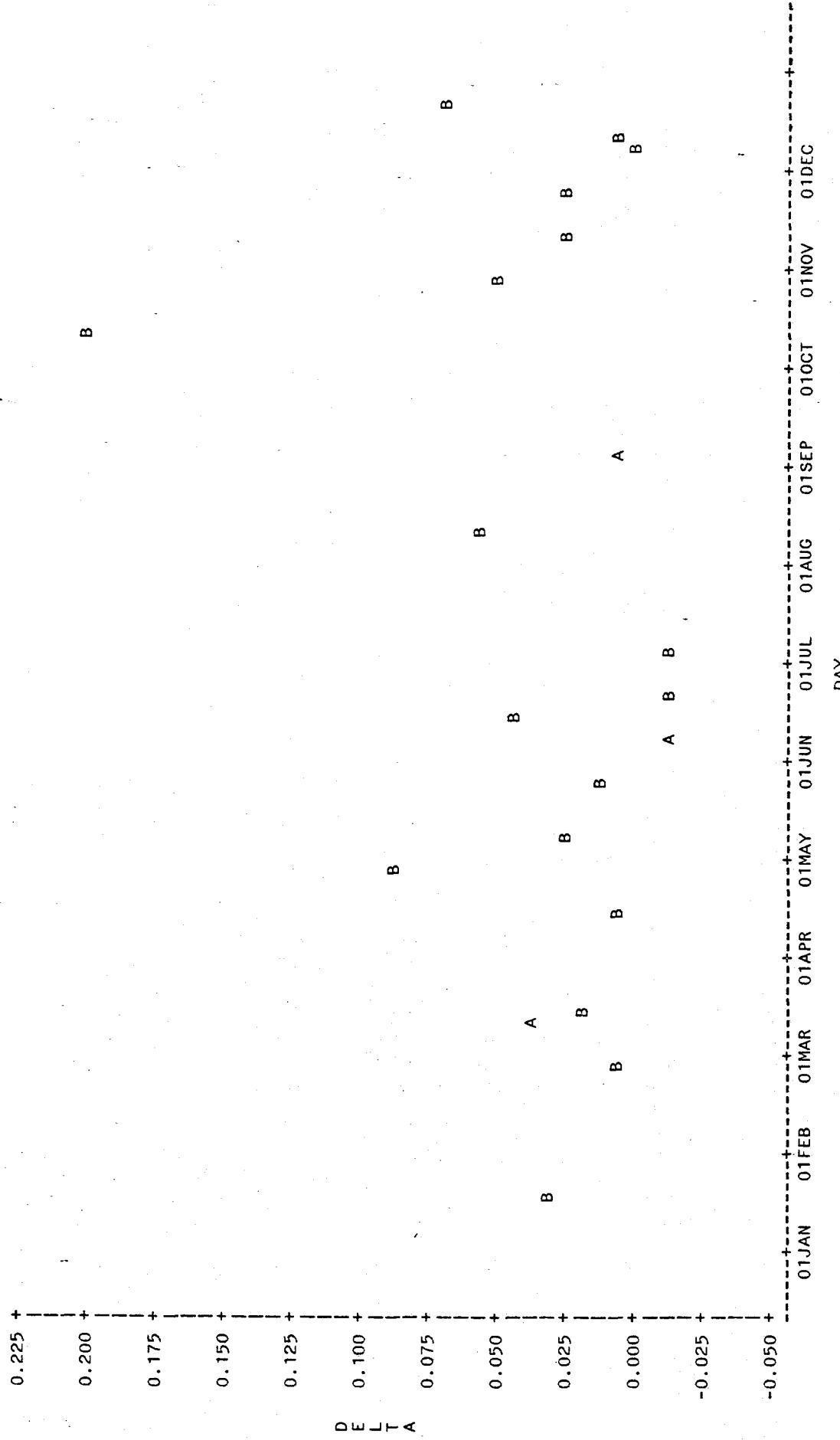
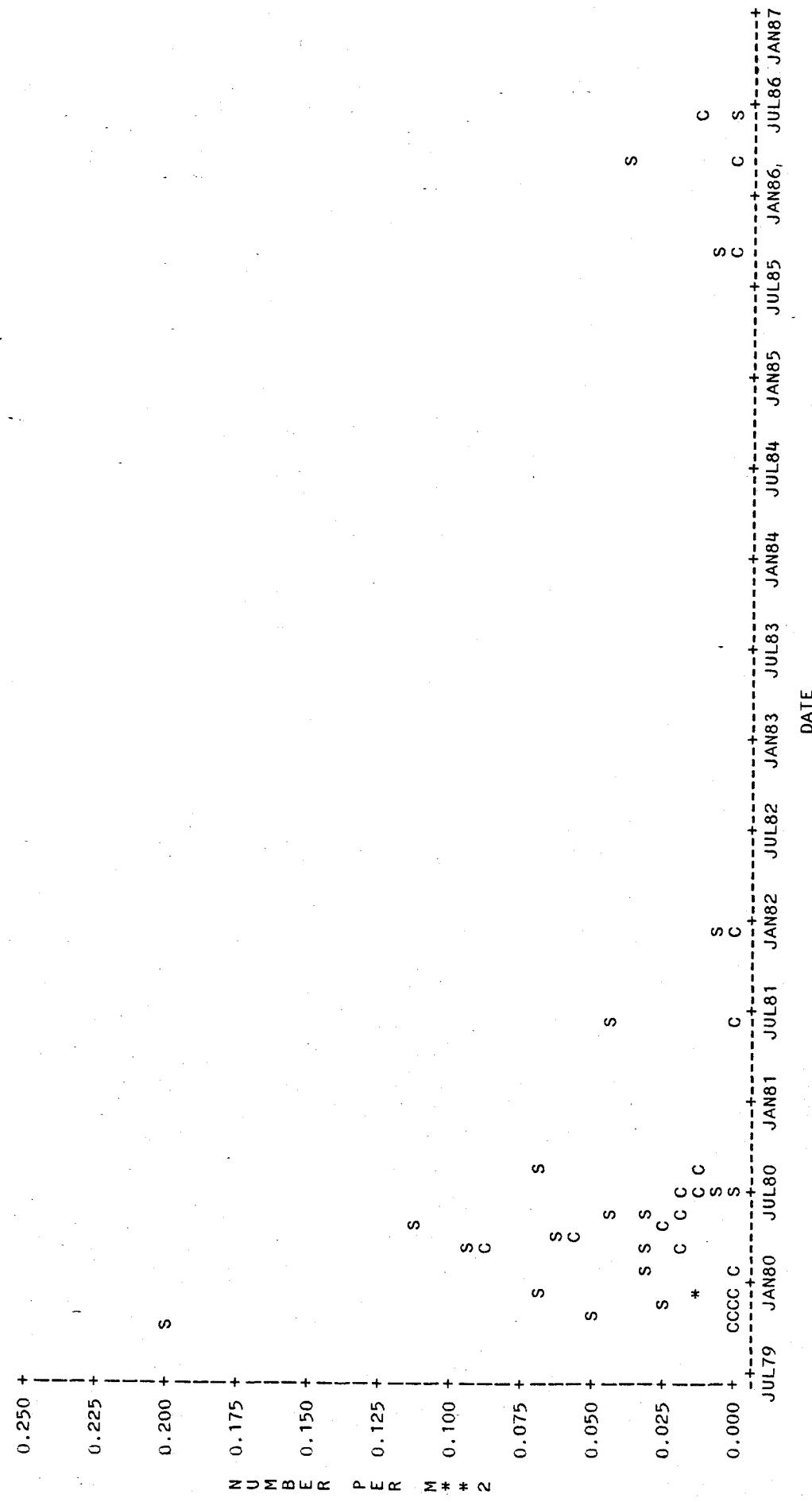


Figure D-61. Plot of preoperational (B) and operational (A) Delta values for *Neomysis rayii* immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Neomysis rayii STAGE=IMMATURE



NOTE:

4 OBS HIDDEN

Figure D-62. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis rayii* immatures. Similar abundances at both locations are designated by asterisks.

D-65

Taxon: Neomysis rayii
Stage: Juvenile

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	9	
$\log(x+0)$	17	0	
$\log(x+\text{constant})$	19	9	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/ Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.10	28.4	1.6/.01
$\log(x+0)$	H					
$\log(x+.1)$	ns	ns/ns	ns/ns	.10	52.1	.16/.02
$\log(x+1)$	ns	ns/ns	ns/ns	.10	37.0	.05/.001

Chi Square; Ho: even distribution of zeroes in BACI cells: sig

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none ; ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$ & $\log(x+1)$: ns

E

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

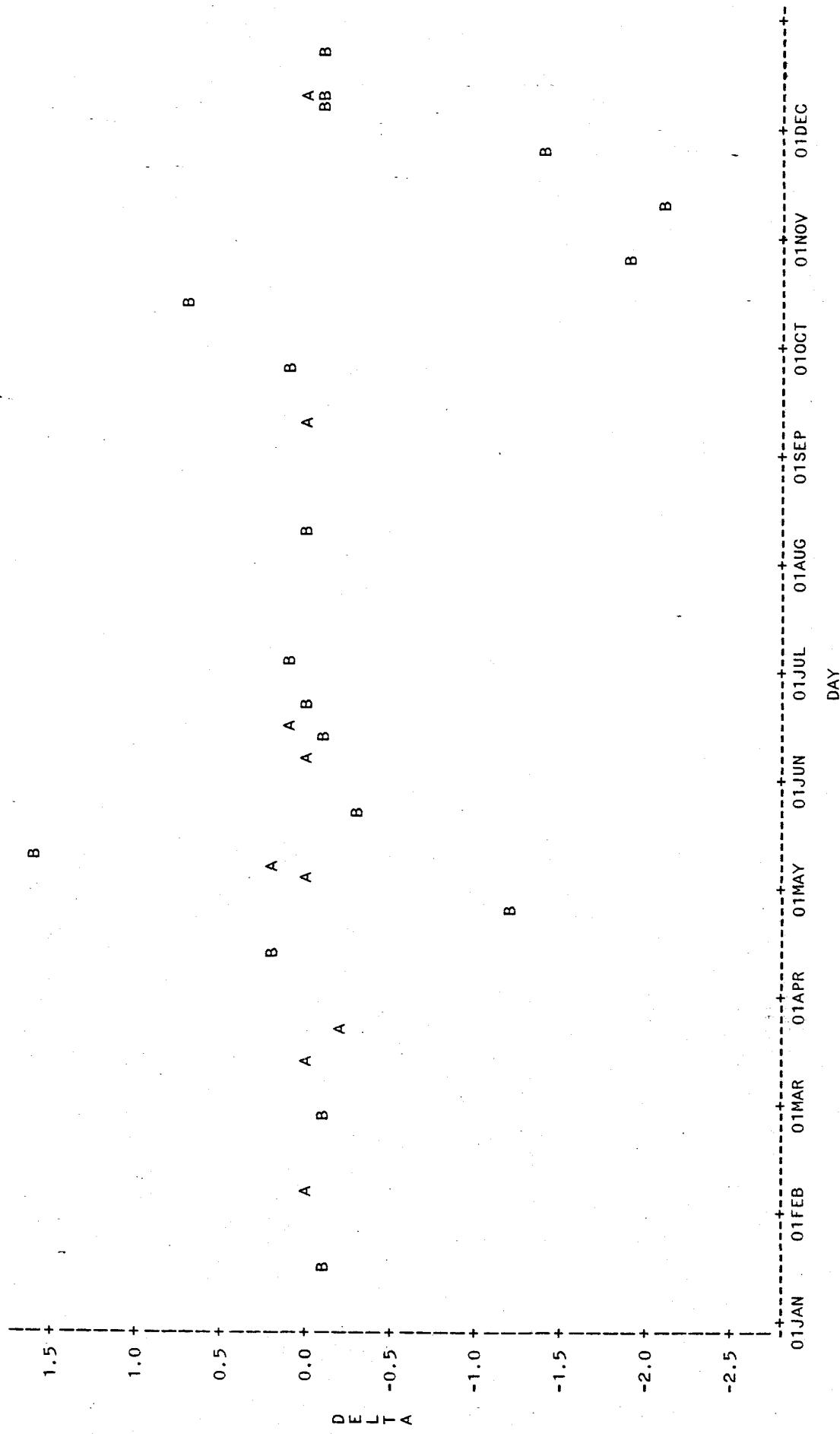
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 63. Summary of Test Results for Neomysis rayii, Juvenile.

SPCODE=Neomysis rayii STAGE=JUVENILE



NOTE:

1 OBS HIDDEN

Figure D-64. Plot of preoperational (B) and operational (A) Delta values for *Neomysis rayii* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-67

SPCODE=Neomysis rayii STAGE=JUVENILE

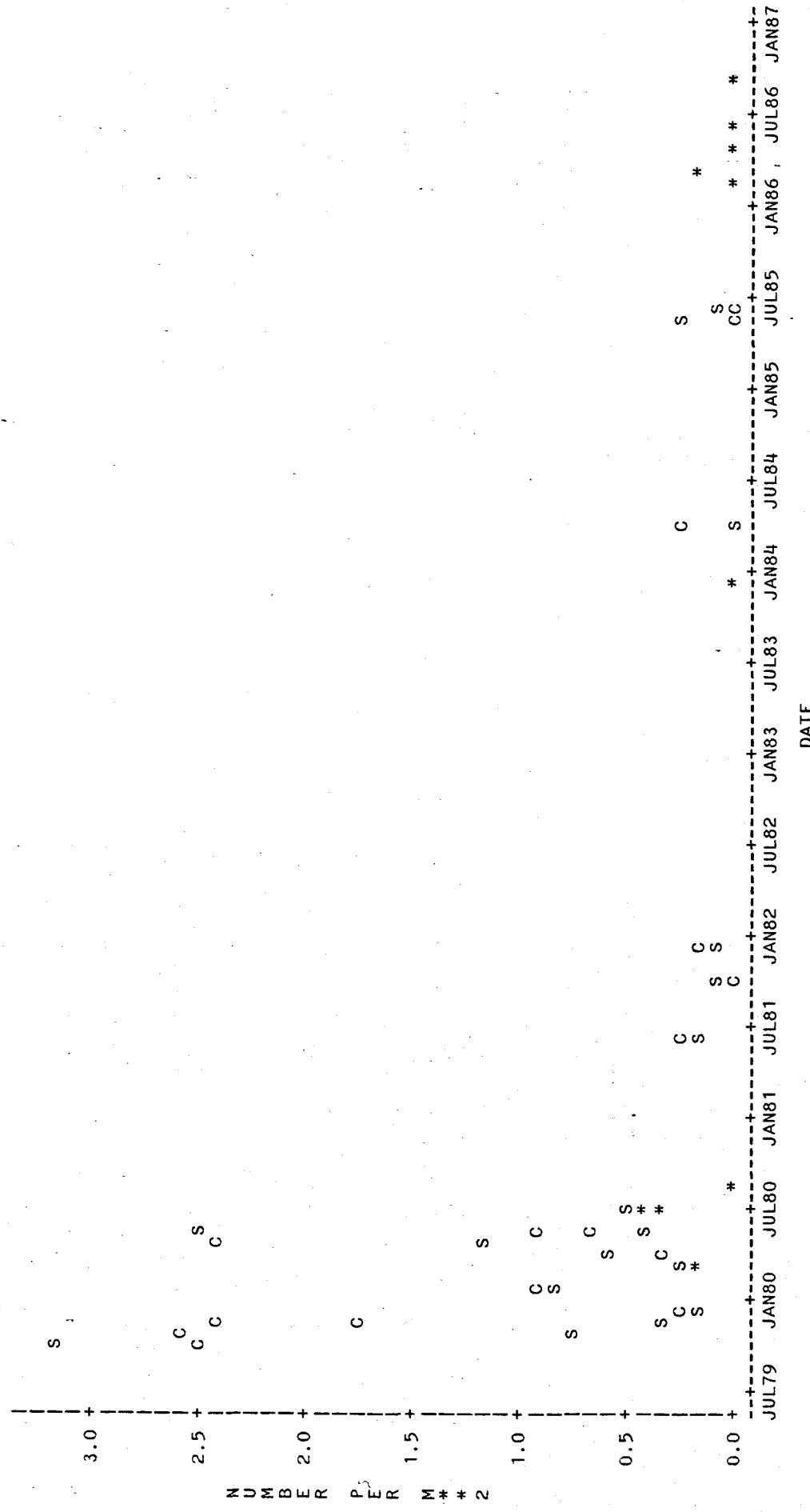


Figure D-65. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis rayii* juveniles. Similar abundances at both locations are designated by asterisks.

D-68

Taxon: Cross-Shelf
Stage: All

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	
	Note:						Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	23.0	278/41.5
$\log(x+0)$	B	ns	sig/ns	ns/ns	.05	84.4	.08/.04
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: sig($p=.057$)
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: sig($p=.071$)
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: none; ns first order model
Transformation 2: $\log(x)$: ns, second order model

C

Binomial: sig

Regression (SONGS vs Control Abundances):
Two straight lines, same intercept(= 0)

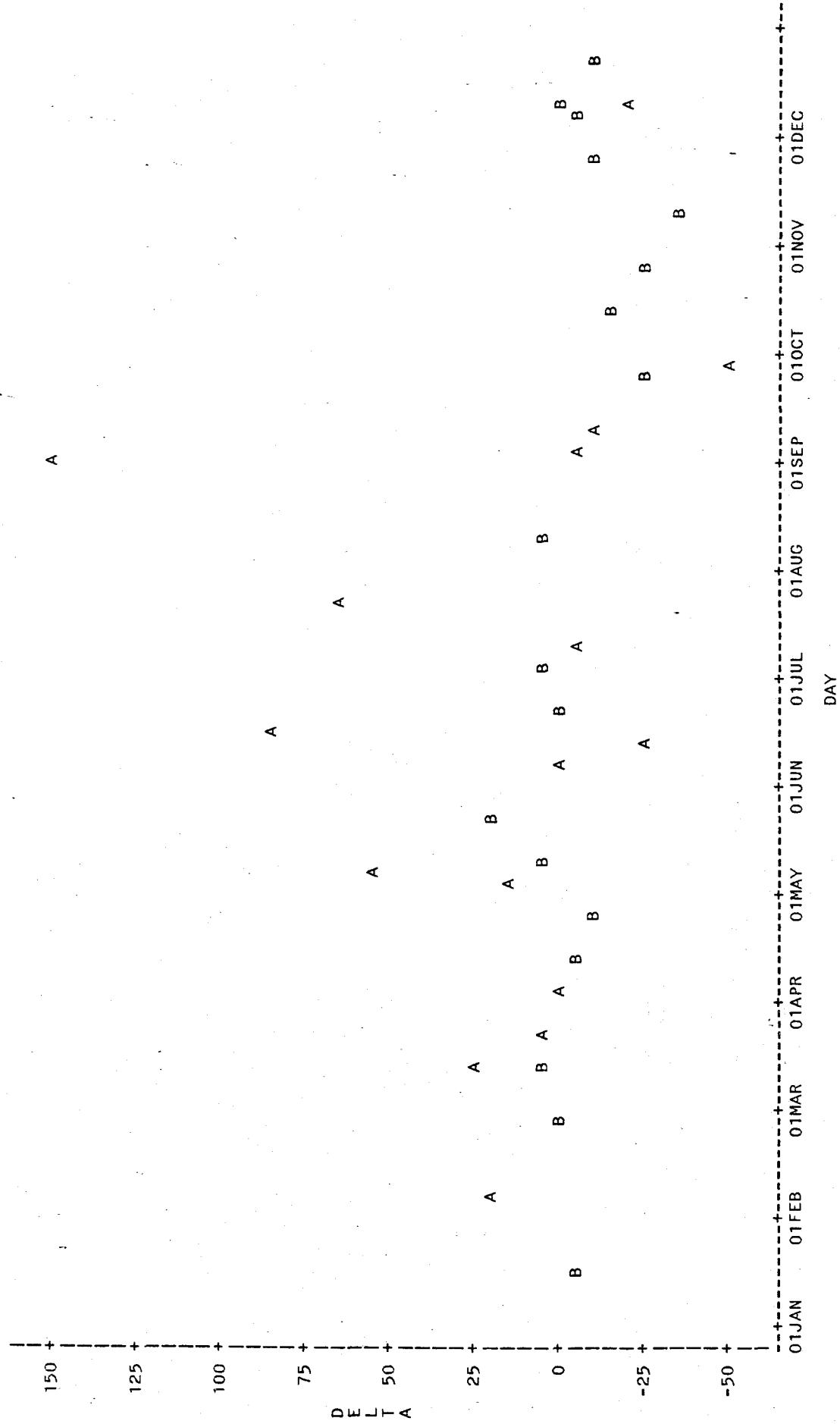
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 66. Summary of Test Results for Cross-Shelf,
All Stages Combined.

SPCODE=Cross-shelf summary group STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE 1 OBS HIDDEN

Figure D-67. Plot of preoperational (B) and operational (A) Delta values for Cross-shelf summary group all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Cross-shelf summary group STAGE=ALL

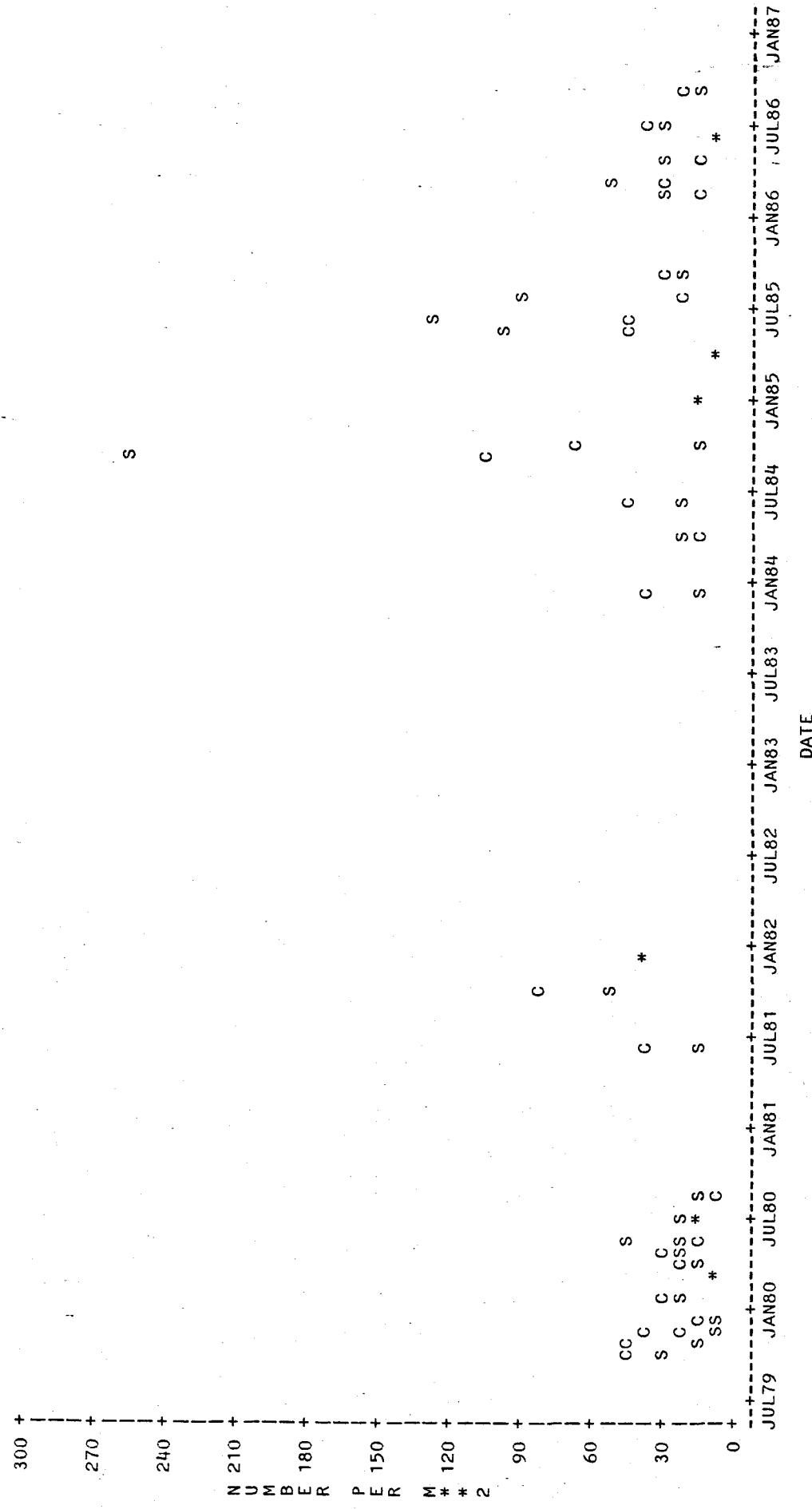


Figure D-68. Abundance values at SONGS (S) and Control (C) plotted through time for Cross-shelf summary group all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages Combined	B or C	6.1	5.2	5.1	5.2	3.1	2.1
	A-S	6.4	5.4	4.7	4.8	3.5	2.3
Adults p=.015	B or C	4.5	4.7	5.7	6.0	3.7	2.4
	A-S	4.1	4.9	5.5	5.3	4.2	3.0
Immatures p=.019	B or C	5.5	5.7	5.5	5.0	3.1	2.0
	A-S	4.5	5.2	5.5	5.4	4.0	2.3
Juveniles	B or C	6.2	5.6	5.1	4.6	3.1	2.0
	A-S	6.9	5.5	4.7	4.3	3.2	2.0

Figure D-69. Cross-shelf distributional patterns for Cross-Shelf Taxa. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Cross-Shelf
Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u> <u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	29.2
$\log(x+0)$	B	ns	ns/sig	ns/ns	.10	83.5
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x)$: ns

Autoregressive Errors t-test

Transformation 1: none: ns first order model
Transformation 2: $\log(x)$: ns first order model

C
C

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

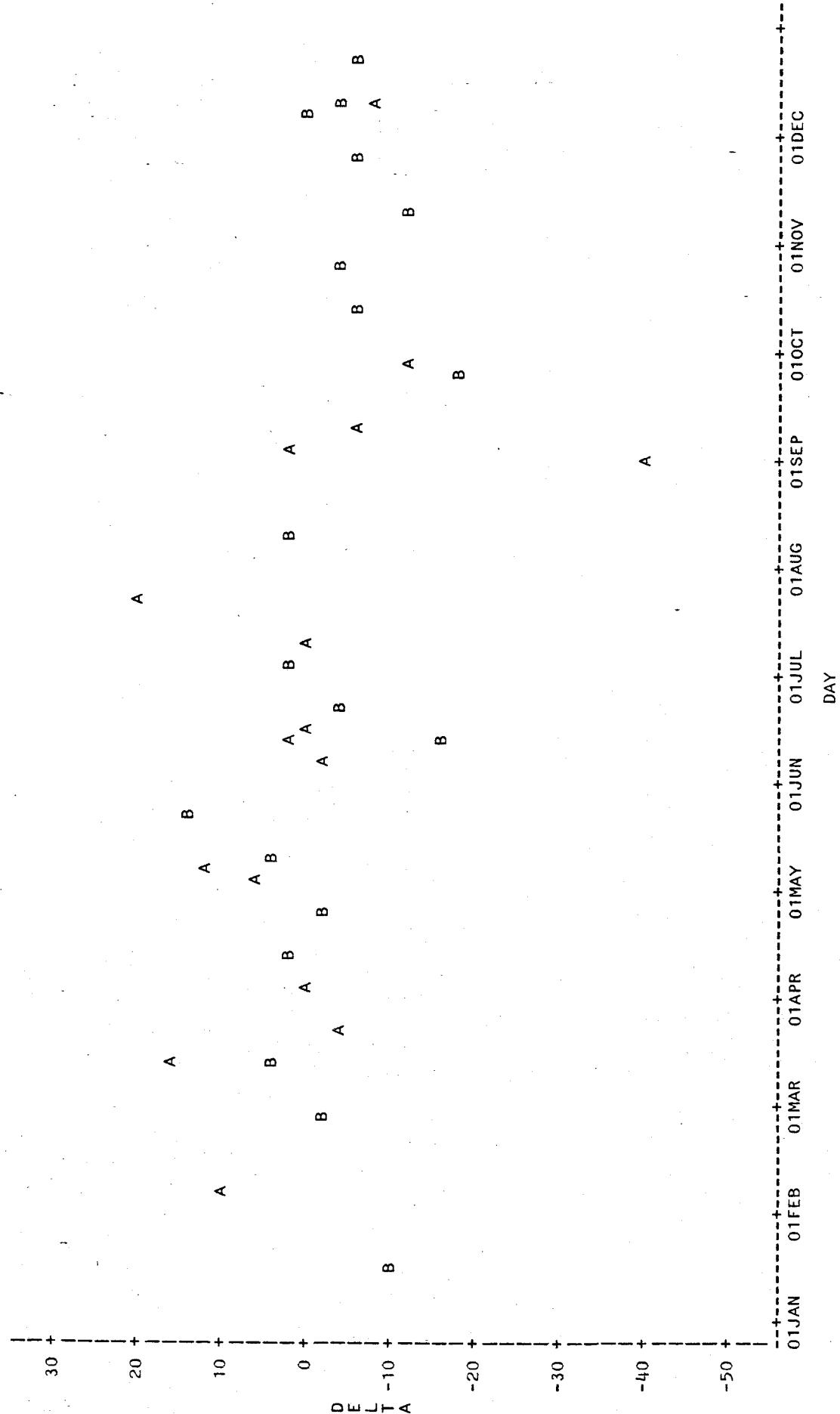
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 70. Summary of Test Results for Cross-Shelf,
Adult.

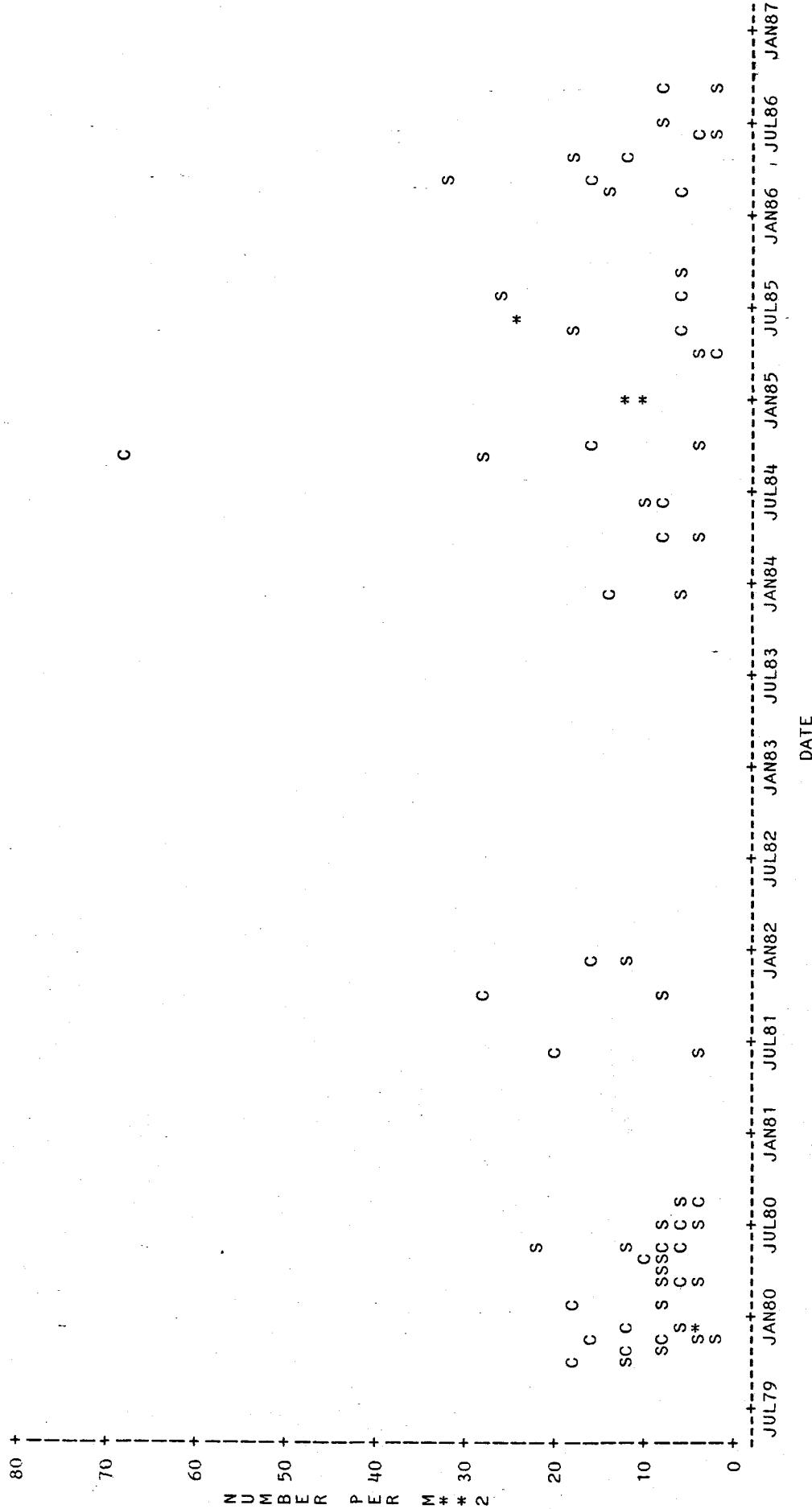
SPCODE=Cross-shelf summary group STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-71. Plot of preoperational (B) and operational (A) Delta values for Cross-shelf summary group adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Cross-shelf summary group STAGE=ADULT



NOTE:

7 OBS HIDDEN

Figure D-72. Abundance values at SONGS (S) and Control (C) plotted through time for Cross-shelf summary group adults. Similar abundances at both locations are designated by asterisks.

D-75

Taxon: Cross-Shelf
Stage: Immature

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	ns	ns/ns	ns/ns	.10	33.2	76.1/8.31	
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	84.3	.13/.06
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: sig($p=.030$)
Transformation 2: $\log(x)$: sig($p=.060$)

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: sig($p=.039$)
Transformation 2: $\log(x)$: sig($p=.057$)

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: $\log(x)$: ns second order model

C

Binomial: sig($p=.000$)

Regression (SONGS vs Control Abundances):

Two different straight lines, same intercept (= 0)

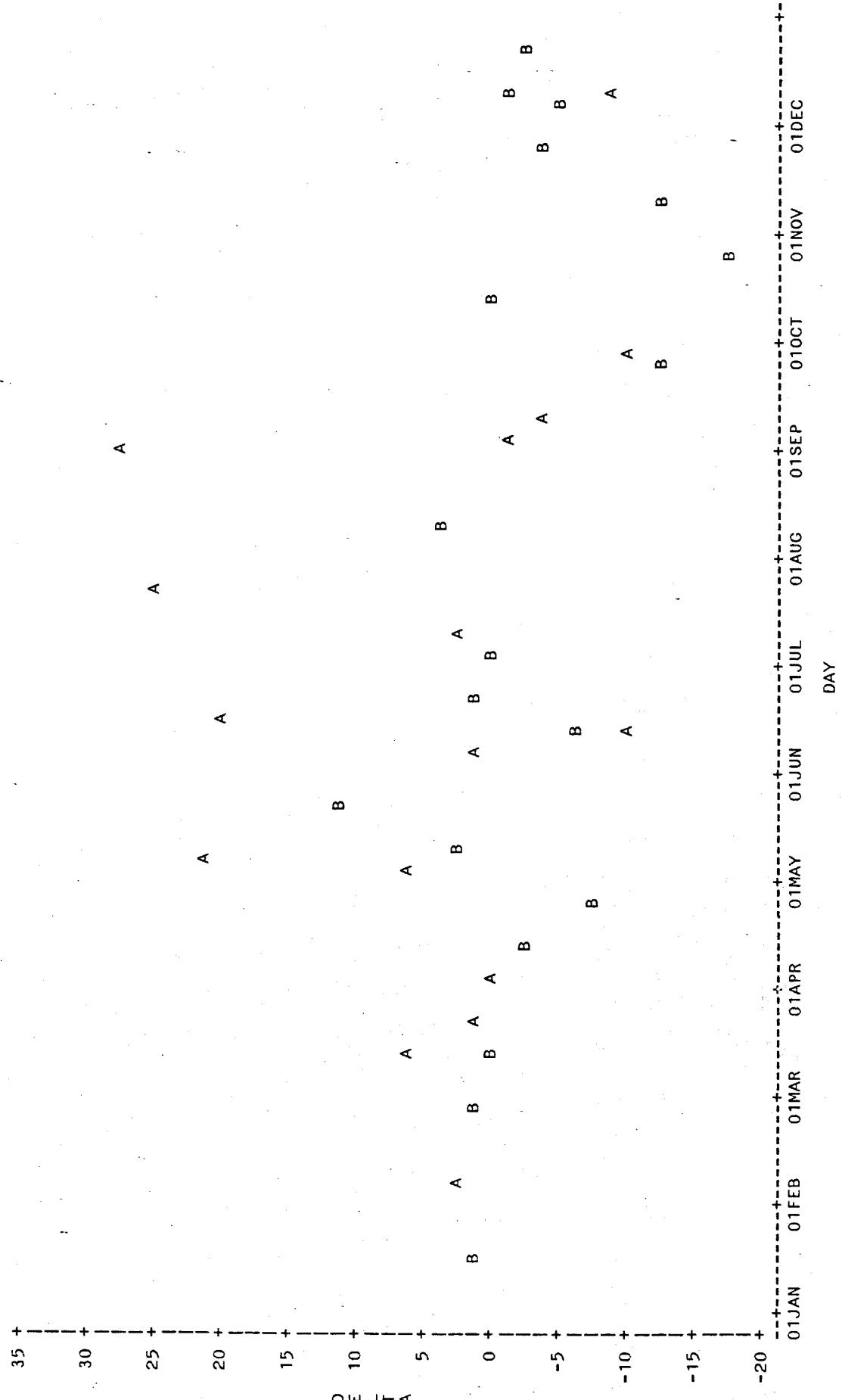
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 73. Summary of Test Results for Cross-Shelf,
Immature.

SPCODE=Cross-shelf summary group STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-74. Plot of preoperational (B) and operational (A) Delta values for Cross-shelf summary group immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Cross-shelf summary group STAGE=IMMATURE

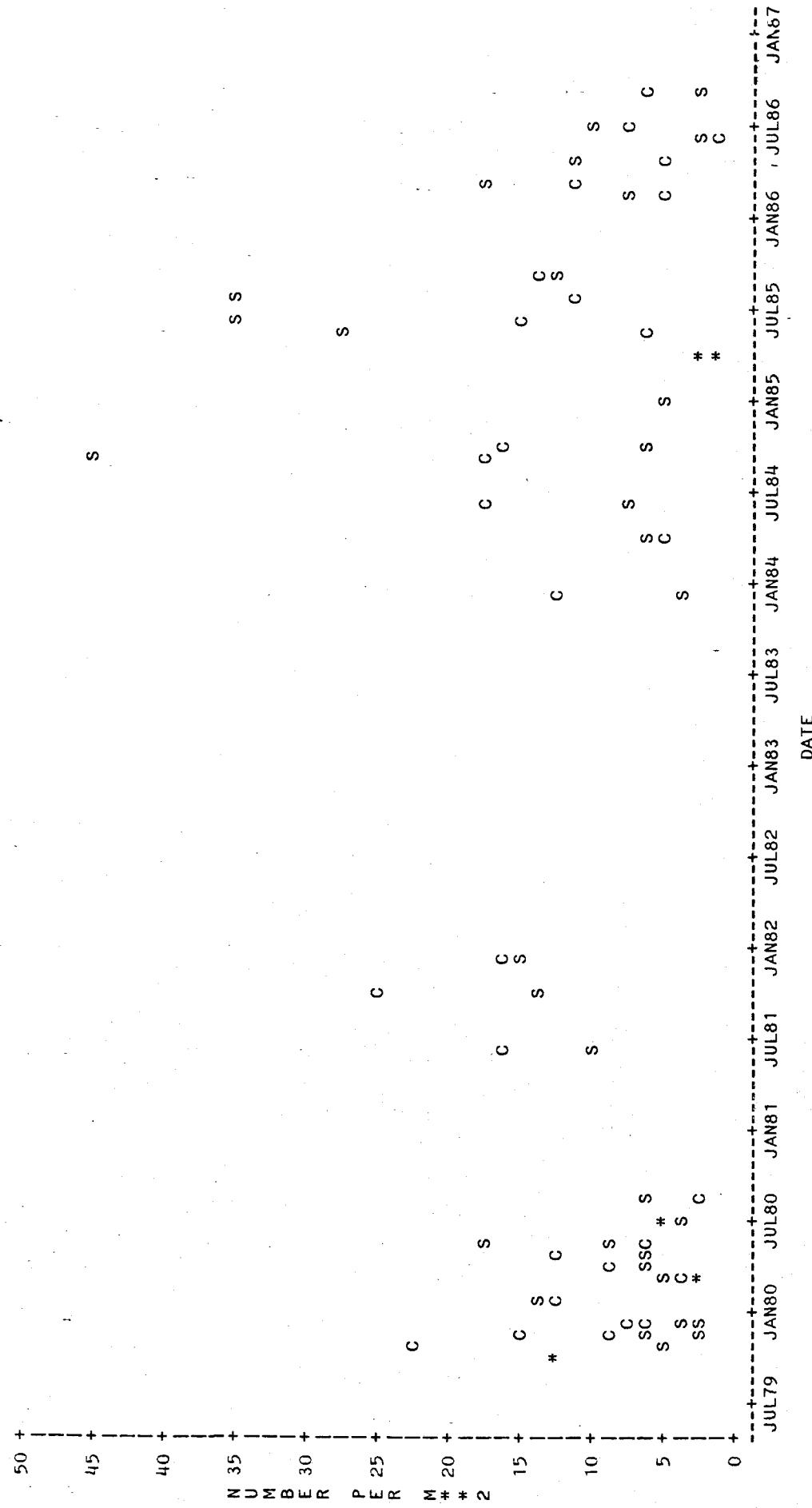


Figure D-75. Abundance values at SONGS (S) and Control (C) plotted through time for Cross-shelf summary group immatures. Similar abundances at both locations are designated by asterisks.

Taxon: Cross-Shelf
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	D	ns	sig/ns	sig/ns		
$\log(x+0)$	D	ns	sig/ns	sig/ns		
$\log(x+.1)$	D	ns	sig/ns	sig/ns		
$\log(x+1)$	D	ns	sig/ns	sig/ns		

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

BACI t-test

See Key Note:

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: sig(.000)**

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0*

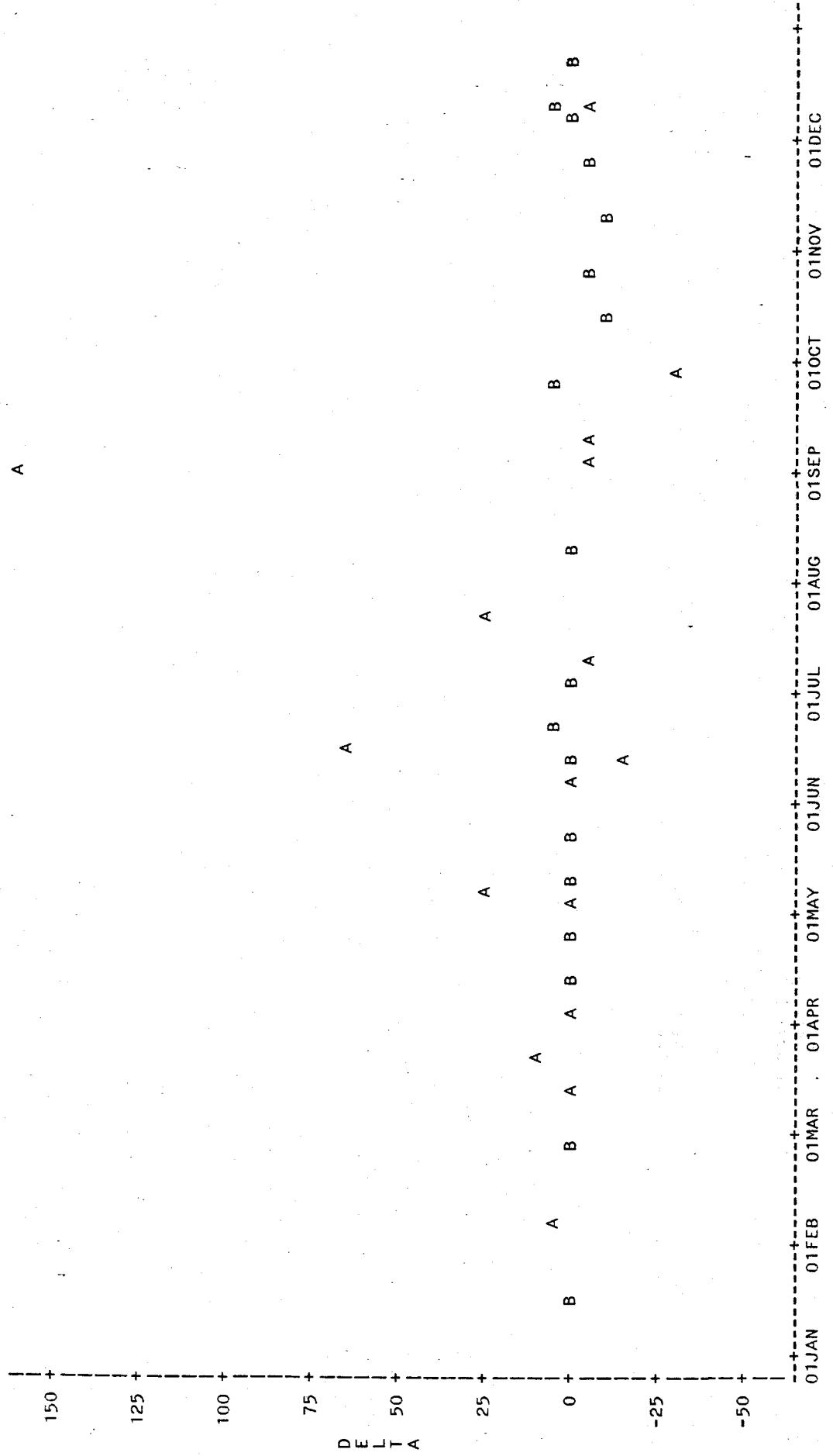
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 76. Summary of Test Results for Cross-Shelf,
Juvenile.

SPCODE=Cross-shelf summary group STAGE=JUVENILE



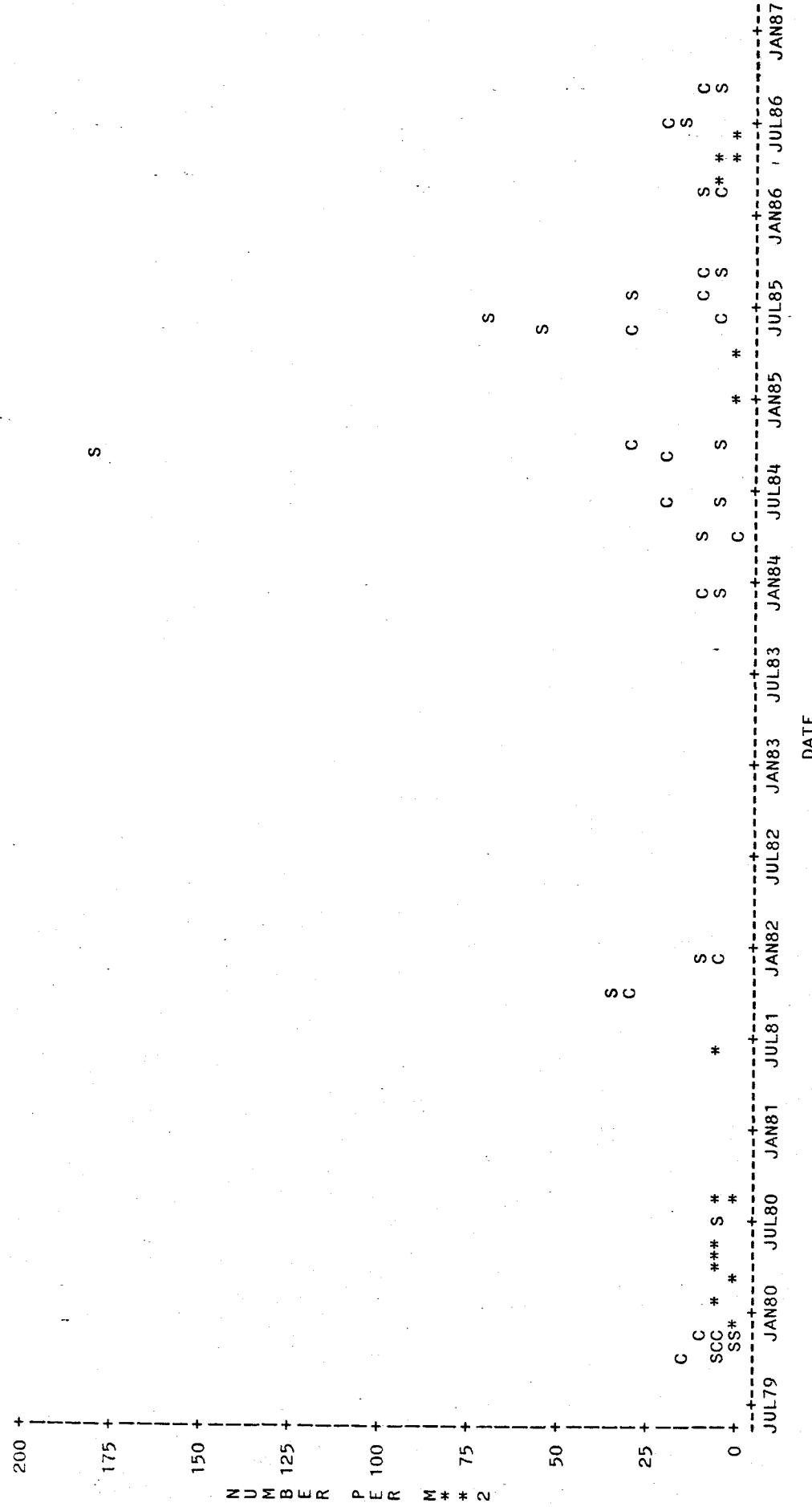
NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

1 OBS HIDDEN

Figure D-77. Plot of preoperational (B) and operational (A) Delta values for Cross-shelf summary group Juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-80

SPCODE=Cross-shelf summary group STAGE=JUVENILE



NOTE: 21 OBS HIDDEN

Figure D-78. Abundance values at SONGS (S) and Control (C) plotted through time for Cross-shelf summary group juveniles. Similar abundances at both locations are designated by asterisks.

D-81

Taxon: Metamysidopsis elongata
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	A	sig+	sig/ns	ns/ns			
$\log(x+0)$		ns	ns/ns	ns/ns	.10	70.0	.18/.16
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	69.3	.18/.15
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: sig

Regression (SONGS vs Control Abundances):

Two straight lines, same intercept(= 0)

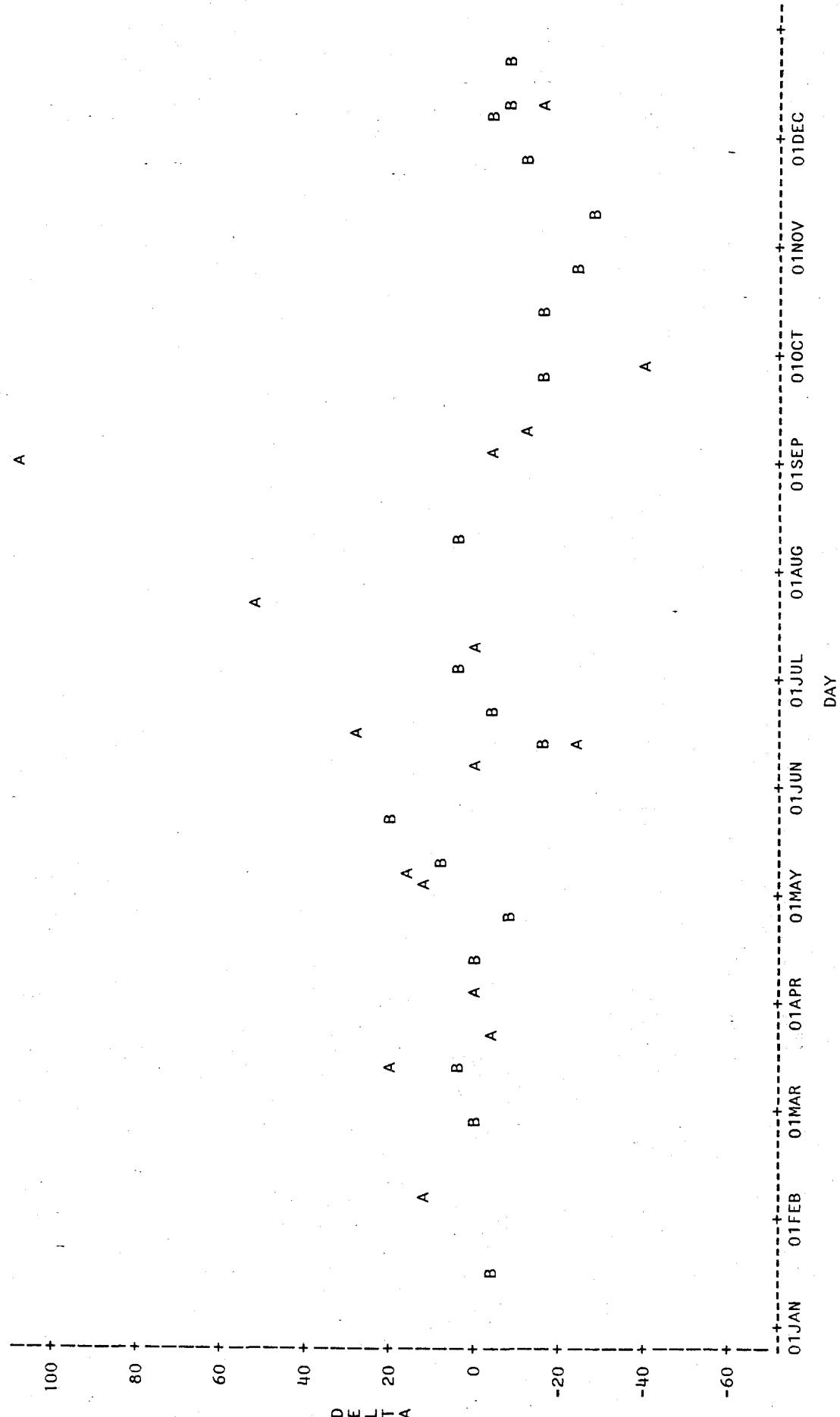
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 79. Summary of Test Results for Metamysidopsis elongata,
All Stages Combined

SPCODE=Metamysidopsis elongata STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-80. Plot of preoperations! (B) and operational (A) Delta values for Metamysidopsis elongata all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Metamysidopsis elongata STAGE=ALL

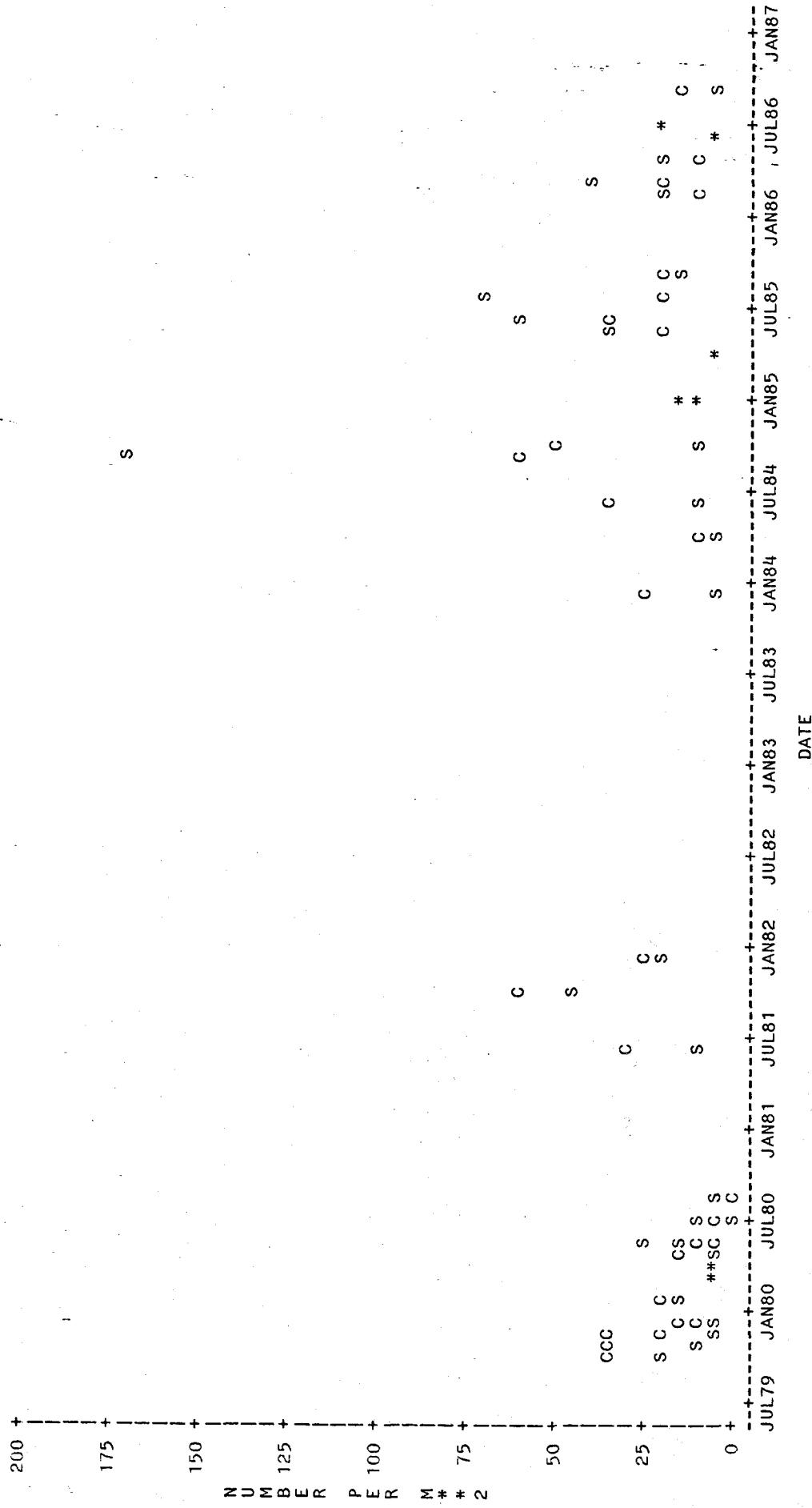


Figure D-81. Abundance values at SONGS (S) and Control (C) plotted through time for *Metamysidopsis elongata* all stages. Similar abundances at both locations are designated by asterisks.

D-84

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages	B or C	6.2	5.4	5.2	5.0	2.9	2.0
	Combined						
	A-S	6.3	5.2	4.9	4.9	3.1	2.2
Adults	B or C	4.8	5.0	5.8	5.7	3.2	2.1
	A-S	4.3	5.2	5.7	5.5	3.6	2.2
Immatures	B or C	5.9	5.9	5.2	4.6	2.5	2.0
	A-S	5.4	5.6	5.8	4.8	2.6	2.2
Juveniles	B or C	4.4	3.7	2.6	2.3		
	A-S	4.7	3.6	2.6	2.2		

Figure D-82. Cross-shelf distributional patterns for Metamysidopsis elongata. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Metamysidopsis elongata
Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	17	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note: Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	A	sig	ns/ns	ns/ns		
$\log(x+0)$	B	ns	ns/sig	ns/ns	.10	65.7
$\log(x+.1)$	B	ns	ns/sig	ns/ns	.10	64.1
$\log(x+1)$	N/A					.18/.21

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

Transformation 1: $\log(x)$: ns first order model
Transformation 2: $\log(x+.1)$: ns first order model

C
C

Binomial: sig

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

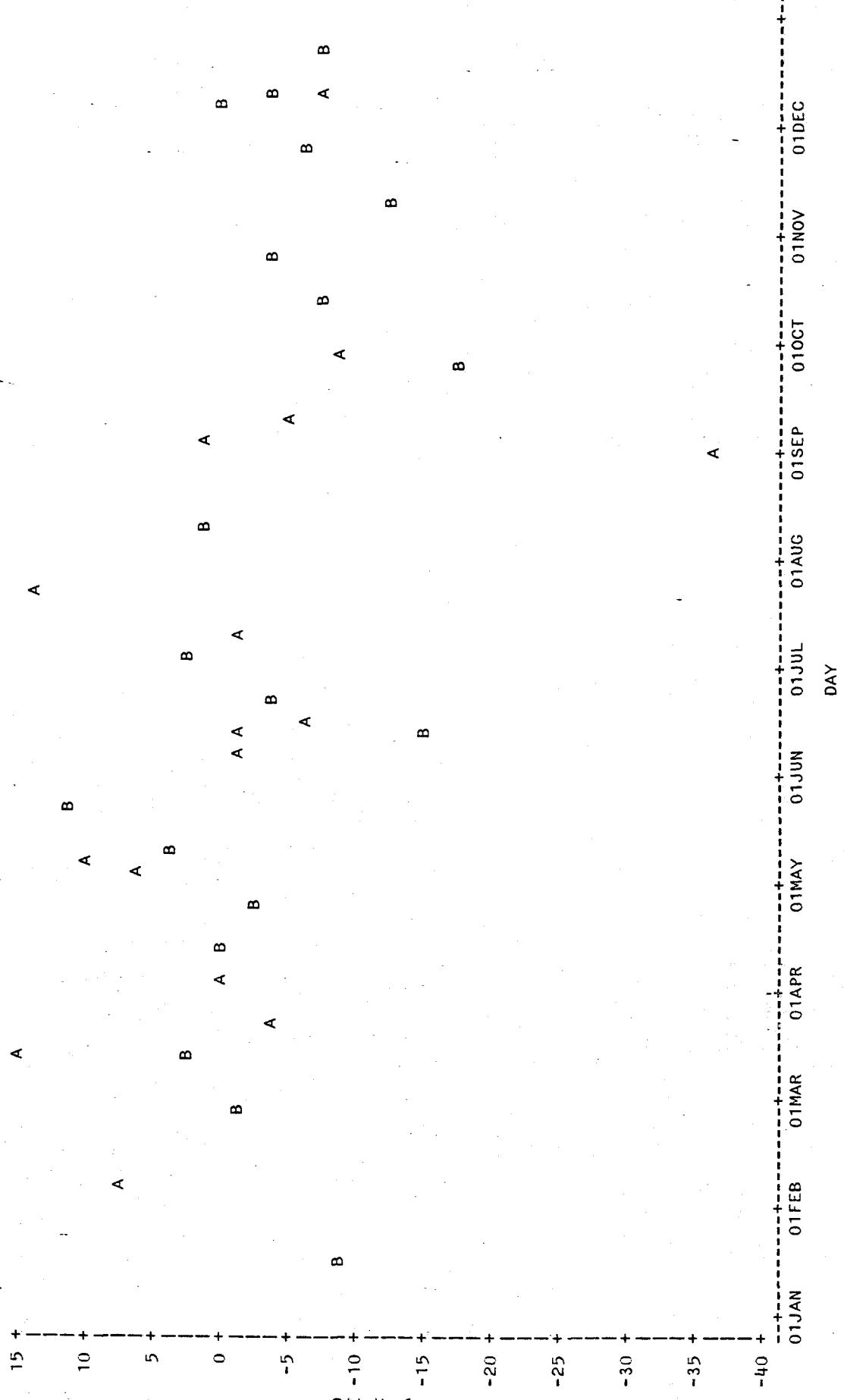
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 83. Summary of Test Results for Metamysidopsis elongata,
Adult.

SPCODE=Metamysidopsis elongata STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-84. Plot of preoperational (B) and operational (A) Delta values for Metamysidopsis elongata adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Metamysidopsis elongata STAGE=ADULT

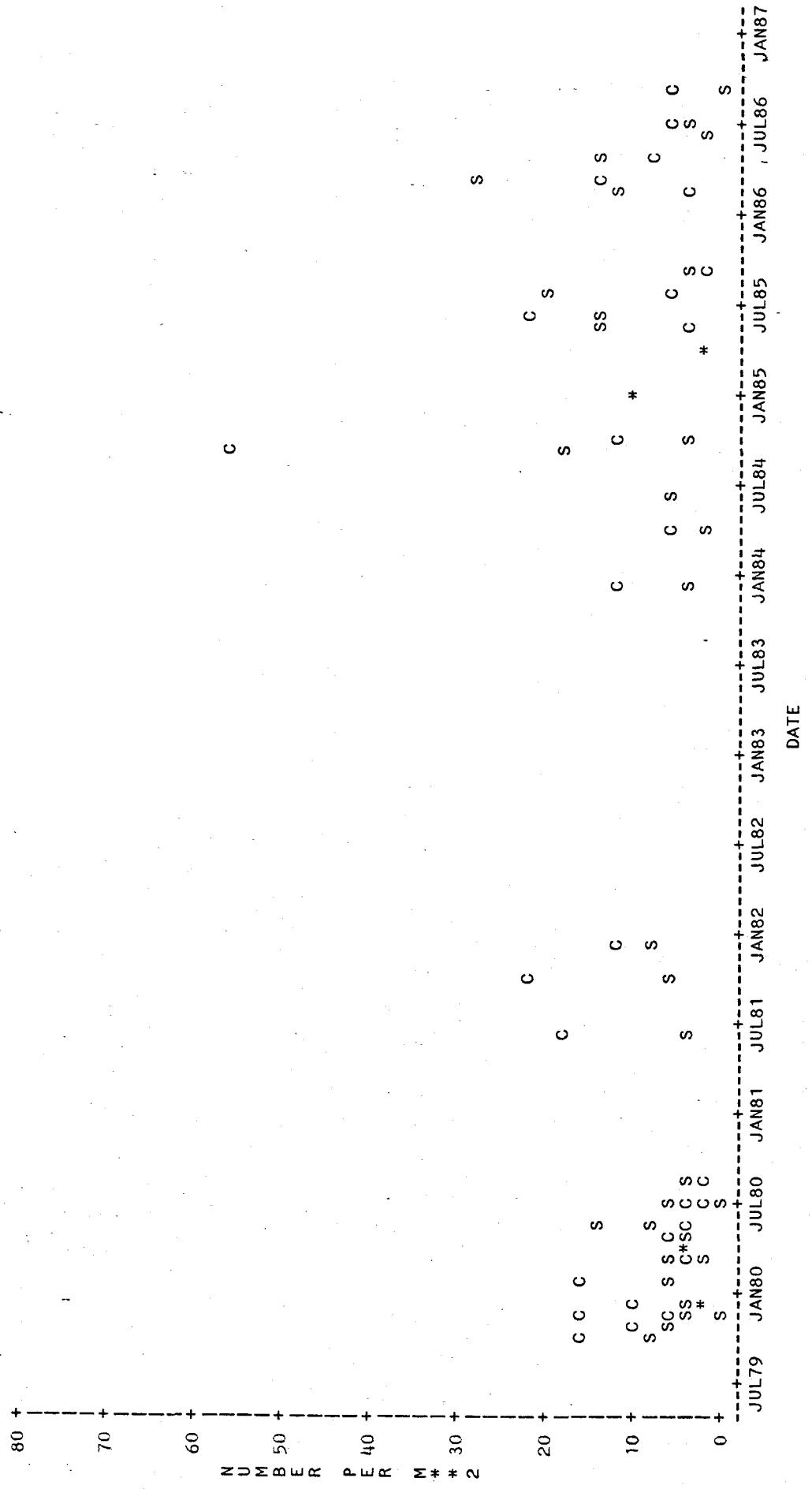


Figure D-85. Abundance values at SONGS (S) and Control (C) plotted through time for *Metamysidopsis elongata* adults. Similar abundances at both locations are designated by asterisks.

D-88

Taxon: Metamysidopsis elongata
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note: Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Abun/Sprse
none	A	sig	ns/ns	ns/ns			
$\log(x+0)$		ns	ns/ns	ns/ns	.10	53.6	.13/.27
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	51.9	.12/.24
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0)

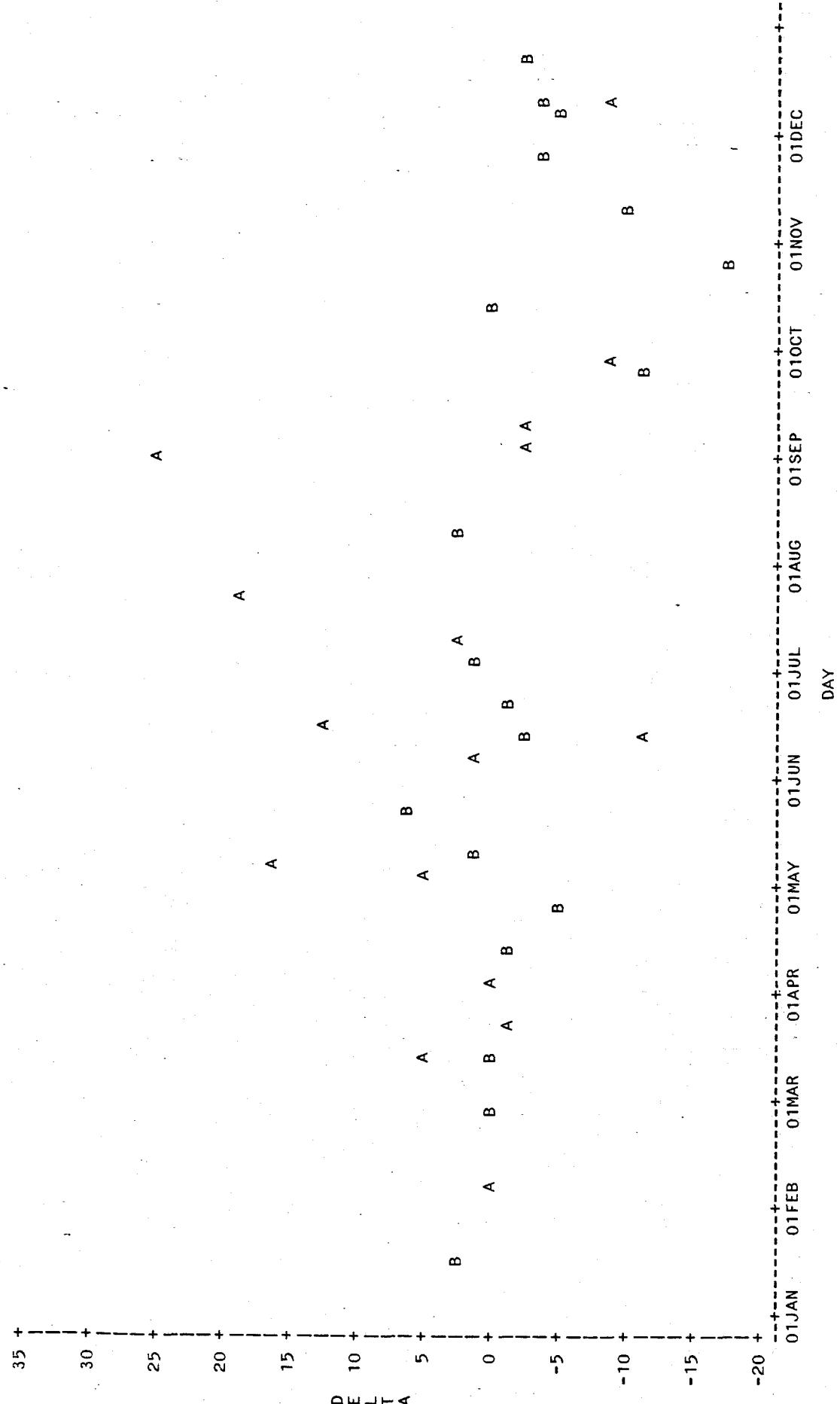
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 86. Summary of Test Results for Metamysidopsis elongata,
Immature.

SPCODE=Metamysidopsis elongata STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-87. Plot of preoperational (B) and operational (A) Delta values for Metamysidopsis elongata immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-90

SPCODE=Metamysidopsis elongata STAGE=IMMATURE

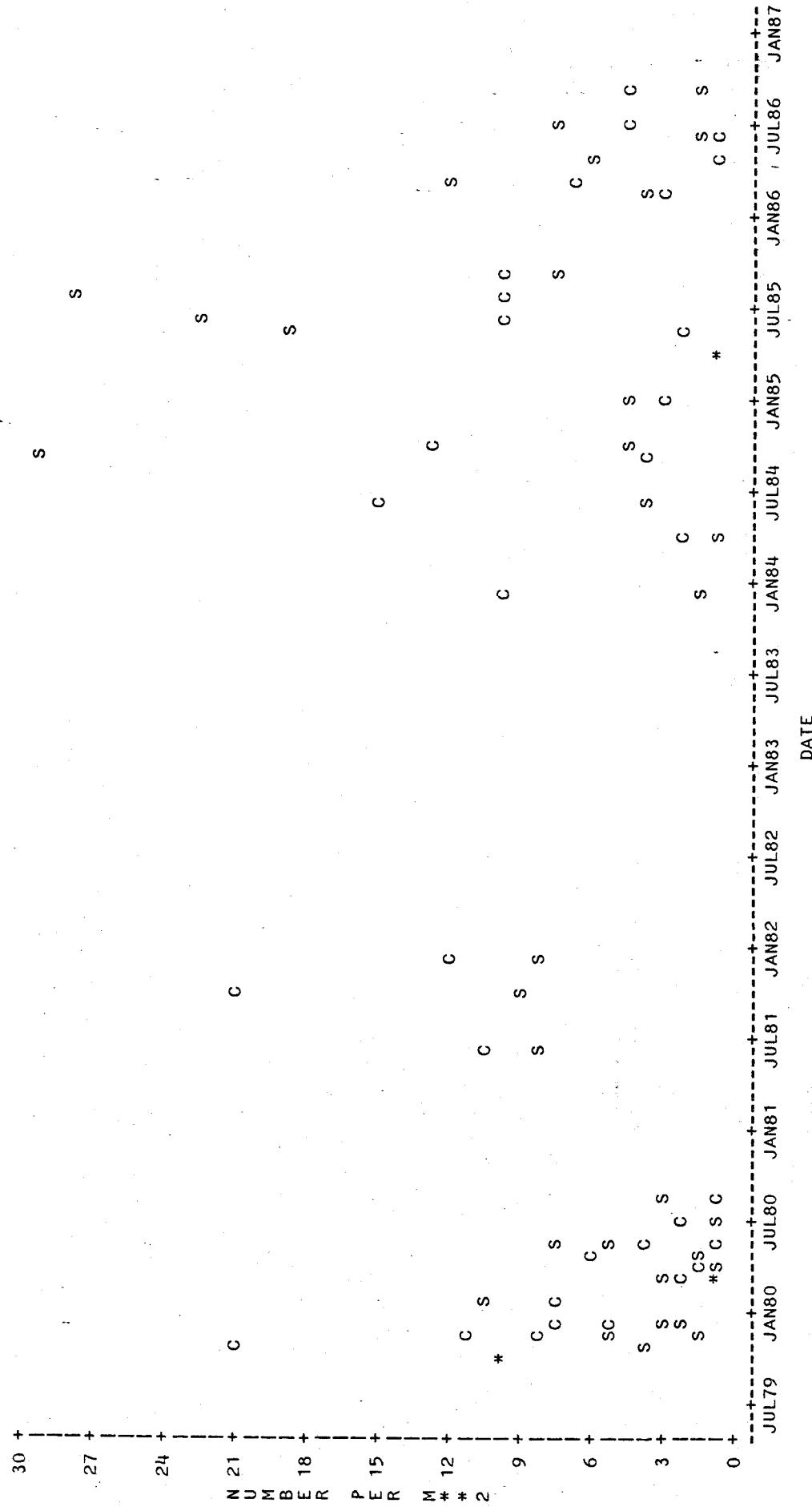


Figure D-88. Abundance values at SONGS (S) and Control (C) plotted through time for *Metamysidopsis elongata* immatures. Similar abundances at both locations are designated by asterisks.

TAXON: Metamysidopsis elongata
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	14	12	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	A	sig	sig/ns		sig/ns		
$\log(x+0)$	N/A						
$\log(x+.1)$	B	ns	sig/ns		ns/ns	.10	20.7
$\log(x+1)$	D	ns	sig/ns		sig/ns		.52/.15

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x+.1)$: ns
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x+.1)$: ns
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: $\log(x+.1)$: ns first order model
Transformation 2: N/A

C

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

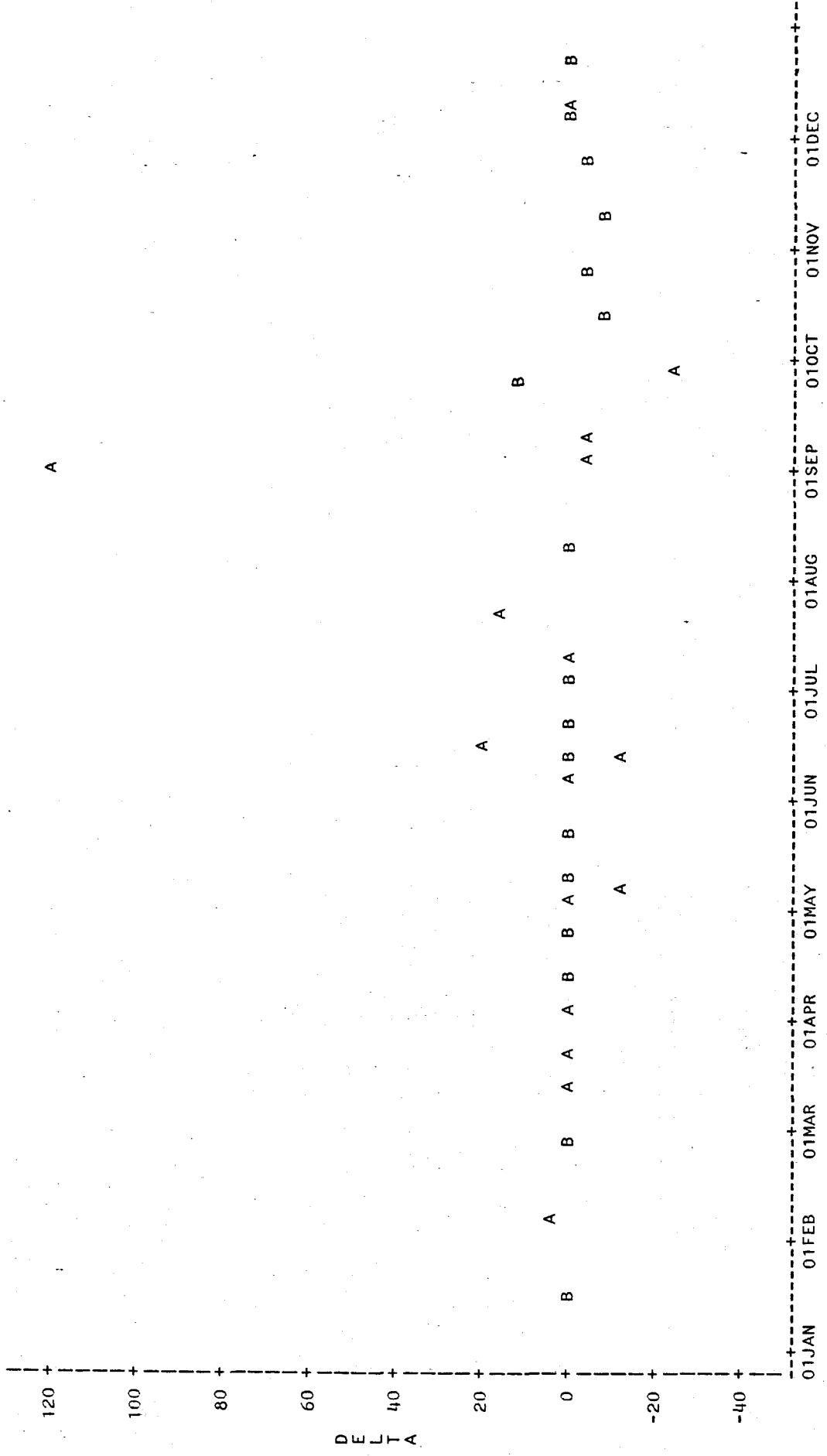
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 89. Summary of Test Results for Metamysidopsis elongata, Juvenile.

SPCODE=Metamysidopsis elongata STAGE=JUVENILE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

2 OBS HIDDEN

Figure D-90. Plot of preoperational (B) and operational (A) Delta values for *Metamysidopsis elongata* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-93

SPCODE=Metamysidopsis elongata STAGE=JUVENILE

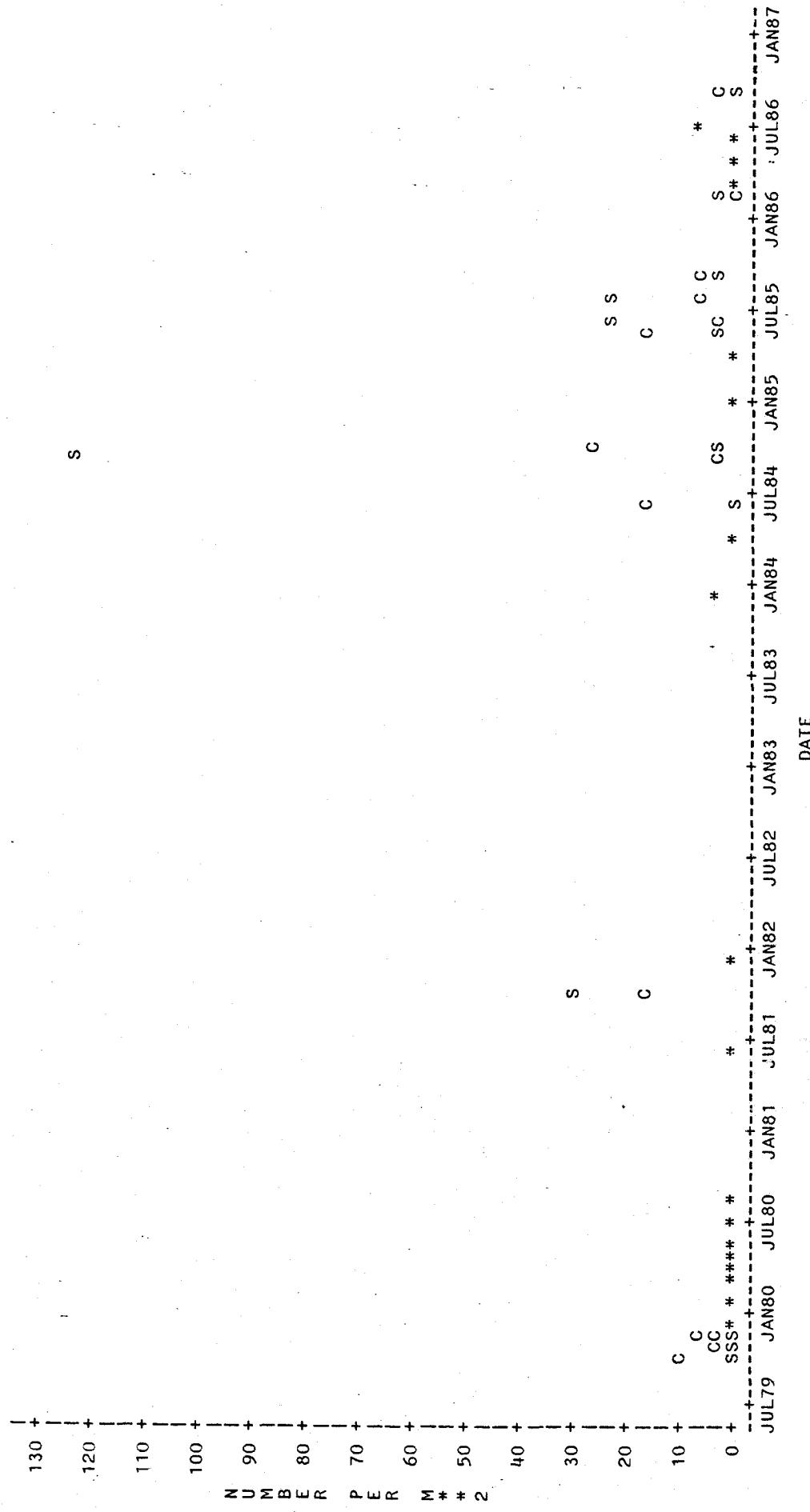


Figure D-91. Abundance values at SONGS (S) and Control (C) plotted through time for *Metamysidopsis elongata* juveniles. Similar abundances at both locations are designated by asterisks.

D-94

Taxon: Mysidopsis intii
Stage: All

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	ns	ns/ns	ns/ns	.05	91.9	9.8/4.2	
$\log(x+0)$	ns	ns/ns	ns/ns	.10	86.6	.02/.09	
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: sig($p=.014$)
Transformation 2: $\log(x)$: sig($p=.007$)

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: sig($p=.019$)
Transformation 2: $\log(x)$: sig($p=.011$)

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: sig($p=.016$)

Regression (SONGS vs Control Abundances):
Two straight lines, same intercept(= 0)

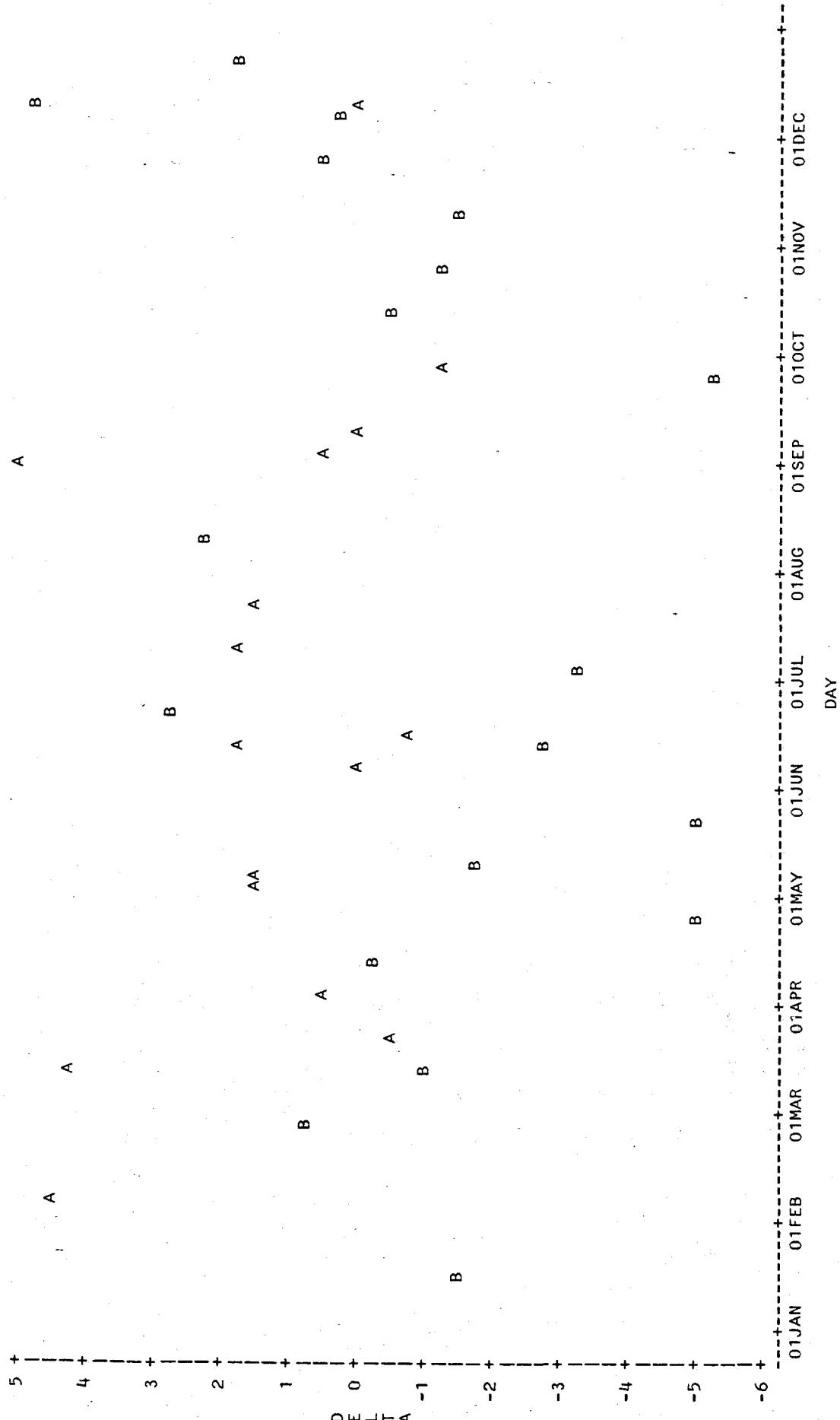
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 92. Summary of Test Results for Mysidopsis intii,
All Stages Combined.

SPCODE=Mysidopsis intii STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-93. Plot of preoperational (B) and operational (A) Delta values for Mysidopsis intii all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-96

SPCODE=Mysidopsis intii STAGE=ALL

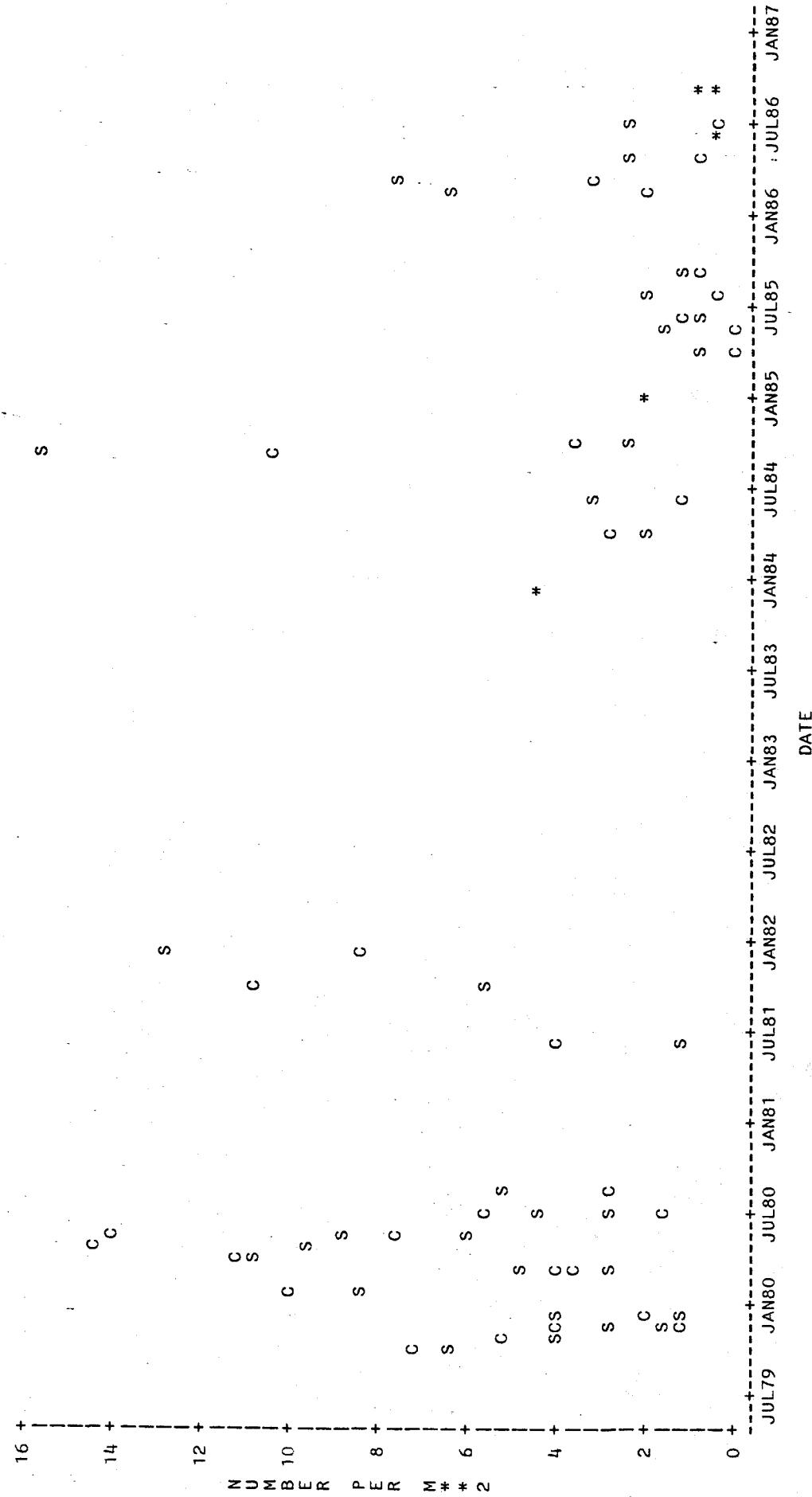


Figure D-94. Abundance values at SONGS (S) and CONTROL (C) plotted through time for *Mysidopsis intii* all stages. Similar abundances at both locations are designated by asterisks.

D-97

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages	B or C	3.8	4.5	6.0	6.0	4.0	2.2
Combined				5.2	6.3	4.6	2.6
Adults	B or C	4.2	4.1	5.2	6.1	4.3	2.4
	A-S	2.9	4.8	5.0	5.8	4.9	2.9
Immatures	B or C	3.4	4.6	6.1	6.0	4.0	2.2
	A-S	2.7	4.2	5.7	6.3	4.4	2.8
Juveniles	B or C	3.2	4.6	6.2	5.7	3.9	2.6
	A-S	3.1	4.0	5.4	6.1	4.5	2.7

Figure D-95. Cross-shelf distributional patterns for *Mysidopsis intii*. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Mysidopsis intii
Stage: Adult

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/ Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.05	96.2	.40/.34
$\log(x+0)$	ns	ns/ns	ns/ns	.05	84.2	.01/.06
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: sig($p=.008$)
Transformation 2: $\log(x)$: sig($p=.005$)

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: sig($p=.009$)
Transformation 2: $\log(x)$: sig($p=.013$)

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

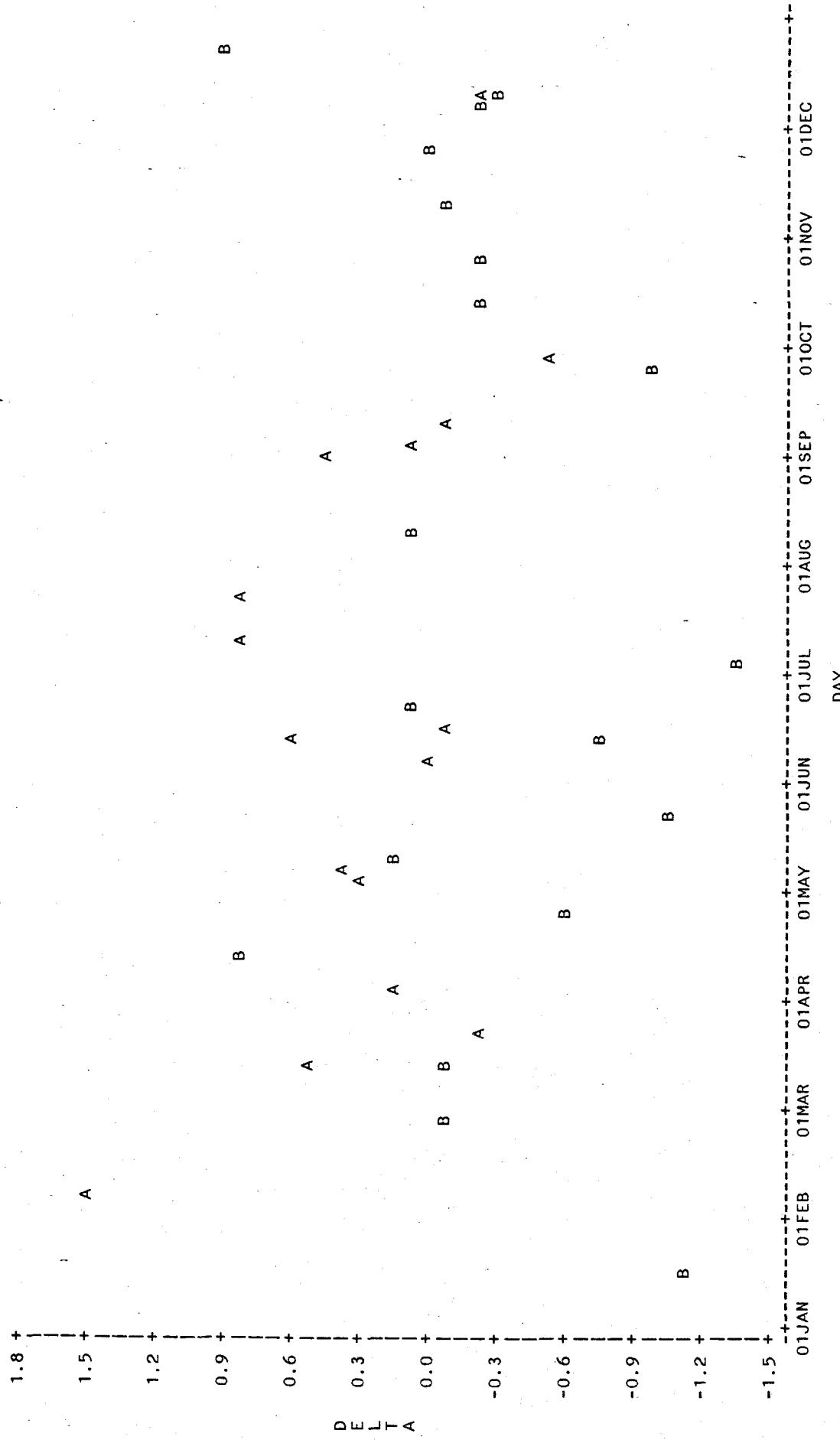
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 96. Summary of Test Results for Mysidopsis intii,
Adult.

SPCODE=Mysidopsis intii STAGE=ADULT

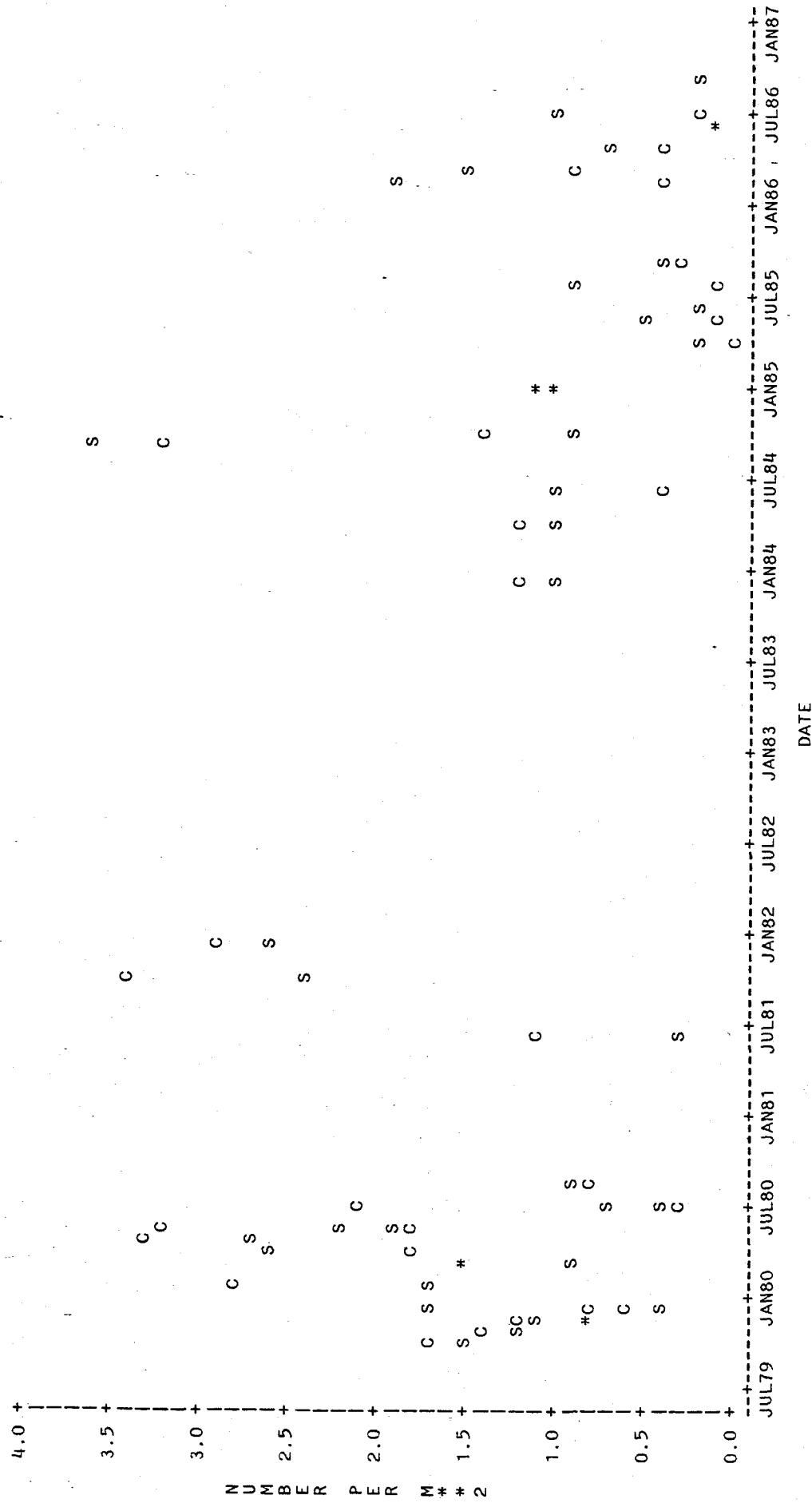


NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-97. Plot of preoperations (B) and operational (A) Delta values for *Mysidopsis intii* adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-100

SPCODE=Mysidopsis intii STAGE=ADULT



NOTE:

6 OBS HIDDEN

Figure D-98. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis intii* adults. Similar abundances at both locations are designated by asterisks.

D-101

TAXON: Mysidopsis intii

Stage: Immature

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.05	83.5	2.21/1.17
$\log(x+0)$	ns	ns/ns	ns/ns	.10	78.9	.04/.14
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns ($p=.063$)
Transformation 2: $\log(x)$: sig ($p=.028$)

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns ($p=.081$)
Transformation 2: $\log(x)$: sig ($p=.053$)

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
Two straight lines, same intercept (= 0)

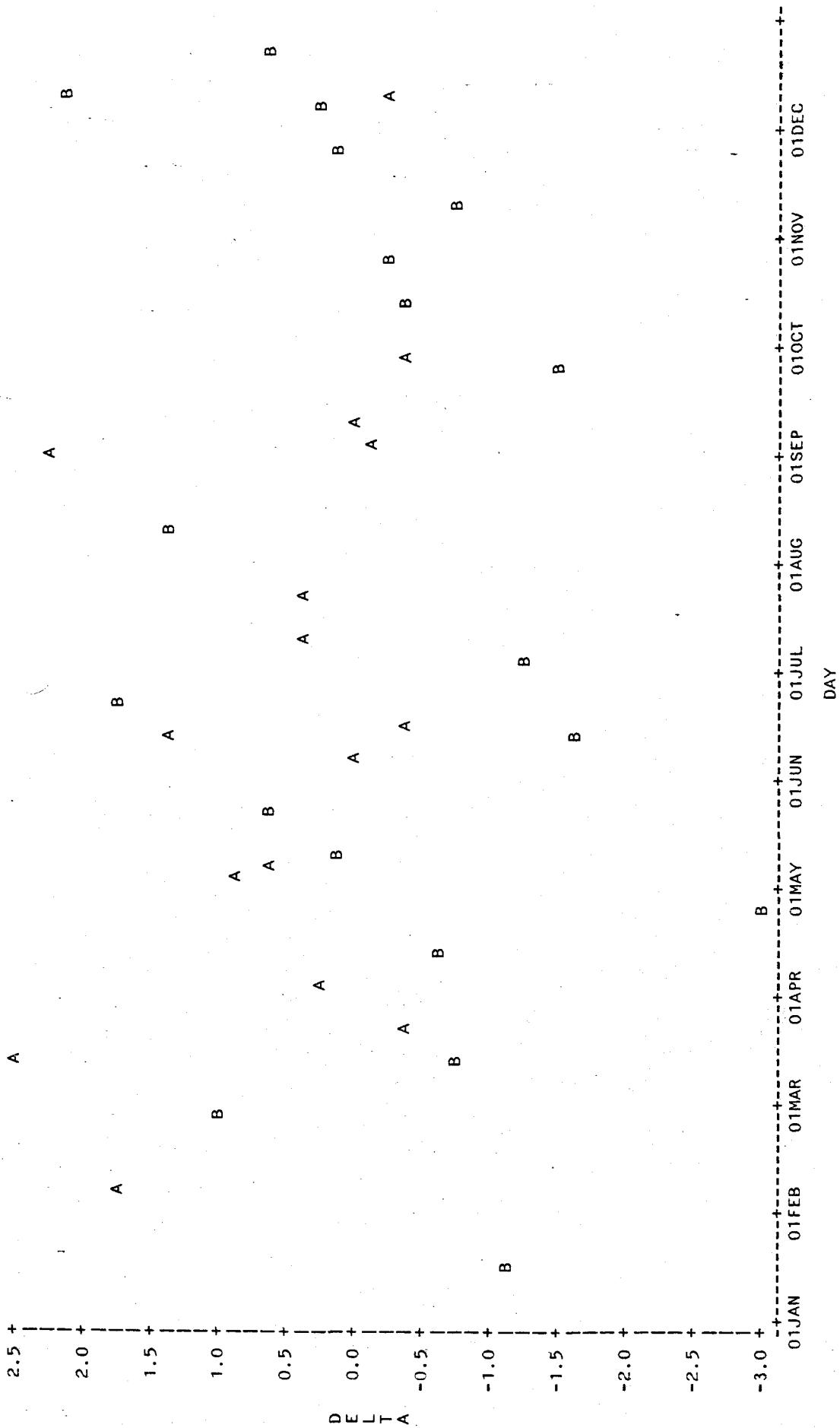
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D- 99. Summary of Test Results for Mysidopsis intii,
Immature.

SPCODE=Mysidopsis intii STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-100. Plot of preoperational (B) and operational (A) Delta values for Mysidopsis intii immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Mysidopsis intii STAGE=IMMATURE

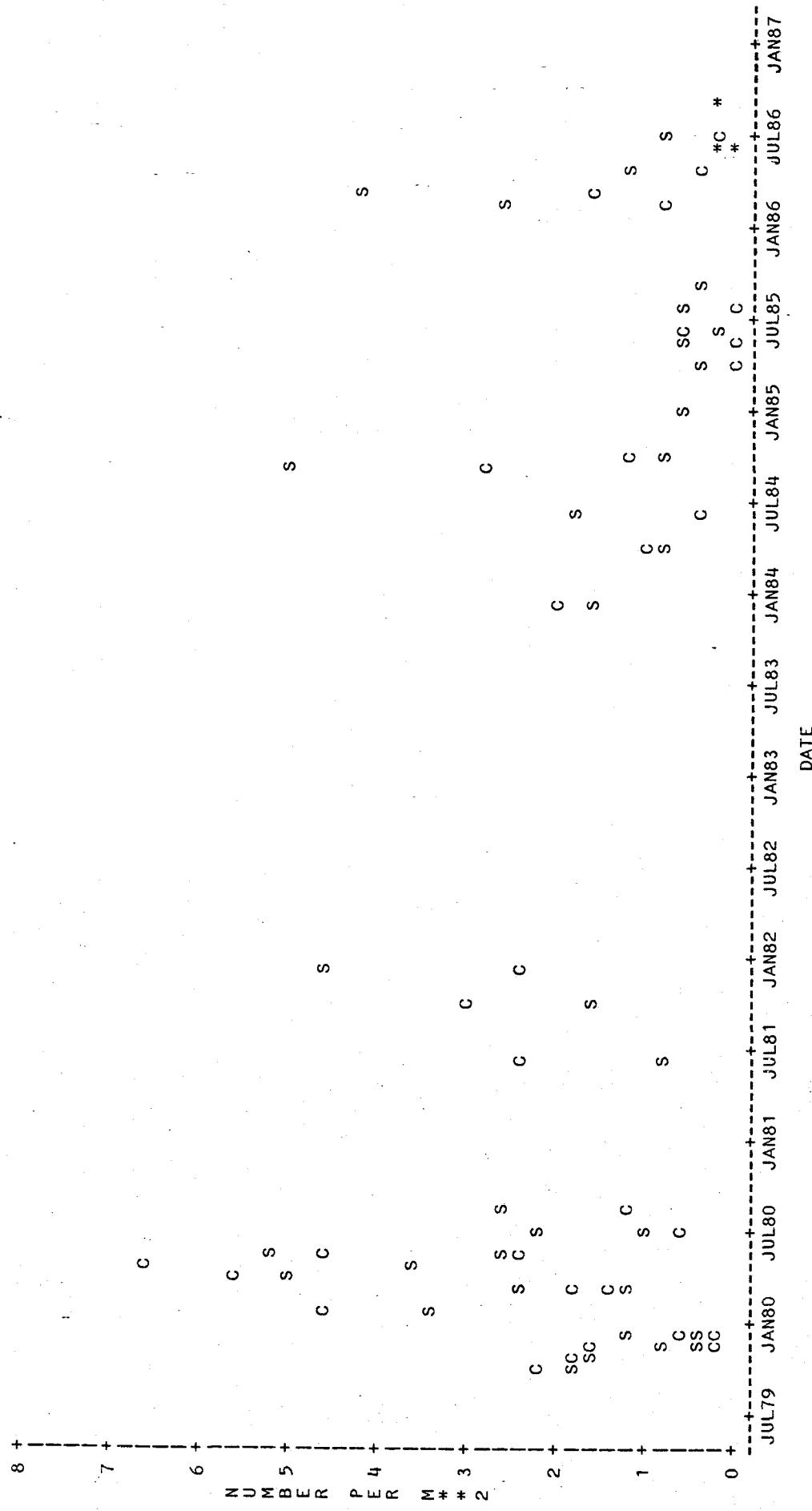


Figure D-101. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis intii* immatures. Similar abundances at both locations are designated by asterisks.

Taxon: Mysidopsis intii

Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>	
			<u>Deleted for Additivity</u>	
Untransformed	19	17		
$\log(x+0)$	19	17		
$\log(x+\text{constant})$	19	17		

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/ Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.10	67.0	.10/.09
$\log(x+0)$	ns	ns/ns	ns/ns	.10	47.5	5.0/.34
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: sig($p=.061$)
Transformation 2: $\log(x)$: sig($p=.041$)

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: sig($p=.039$)
Transformation 2: $\log(x)$: sig($p=.037$)

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):

Two different lines, atleast one curved

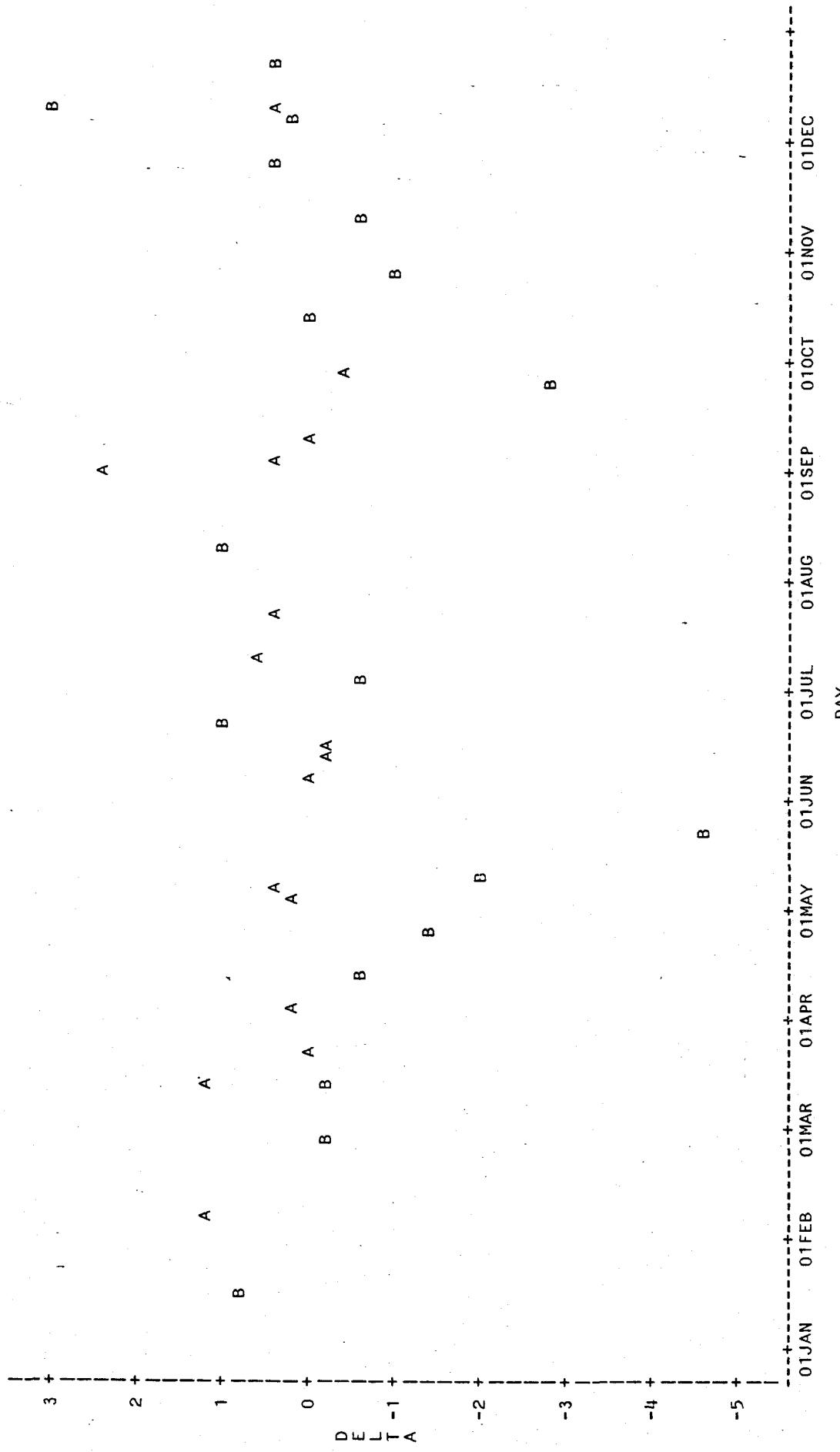
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-102. Summary of Test Results for Mysidopsis intii, Juvenile.

SPCODE=Mysidopsis intii STAGE=JUVENILE



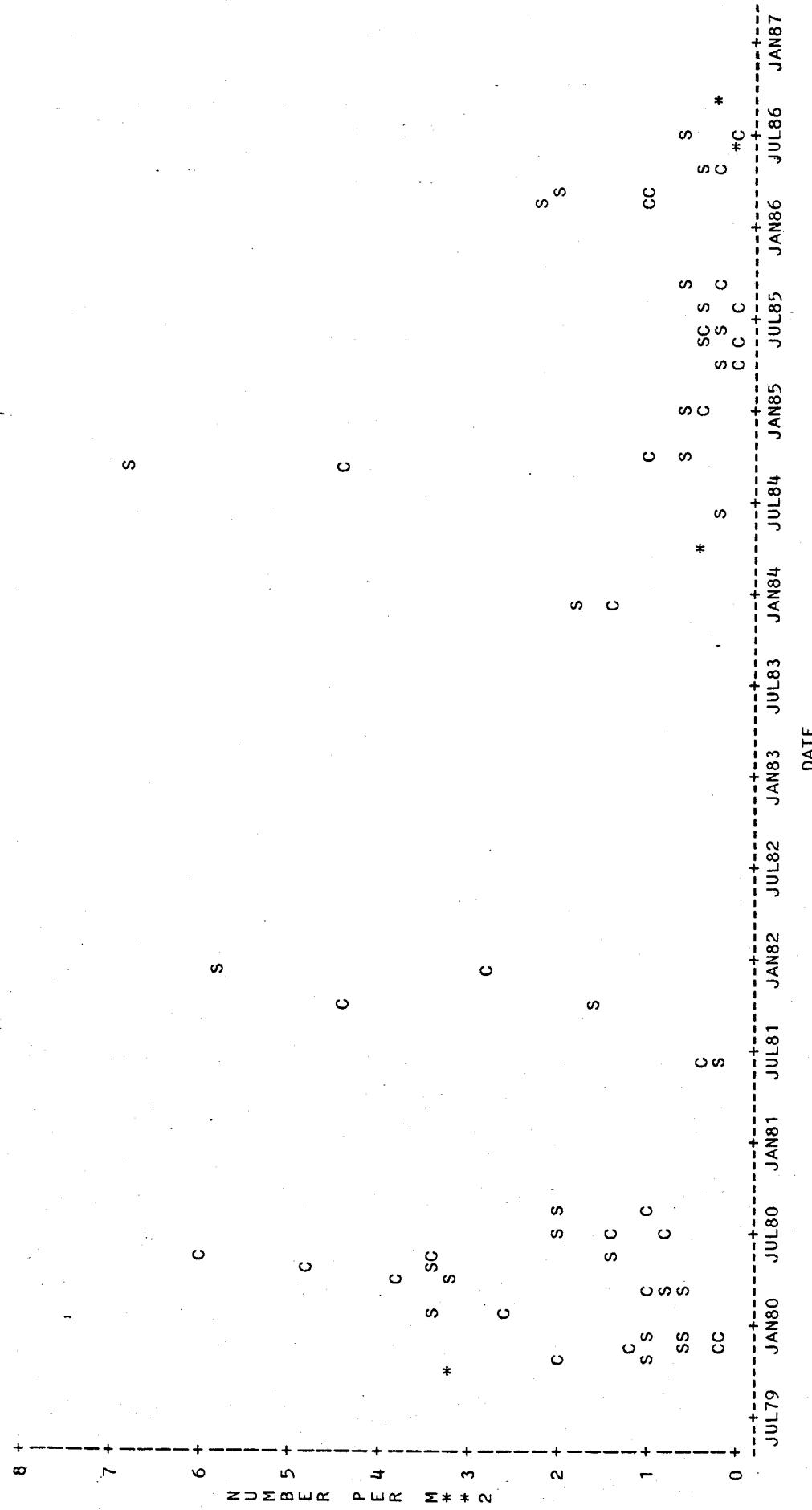
NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

1 OBS HIDDEN

Figure D-103. Plot of preoperational (B) and operational (A) Delta values for Mysidopsis intii juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-106

SPCODE=Mysidopsis intili STAGE=JUVENILE



NOTE: 10 OBS HIDDEN

Figure D-104. Abundance values at SONGS (S) and Control (C) plotted through time for *Mysidopsis intili* juveniles. Similar abundances at both locations are designated by asterisks.

D-107

TAXON: Acanthomysis macropsis
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note: Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	13.1	14.2/1.9
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	80.6	.07/.10
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns

* Transformation 2: $\log(x)$: ns

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: none: ns

Transformation 2: $\log(x)$: ns

Autoregressive Errors t-test

Transformation 1: none: ns first order model

Transformation 2: $\log(x)$: ns first order model

C

C

Binomial: sig

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

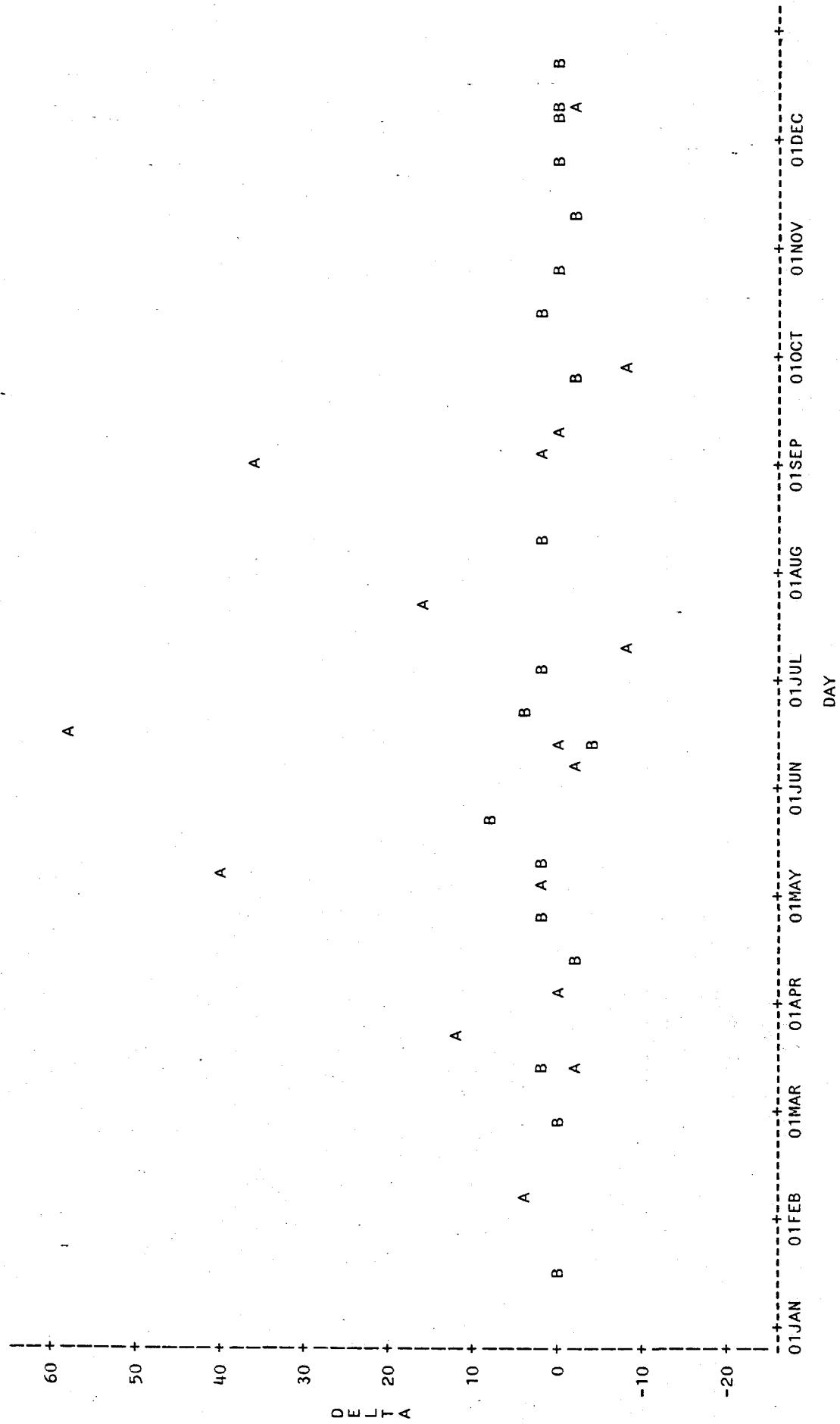
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-105. Summary of Test Results for Acanthomysis macropsis,
All Stages Combined

SPCODE=Acanthomyysis macropsis STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-106. Plot of preoperational (B) and operational (A) Delta values for Acanthomyysis macropsis all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-109

SPCODE=Acanthomysis macropsis STAGE=ALL

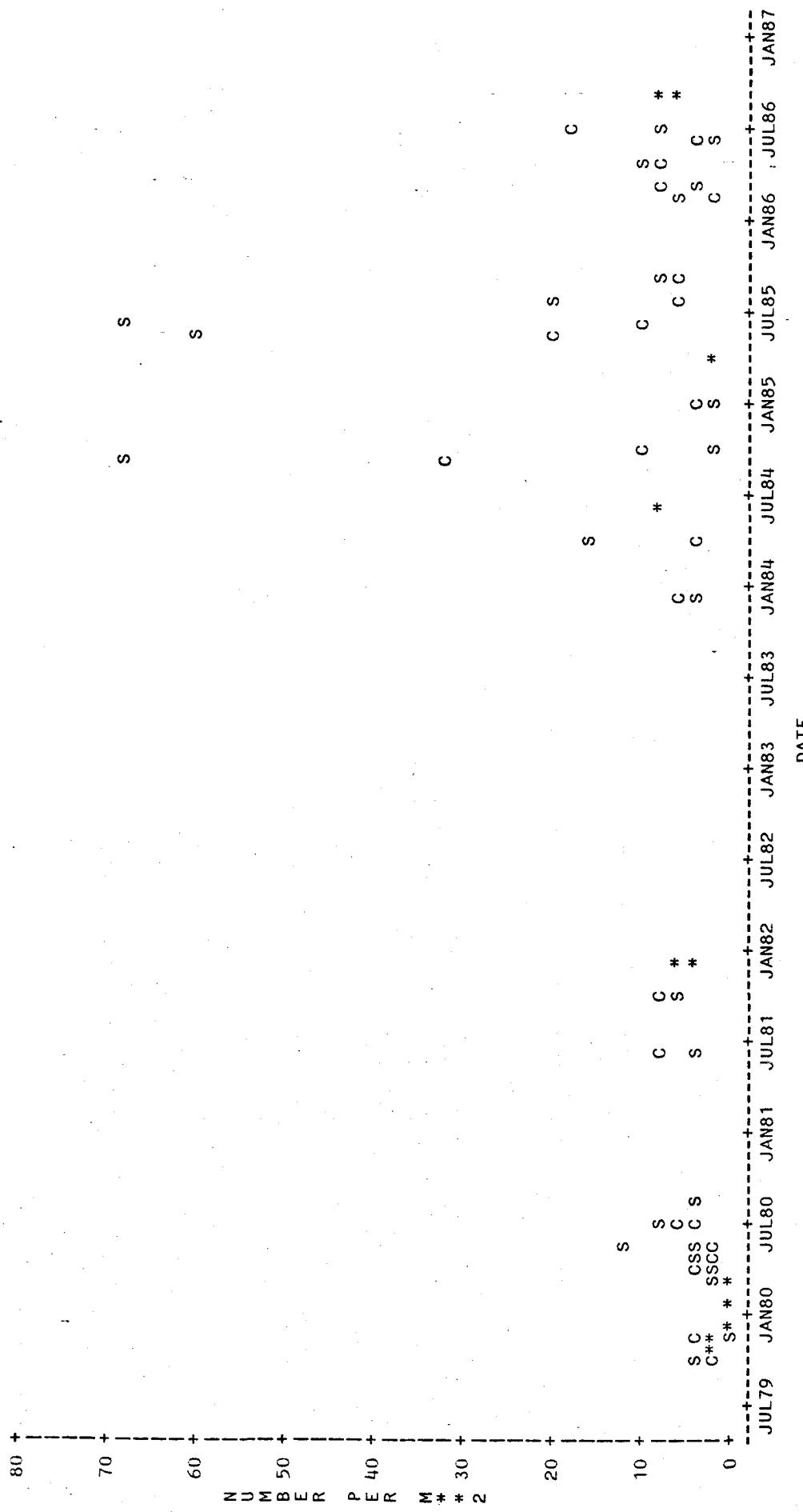


Figure D-107. Abundance values at SONGS (S) and Control (C) plotted through time for Acanthomysis macropsis all stages. Similar abundances at both locations are designated by asterisks.

D-110

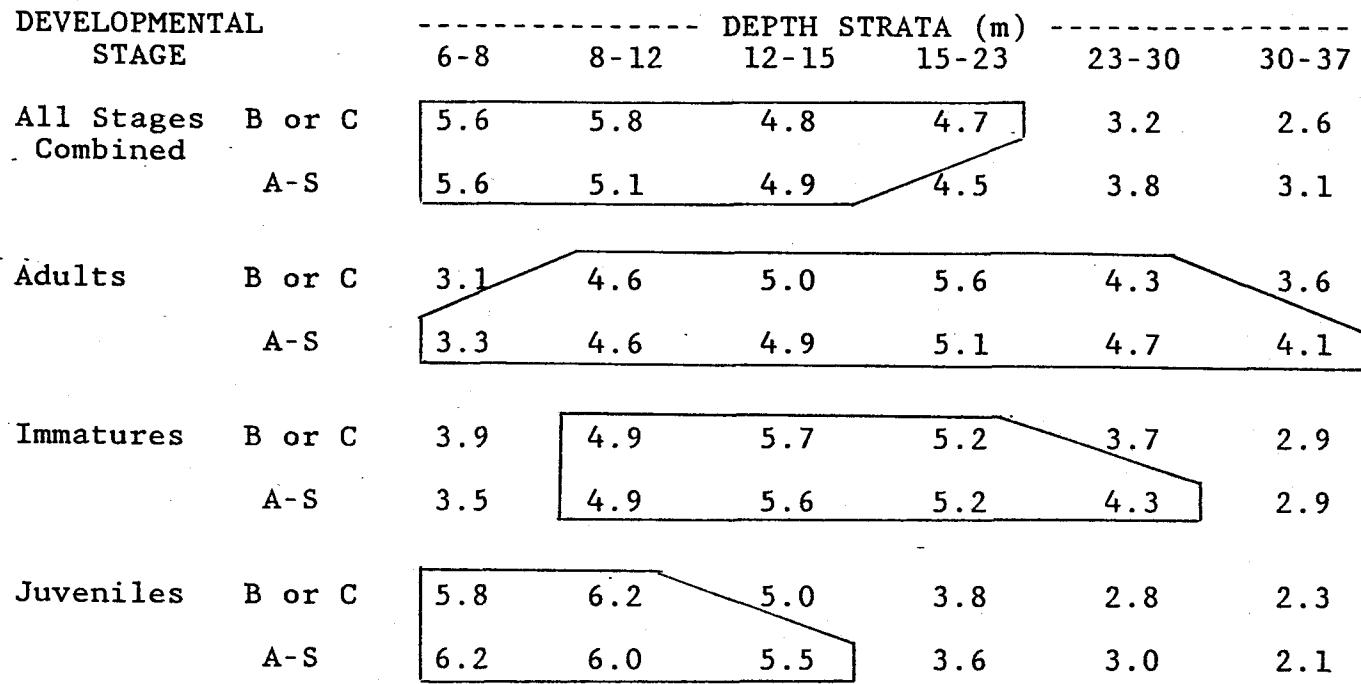


Figure D-108. Cross-shelf distributional patterns for *Acanthomysis macropsis*. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

TAXON: Acanthomysis macropsis

Stage: Adult

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	A	sig	ns/sig	ns/ns			
$\log(x+0)$	B	ns	ns/sig	ns/ns	.10	84.7	.03/.13
$\log(x+.1)$	B	ns	ns/sig	ns/ns	.10	77.2	.03/.07
$\log(x+1)$	B	ns	ns/sig	ns/ns	.10	54.7	.01/.01

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

Transformation 1: $\log(x)$: ns first order model
Transformation 2: $\log(x+.1)$: ns first order model

C
C

Binomial: ns

Regression (SONGS vs Control Abundances):

Two parallel straight lines, different intercepts

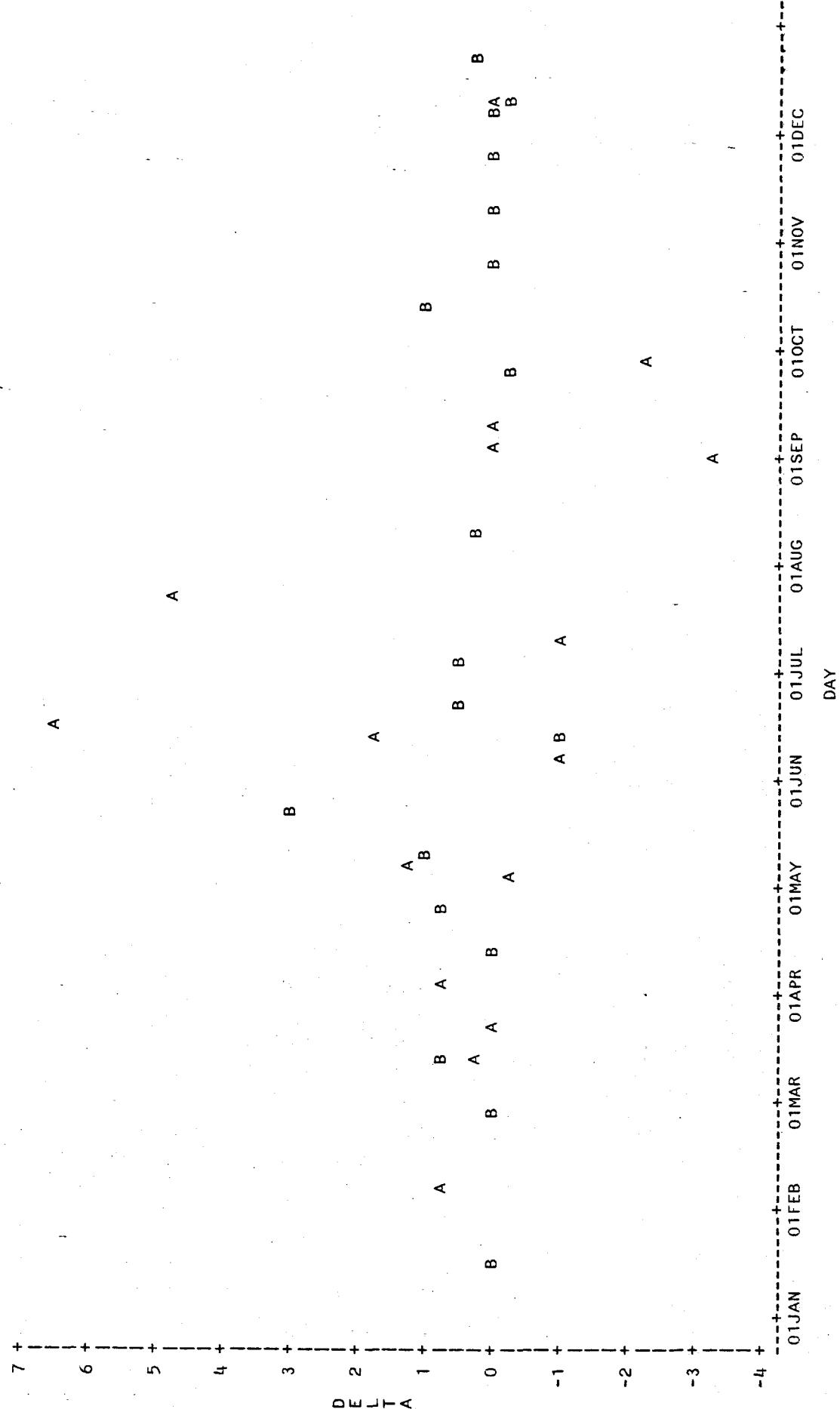
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-109. Summary of Test Results for Acanthomysis macropsis,
Adult.

SPCODE=Acanthomysis macropsis STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-110. Plot of preoperational (B) and operational (A) Delta values for Acanthomysis macropsis adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-113

SPCODE=Acanthomysis macropsis STAGE=ADULT

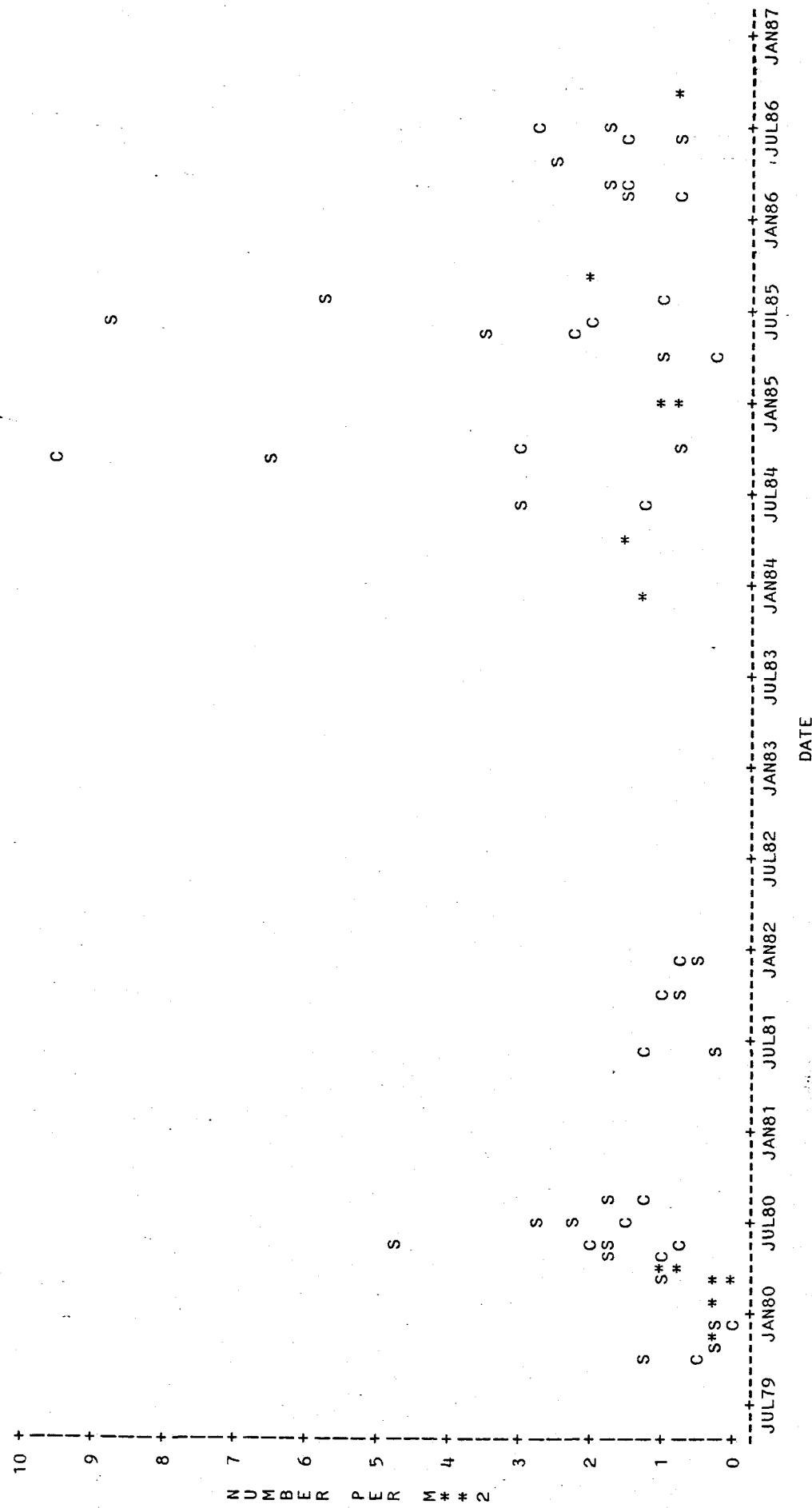


Figure D-111. Abundance values at SONGS (S) and Control (C) plotted through time for Acanthomysis macropsis adults. Similar abundances at both locations are designated by asterisks.

D-114

TAXON: Acanthomysis macropsis
Stage: Immature

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns	ns/sig	ns/ns	.10	20.0
$\log(x+0)$	B	ns	ns/sig	ns/ns	.10	68.0
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A

* Transformation 2: $\log(x)$: ns

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A

Transformation 2: $\log(x)$: ns

Autoregressive Errors t-test

** Transformation 1: none: ns, first order model

Transformation 2: $\log(x)$: ns first order model

C

Binomial: ns

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

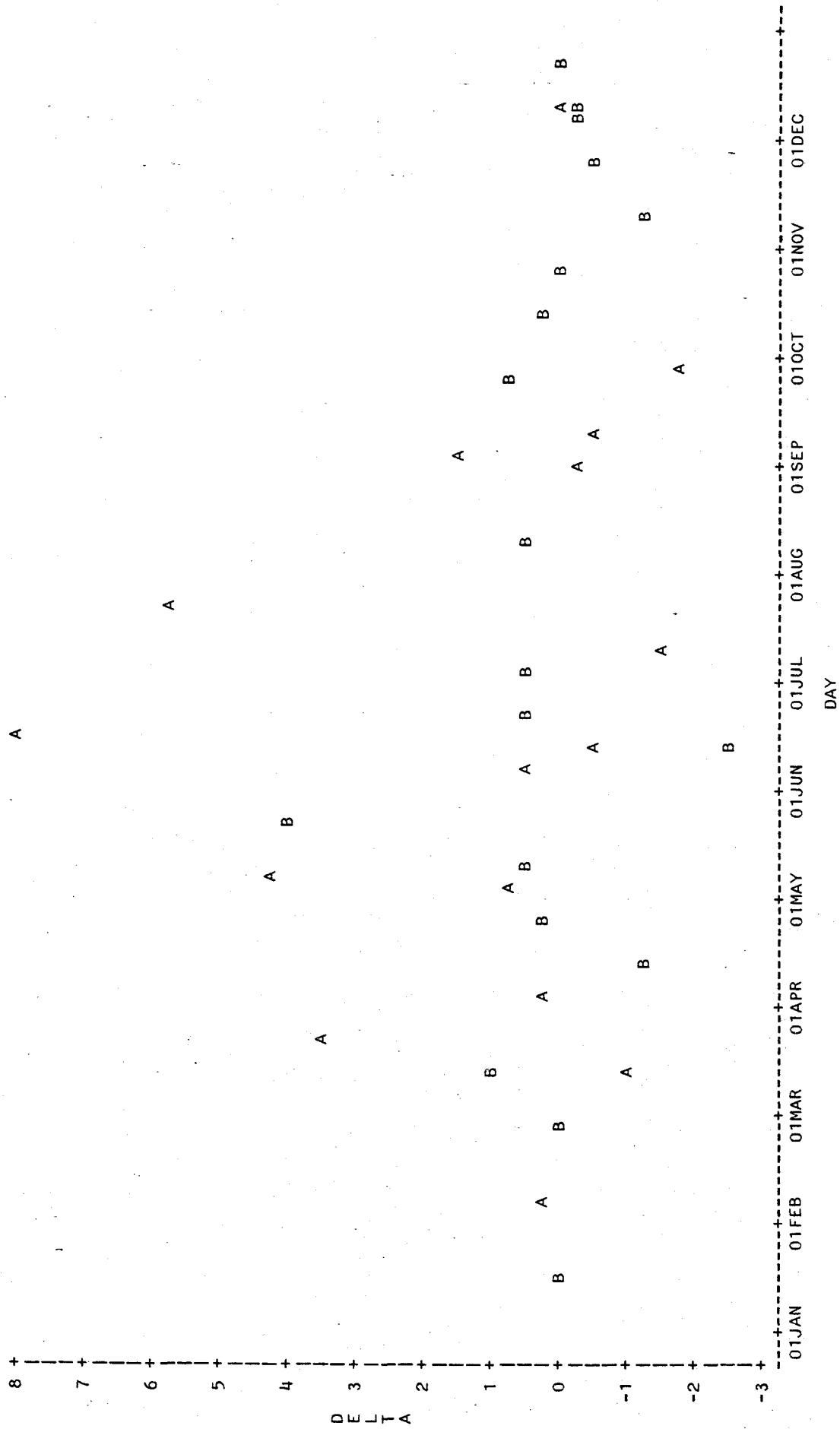
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-112. Summary of Test Results for Acanthomysis macropsis, Immature.

SPCODE=Acanthomysis macropsis STAGE=IMMATURE



NOTE:

1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-113. Plot of preoperational (B) and operational (A) Delta values for Acanthomysis macropsis immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-116

SPCODE=Acanthomysis macropsis STAGE=IMMATURE

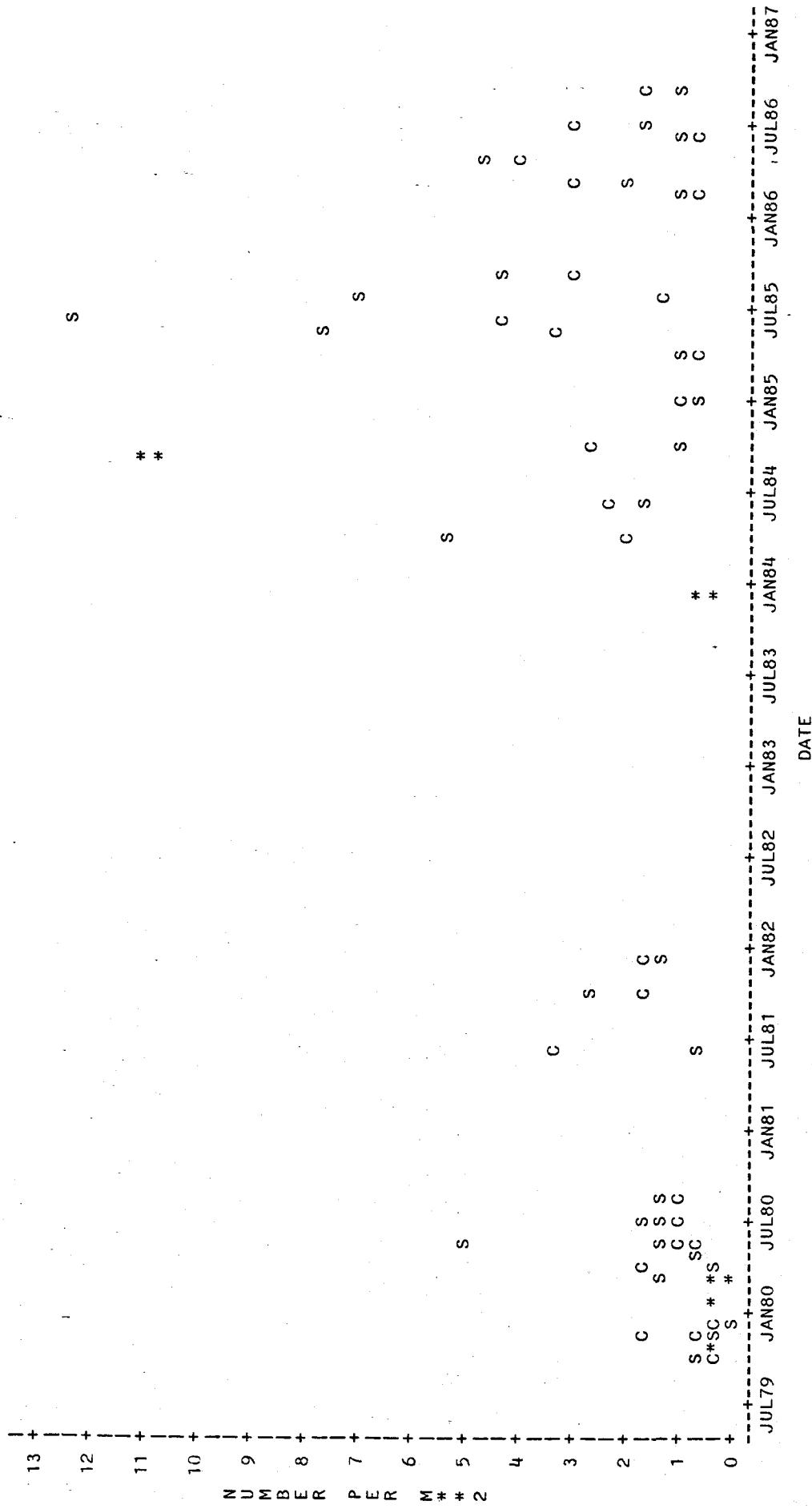


Figure D-114. Abundance values at SONGS (S) and Control (C) plotted through time for *Acanthomysis macropsis* immatures. Similar abundances at both locations are designated by asterisks.

D-117

TAXON: Acanthomysis macropsis
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends Before/ After	α	Power % at α	Delta Variance	
	Note:	Before/After	After				Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	<10	2.7/.50
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	58.0	.09/.16
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x)$: ns

Autoregressive Errors t-test

Transformation 1: none: ns first order model
Transformation 2: $\log(x)$: ns first order model

C
C

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

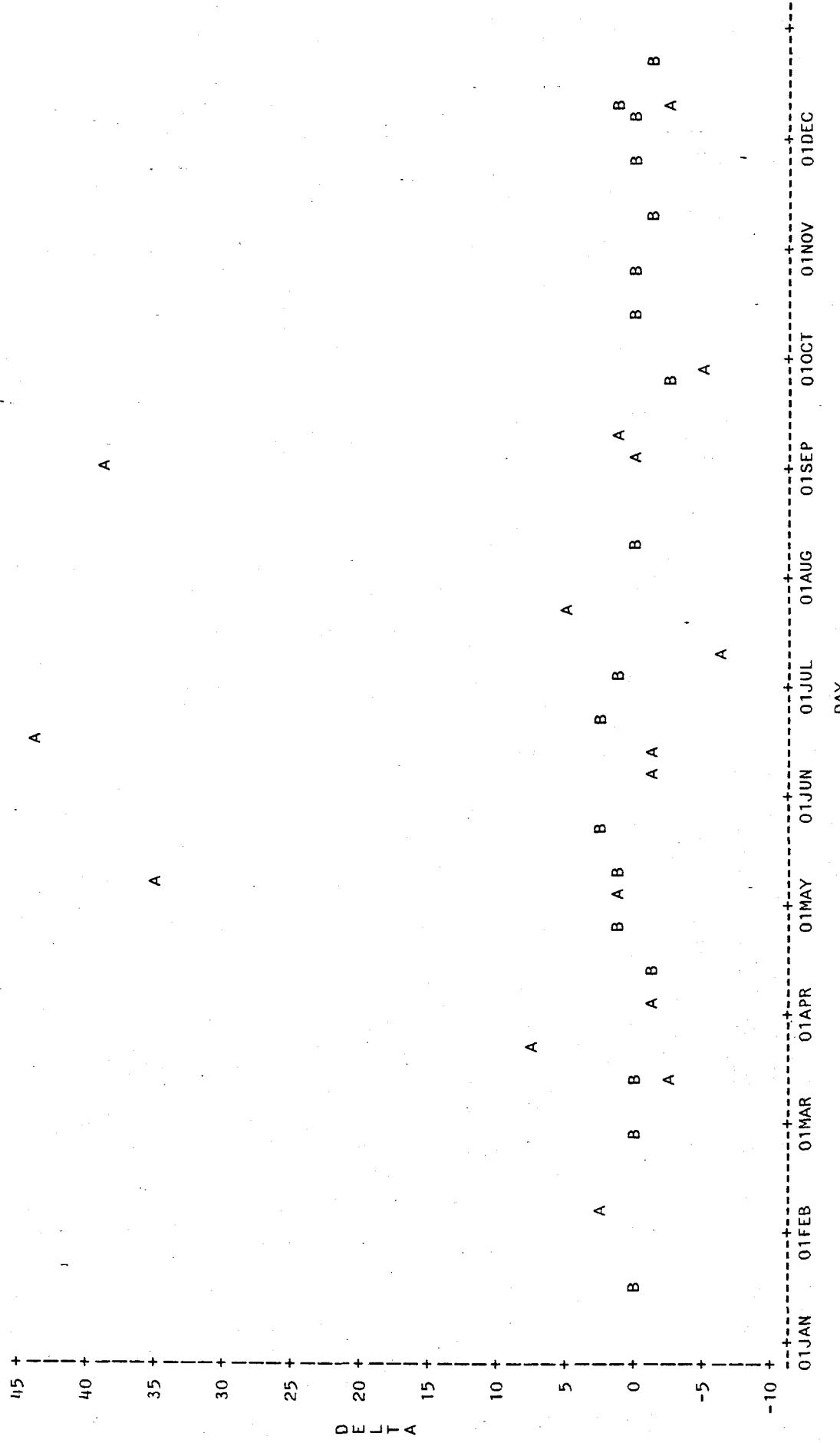
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-115. Summary of Test Results for Acanthomysis macropsis, Juvenile.

SPCODE=Acanthomysis macropsis STAGE=JUVENILE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE 1 OBS HIDDEN

Figure D-116. Plot of preoperations (B) and operational (A) Delta values for *Acanthomysis macropsis* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-116

SPCODE=Acanthomysis macropsis STAGE=JUVENILE

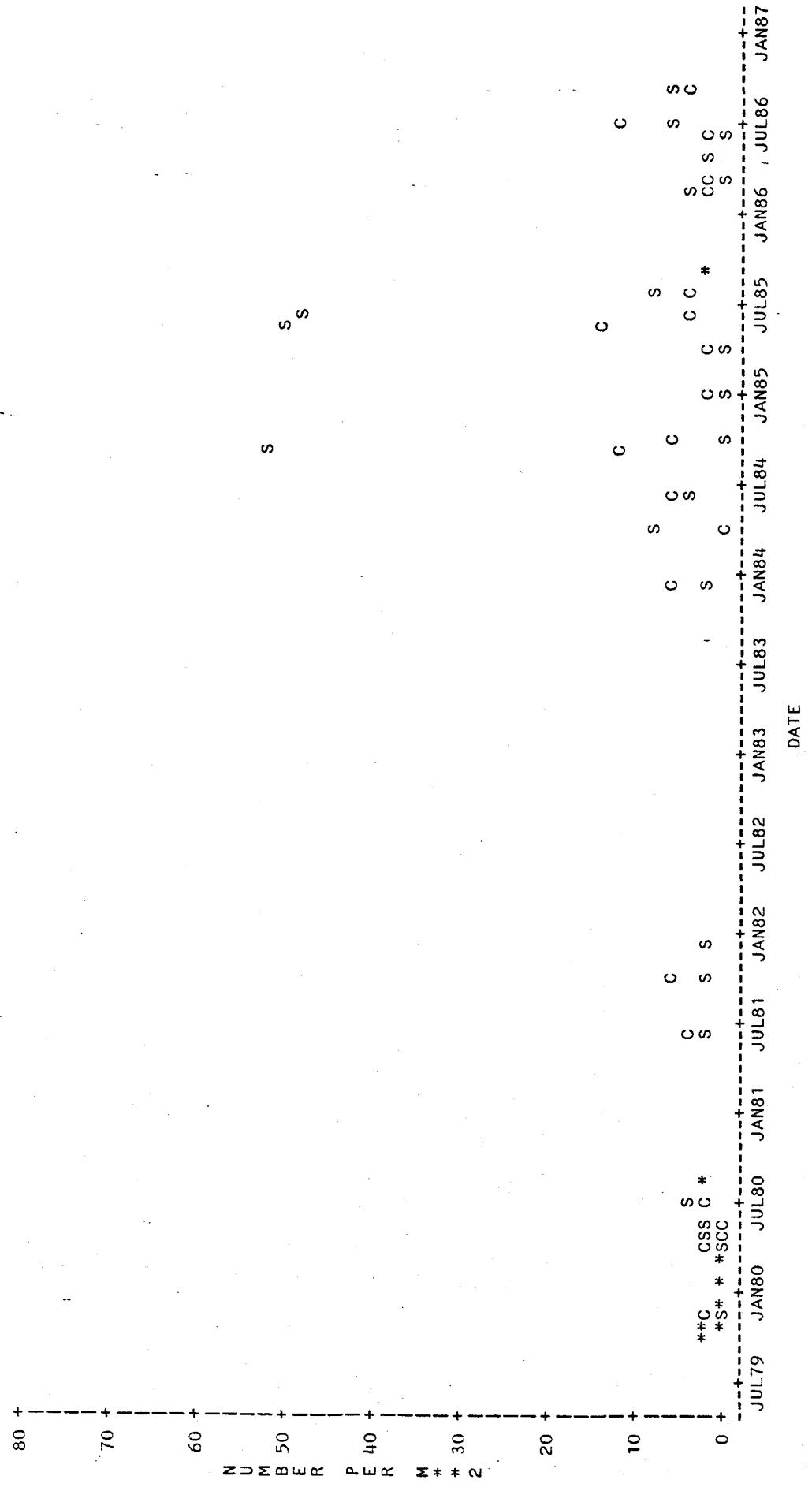


Figure D-117. Abundance values at SONGS (S) and Control (C) plotted through time for *Acanthomysis macropsis* juveniles. Similar abundances at both locations are designated by asterisks.

D-120

Taxon: Offshore
Stage: All

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note:	Trends Before/ Before/After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	65.5	27.08/.84
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	78.1	.18/.05
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: none: sig, ($p=.083$) first order model
* Transformation 2: $\log(x)$: sig, ($p=.062$) first order model

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-118. Summary of Test Results for Offshore,
All Stages Combined.

SPCODE=Offshore summary group STAGE=ALL

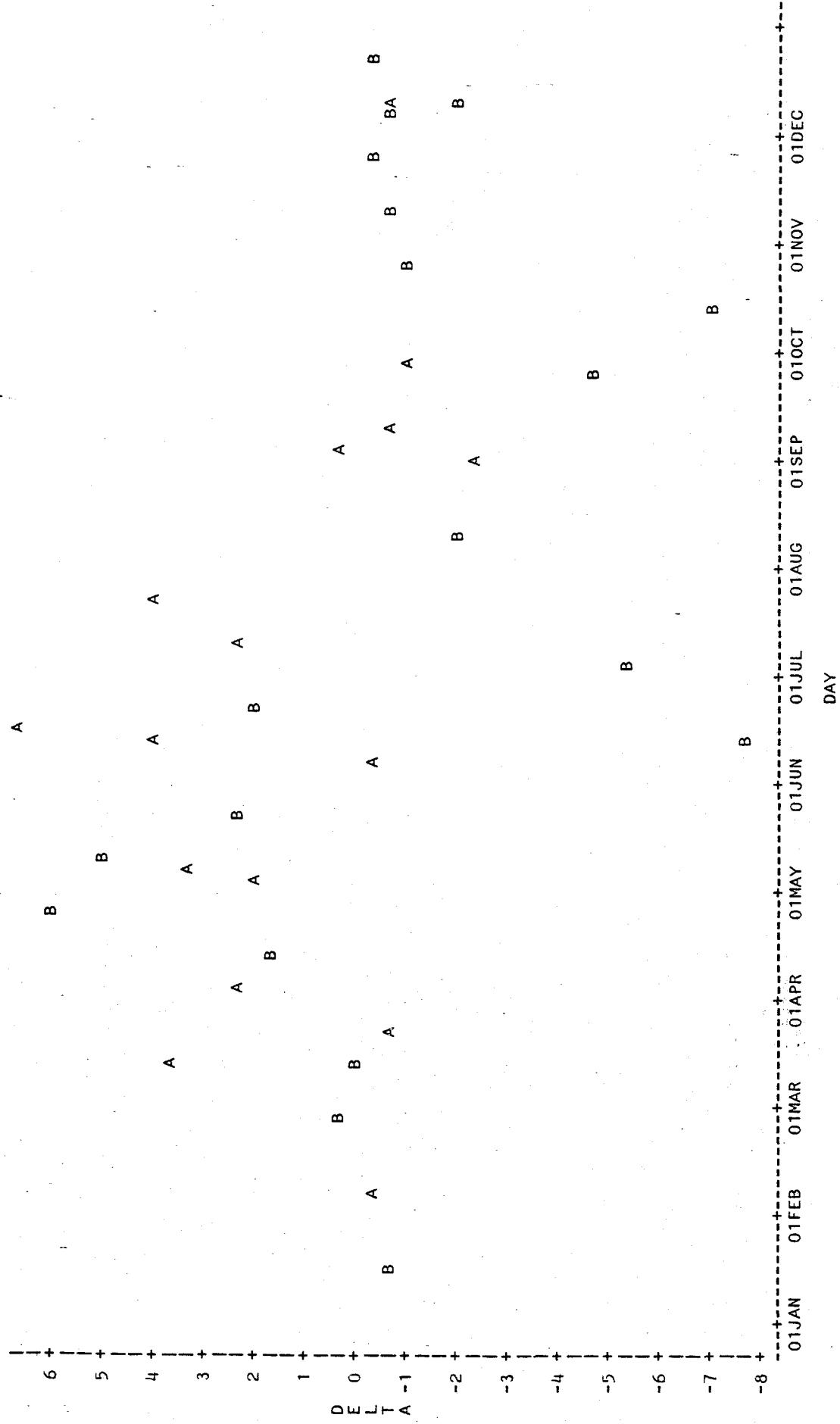


Figure D-119. Plot of preoperational (B) and operational (A) Delta values for Offshore summary group all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Offshore summary group STAGE=ALL

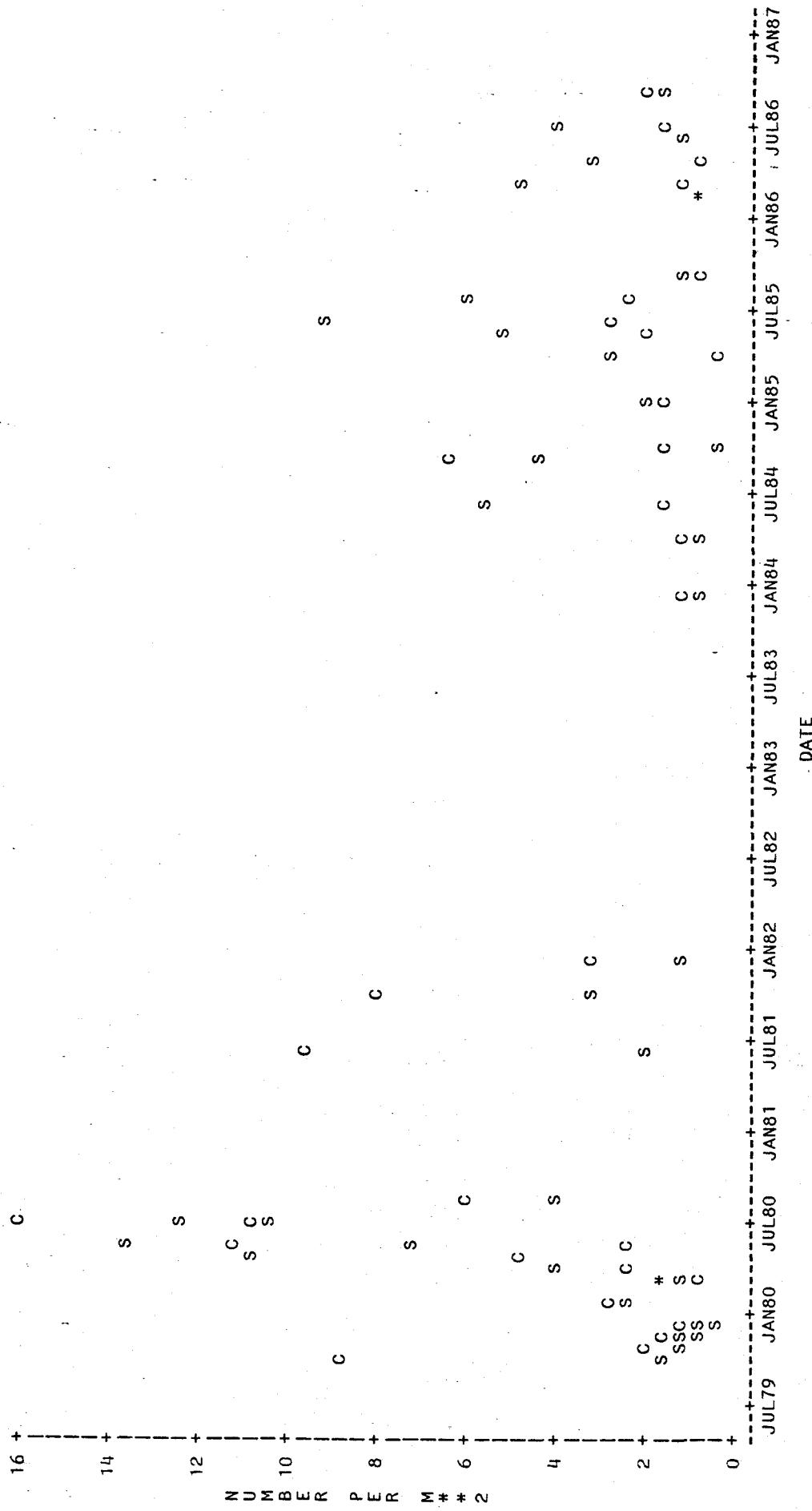


Figure D-120. Abundance values at SONGS (S) and Control (C) plotted through time for offshore summary group all stages. Similar abundances at both locations are designated by asterisks.

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages Combined	B or C	2.3	2.4	3.8	5.7	5.9	6.0
	A-S	2.1	2.3	3.5	5.1	6.4	6.2
Adults	B or C		2.0	2.5	3.8	5.3	5.3
	A-S		2.1	2.5	3.4	5.4	5.5
Immatures	B or C	2.4	2.4	3.2	5.3	6.2	6.1
	A-S	2.5	2.5	2.9	5.1	6.2	6.2
Juveniles	B or C		1.9	3.3	5.0	4.4	4.7
	A-S		1.8	3.0	4.6	5.1	4.7

Figure D-121. Cross-shelf distributional patterns for Offshore Taxa. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Offshore
Stage: Adult

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	A	sig	ns/ns	ns/ns			
$\log(x+0)$		ns	ns/ns	ns/ns	.10	75.3	.19/.02
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	67.6	.16/.01
$\log(x+1)$	A	sig	ns/ns	ns/ns			

Chi Square; H_0 : even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$: sig($p=.013$)
Transformation 2: $\log(x+.1)$: sig($p=.006$)

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: sig($p=.009$)
Transformation 2: $\log(x+.1)$: sig($p=.005$)

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

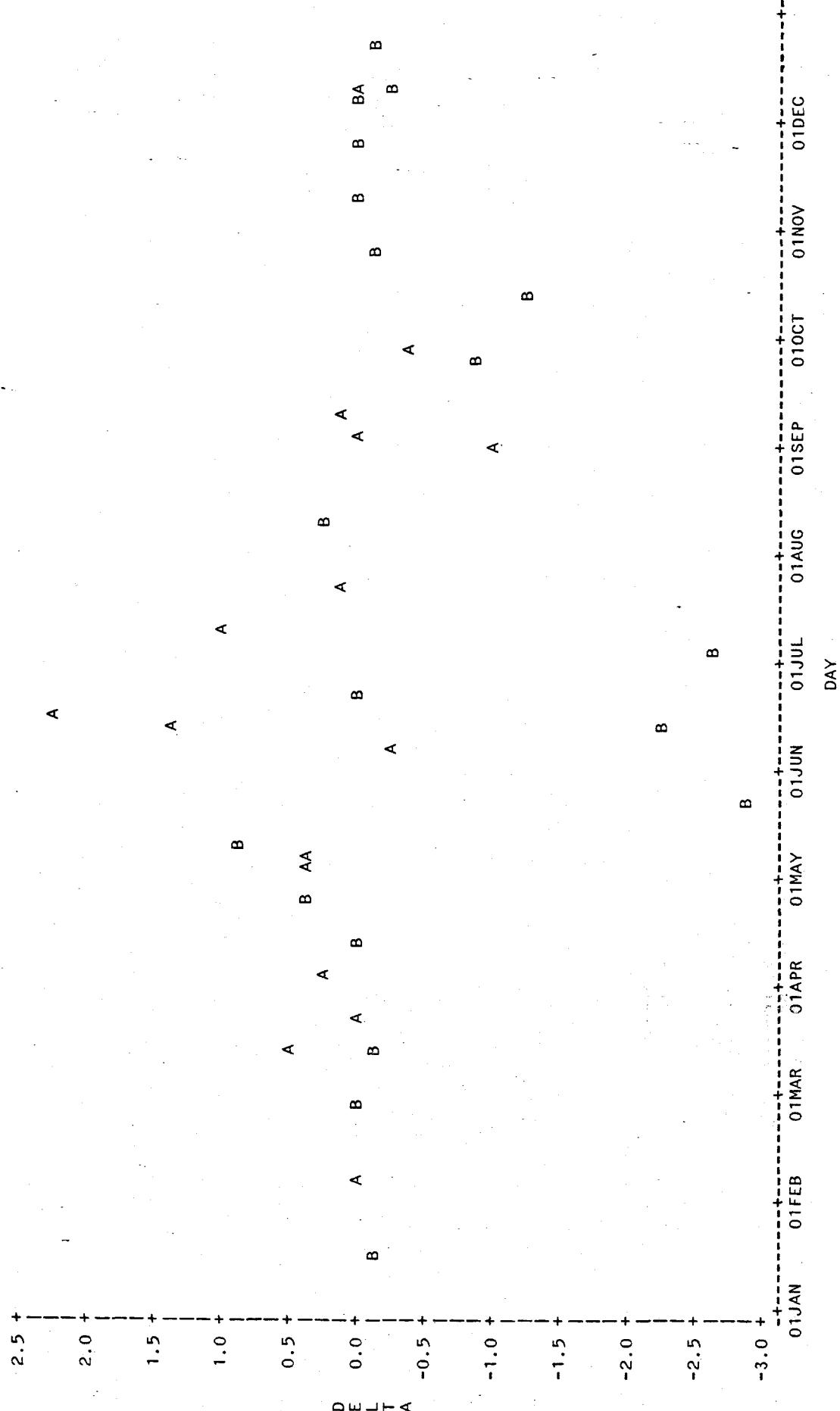
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-122. Summary of Test Results for Offshore,
Adult.

SPCODE=Offshore summary group STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-123. Plot of preoperational (B) and operational (A) Delta values for Offshore summary group adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Offshore summary group STAGE=ADULT

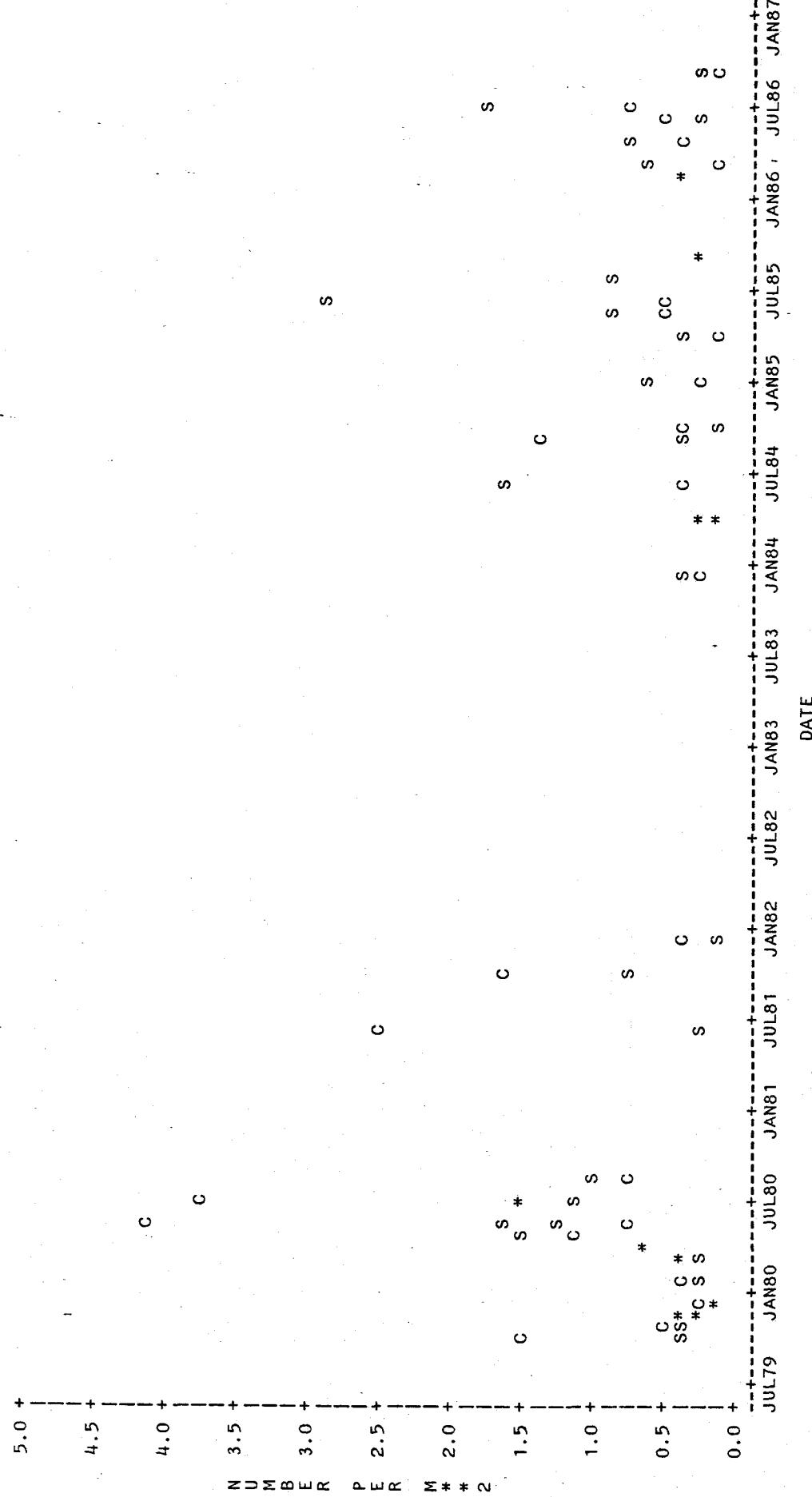


Figure D-124. Abundance values at SONGS (S) and Control (C) plotted through time for Offshore summary group adults. Similar abundances at both locations are designated by asterisks.

Taxon: Offshore
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends Before/ After	α	Power % at α	Delta Variance	
	Note:	Before/After	After				Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	48.7	2.81/.10
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	71.5	.20/.06
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A

* Transformation 2: $\log(x)$: sig($p=.055$)

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A

Transformation 2: $\log(x)$: sig($p=.066$)

Autoregressive Errors t-test

** Transformation 1: none: ns, first order model

Transformation 2: $\log(x)$: ns first order model

C

Binomial: ns

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

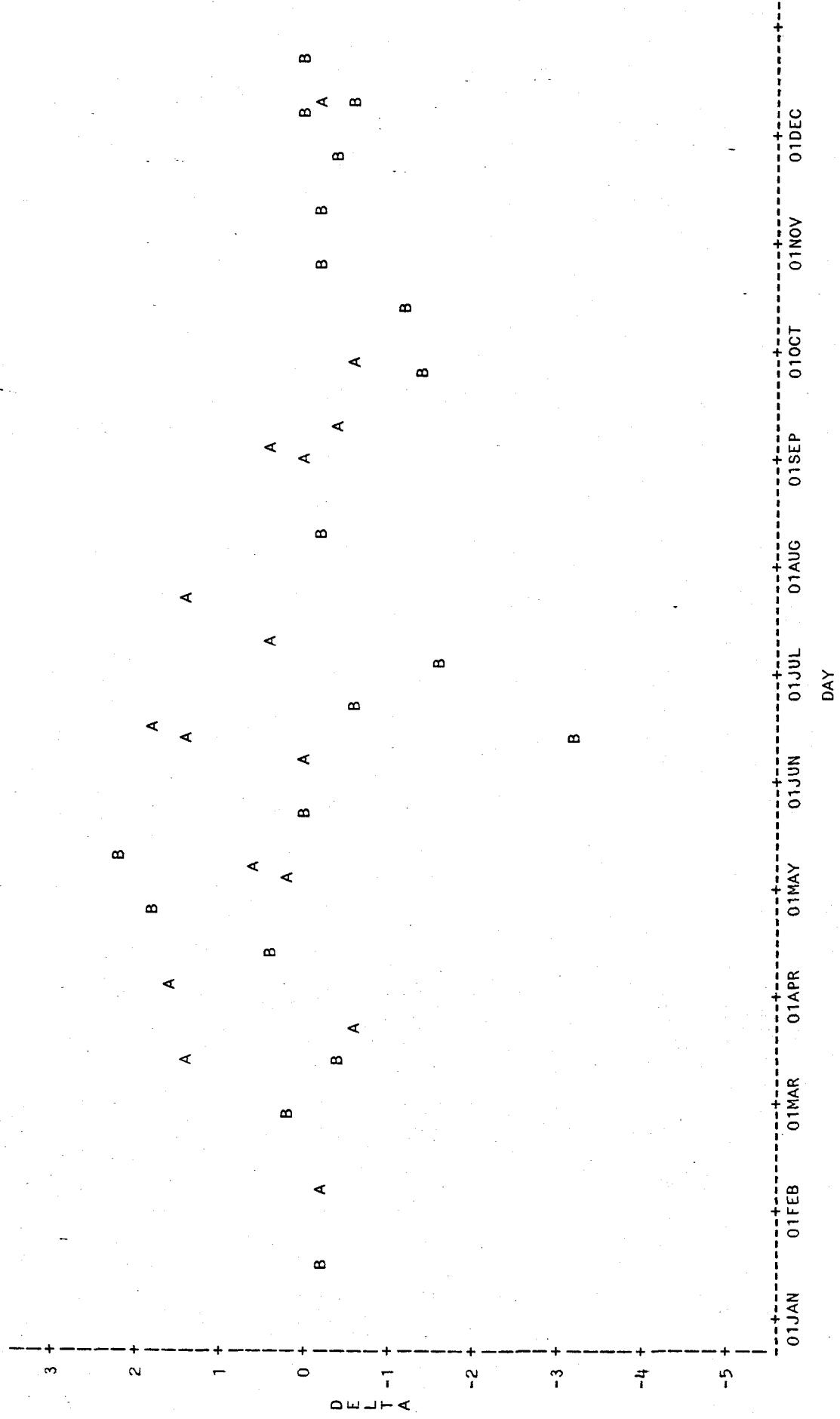
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-125. Summary of Test Results for Offshore,
Immature.

SPCODE=Offshore summary group STAGE=IMMATURE

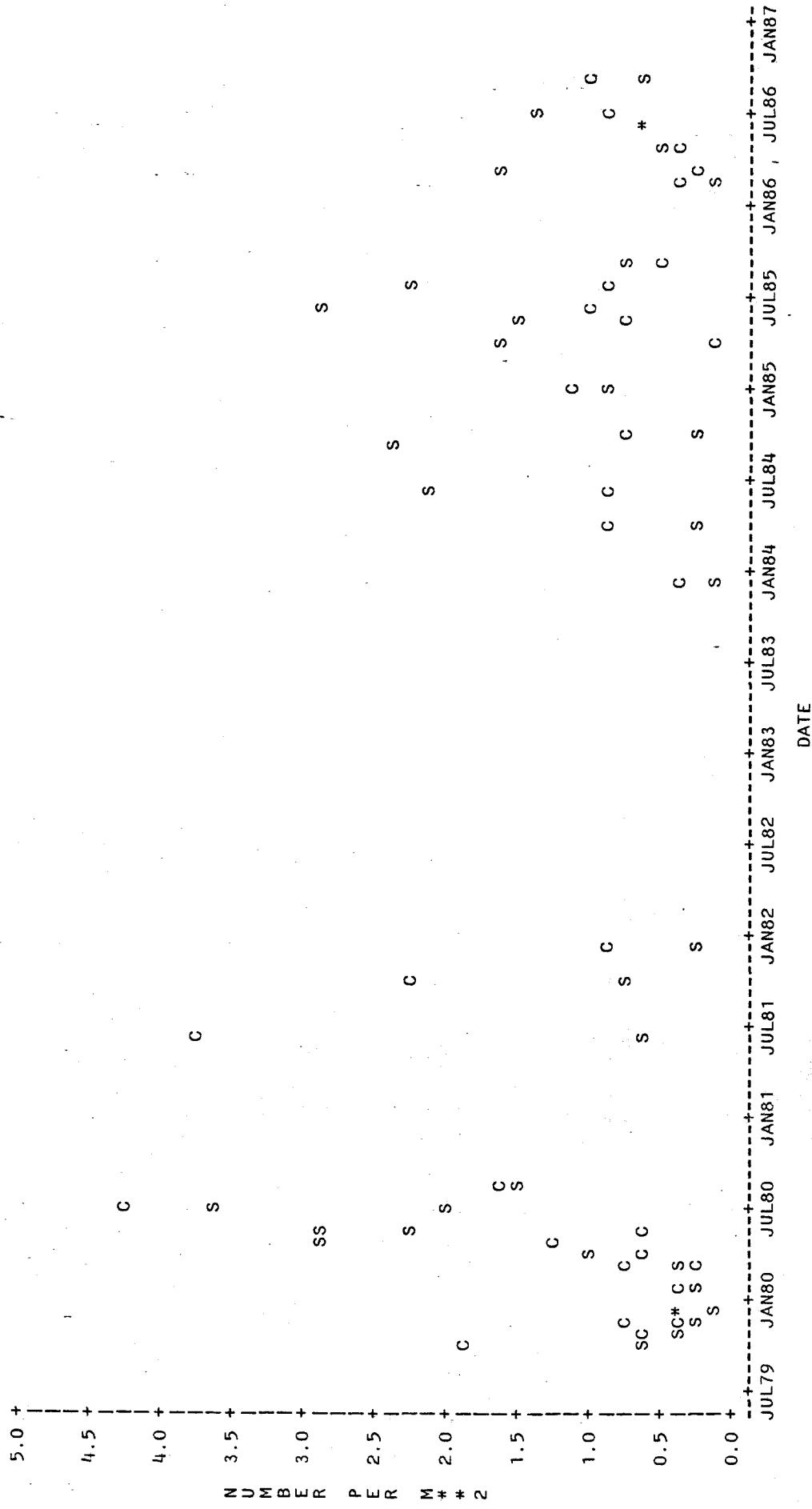


NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-126. Plot of preoperational (B) and operational (A) Delta values for Offshore summary group immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-129

SPCODE=Offshore summary group STAGE=IMMATURE



NOTE:

8 OBS HIDDEN

Figure D-127. Abundance values at SONGS (S) and Control (C) plotted through time for offshore summary group immatures. Similar abundances at both locations are designated by asterisks.

D-130

Taxon: Offshore
Stage: Juvenile

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	
	Note:						Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	64.6	10.87/.7
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	61.7	.17/.15
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A

* Transformation 2: $\log(x)$: sig($p=.014$)

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A

Transformation 2: $\log(x)$: sig($p=.015$)

Autoregressive Errors t-test

** Transformation 1: none: ns, first order model

Transformation 2: $\log(x)$: ns first order model

C

Binomial: ns($p=.054$)

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0

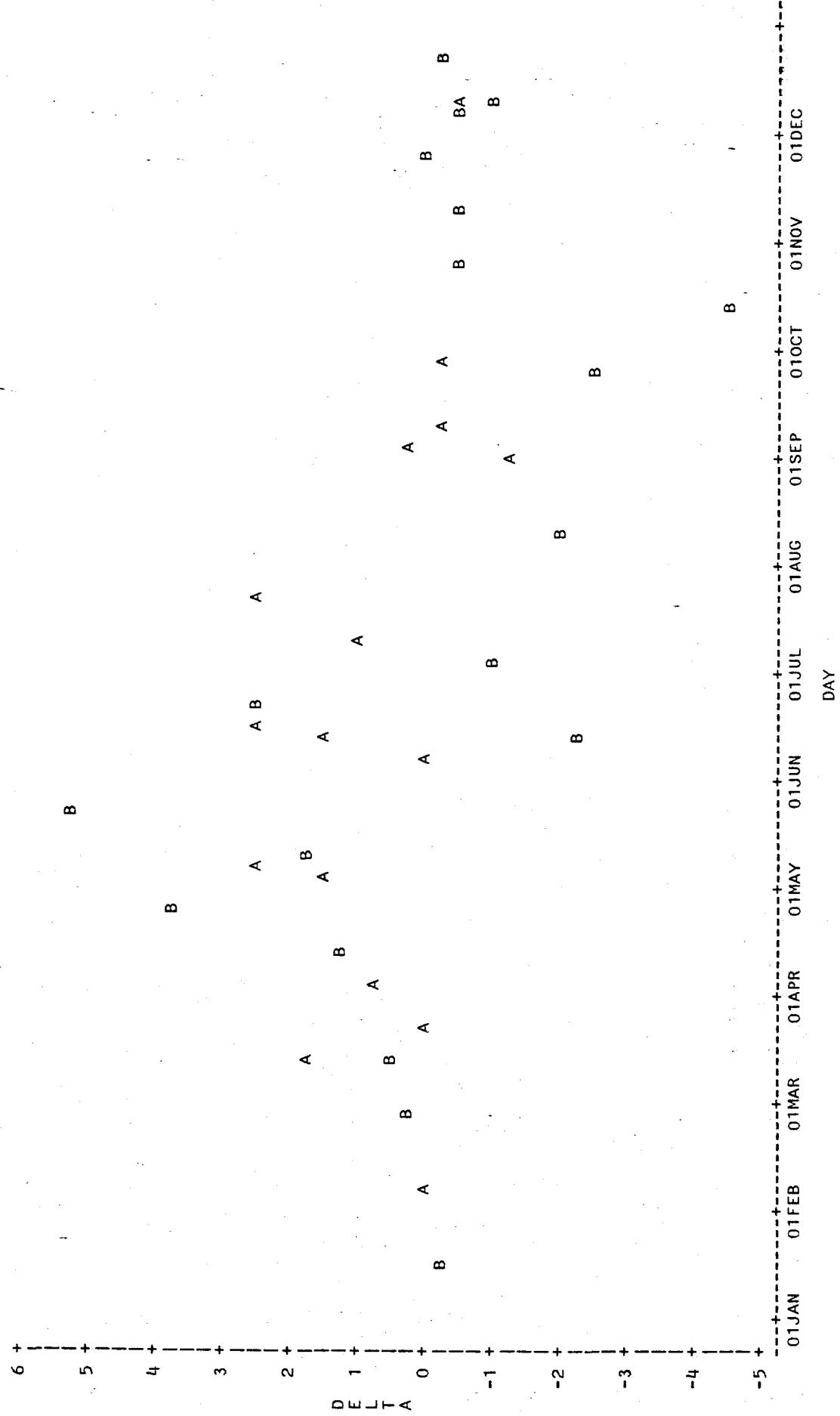
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-128. Summary of Test Results for Offshore,
Juvenile.

SPCODE=Offshore summary group STAGE=JUVENILE

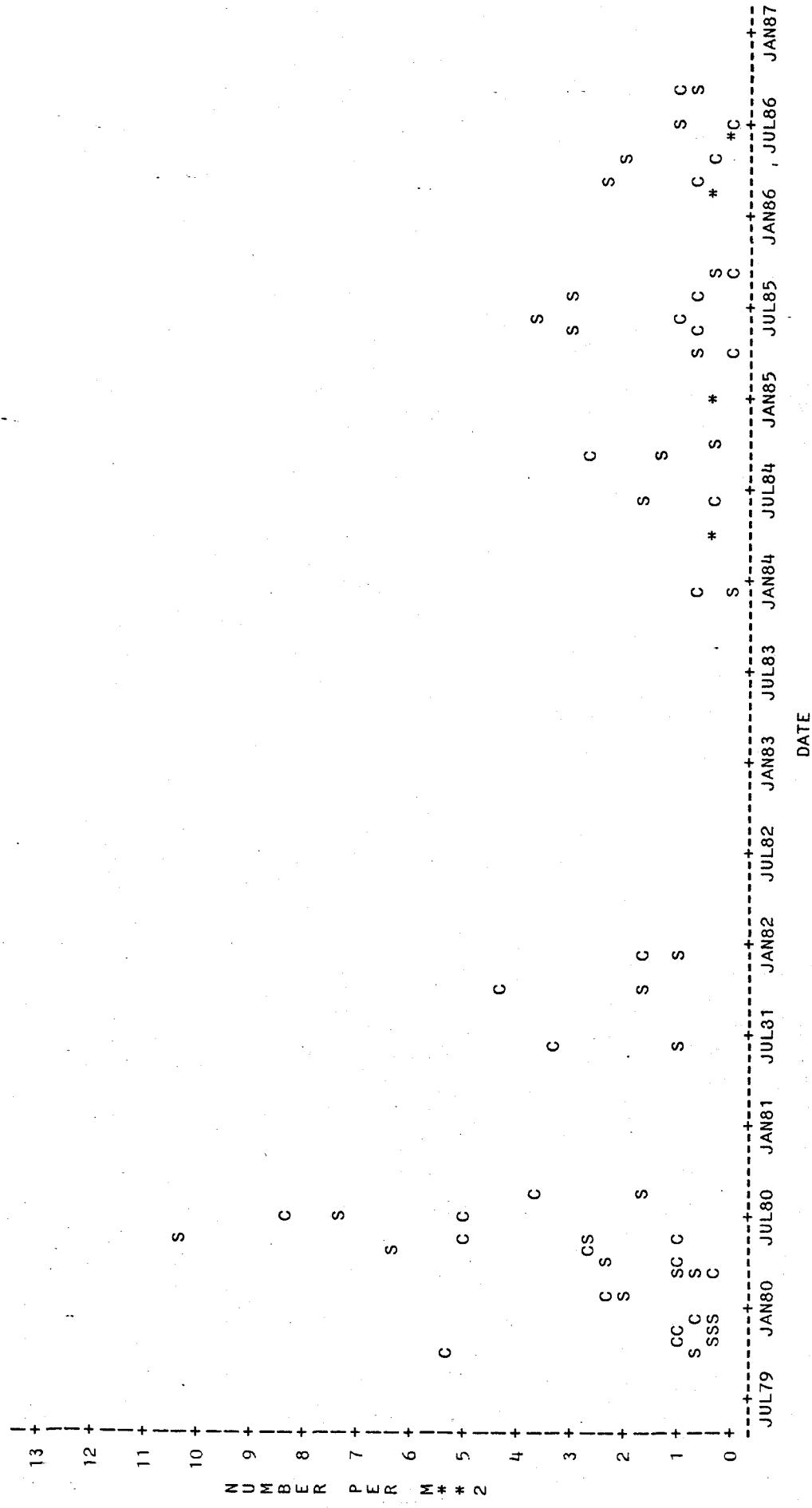


NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-129. Plot of preoperational (B) and operational (A) Delta values for Offshore summary group juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-132

SPCODE=offshore summary group STAGE=JUVENILE



NOTE: 11 OBS HIDDEN

Figure D-130. Abundance values at SONGS (S) and Control (C) plotted through time for offshore summary group juveniles. Similar abundances at both locations are designated by asterisks.

D-133

Taxon: Neomysis kadiakensis
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u> <u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note:	Trends Before/ Before/After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	61.7
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	73.1
$\log(x+.1)$	N/A					.21/.07
$\log(x+1)$	N/A					

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: none: sig(.093), first order model
* Transformation 2: $\log(x)$: sig(.062), first order model

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

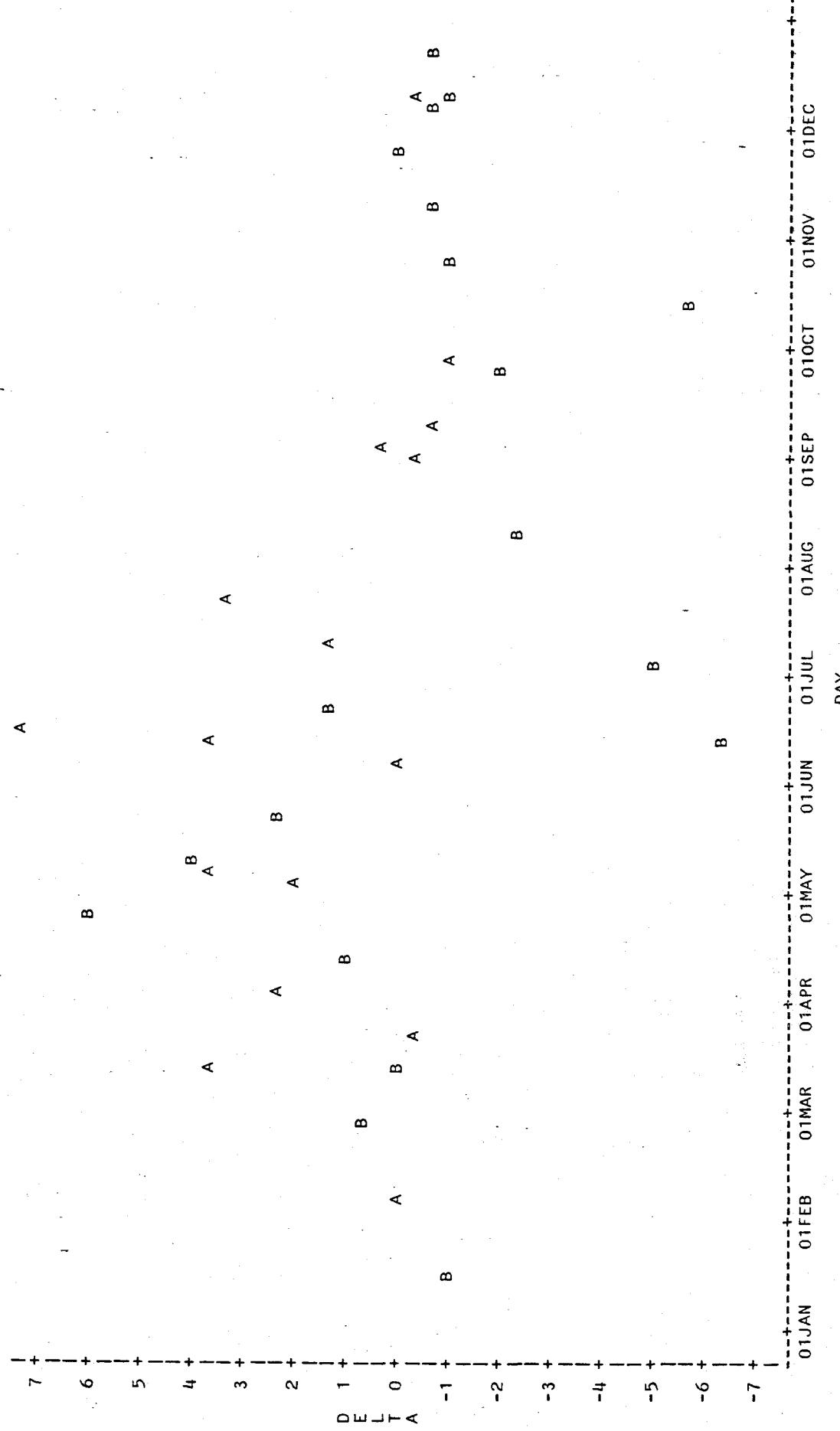
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-131. Summary of Test Results for Neomysis kadiakensis,
All Stages Combined.

SPCODE=Neomysis kadiakensis STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-132. Plot of preoperational (B) and operational (A) Delta values for *Neomysis kadiakensis* all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-135

SPCODE=Neomysis kadiakensis STAGE=ALL

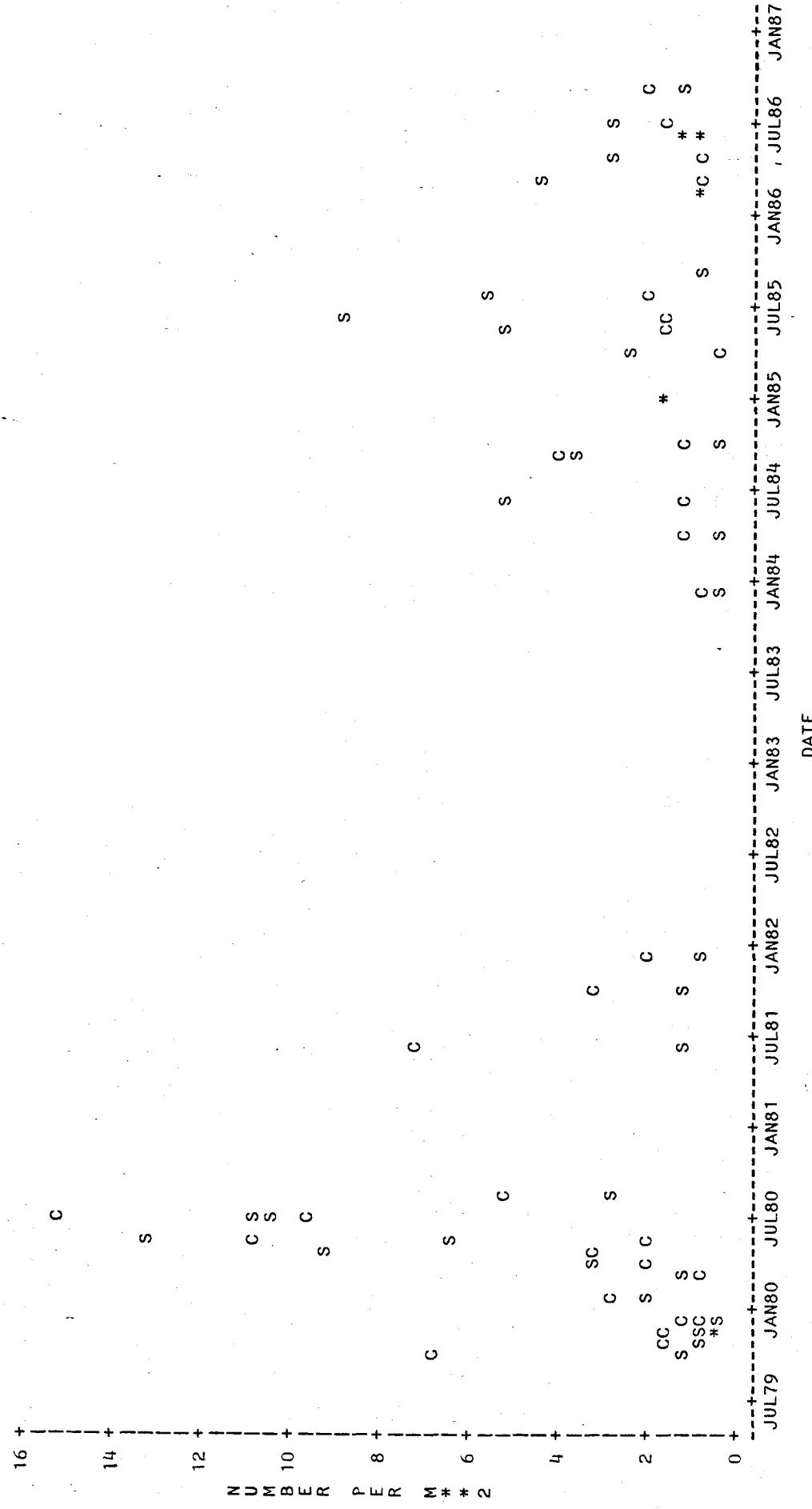


Figure D-133. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis kadiakensis* all stages. Similar abundances at both locations are designated by asterisks.

D-136

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages Combined	B or C	2.1	2.4	4.0	6.1	6.1	5.2
	A-S	2.3	2.3	3.4	5.3	6.5	5.8
Adults	B or C		2.1	2.6	4.1	5.4	4.7
	A-S		2.1	2.5	3.4	5.4	5.5
Immatures	B or C	2.4	2.5	3.3	5.7	6.4	5.3
	A-S	2.5	2.5	2.9	5.1	6.4	6.0
Juveniles	B or C		2.0	3.7	5.4	4.6	3.6
	A-S		2.0	3.2	4.9	5.1	3.7

Figure D-134. Cross-shelf distributional patterns for Neomysis kadiakensis. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

TAXON: Neomysis kadiakensis
Stage: Adult

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance	
	Note:						Abun/Sprse
none	A	sig	ns/ns	ns/ns			
$\log(x+0)$	D	ns	ns/ns	sig/ns			
$\log(x+.1)$	D	ns	ns/ns	sig/ns			
$\log(x+1)$	A	sig	ns/ns	ns/ns			
$\log(x+10)$	A	sig	ns/ns	ns/ns			

Chi Square; Ho:even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: sig($p=.033$) **

Regression (SONGS vs Control Abundances):

One straight line, intercept = 0*

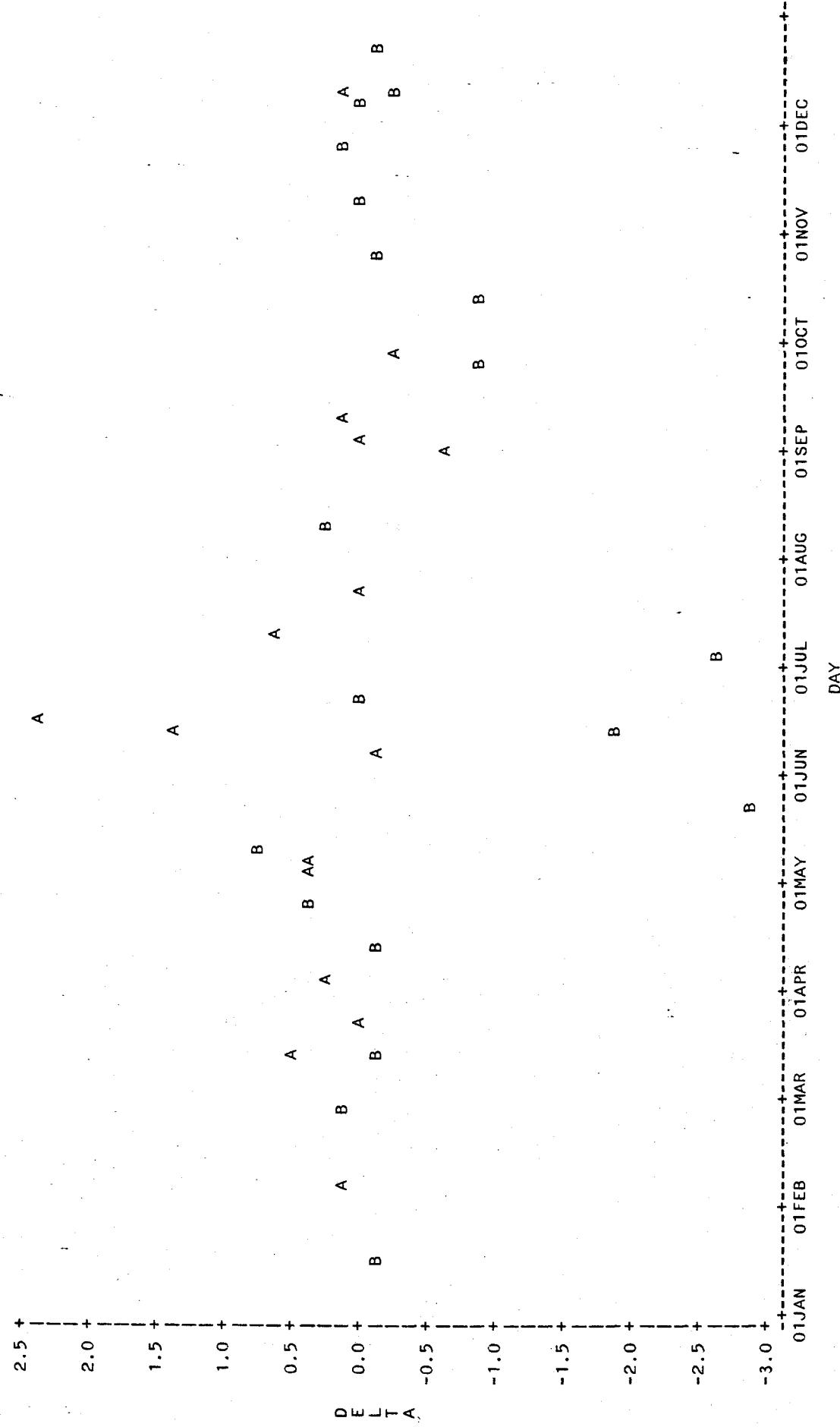
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-135. Summary of Test Results for Neomysis kadiakensis,
Adult.

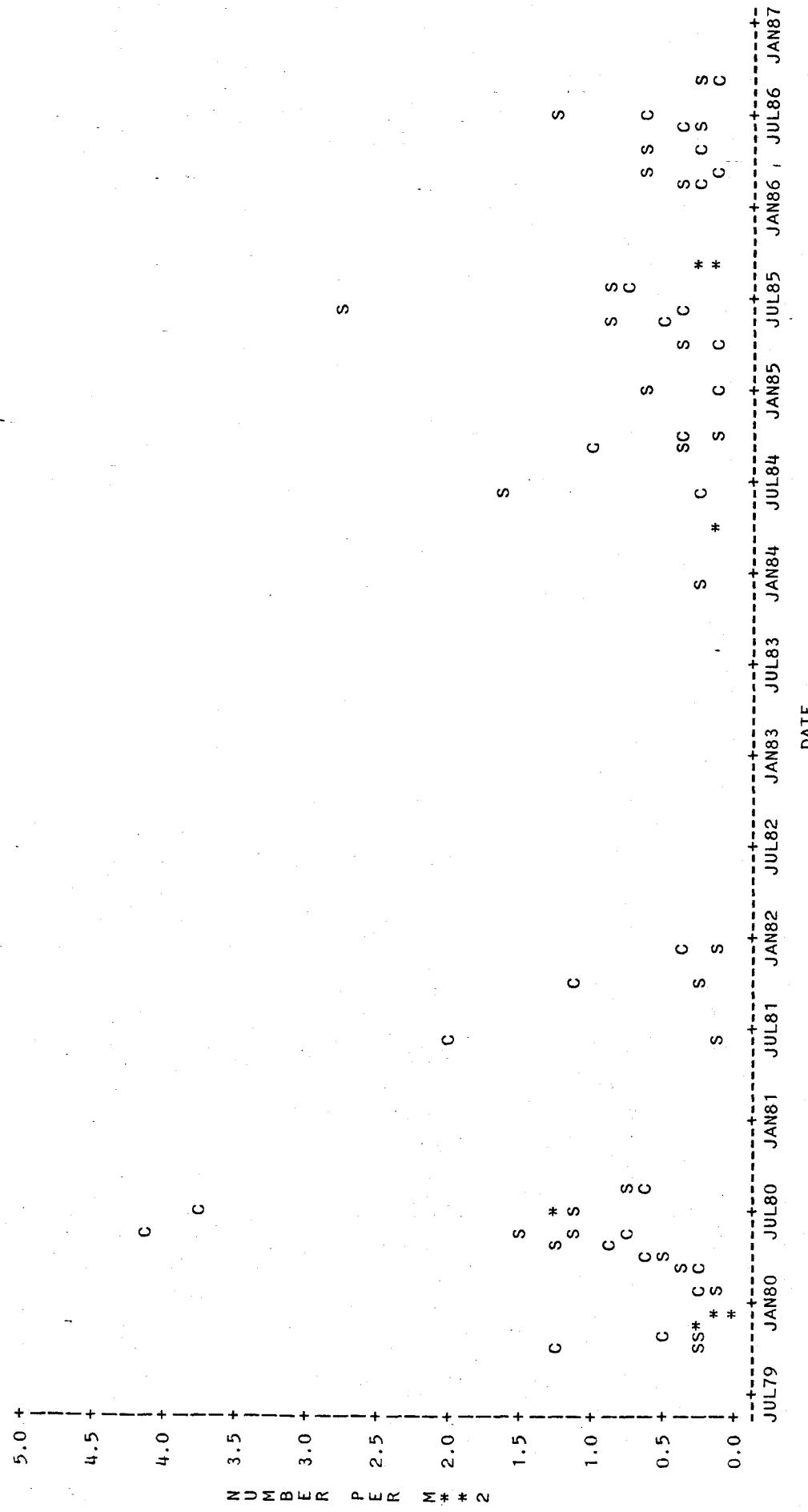
SPCODE=Neomysis kadiakensis STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-136. Plot of preoperational (B) and operational (A) Delta values for *Neomysis kadiakensis* adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Neomysis kadiakensis STAGE=ADULT



TAXON: Neomysis kadiakensis
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>
			<u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	B	ns	sig/ns	ns/ns	.10	38.7
$\log(x+0)$		ns	ns/ns	ns/ns	.10	63.9
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

* Transformation 1: $\log(x)$: sig($p=.043$)
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: $\log(x)$: sig($p=.036$)
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: none: ns, first order model
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

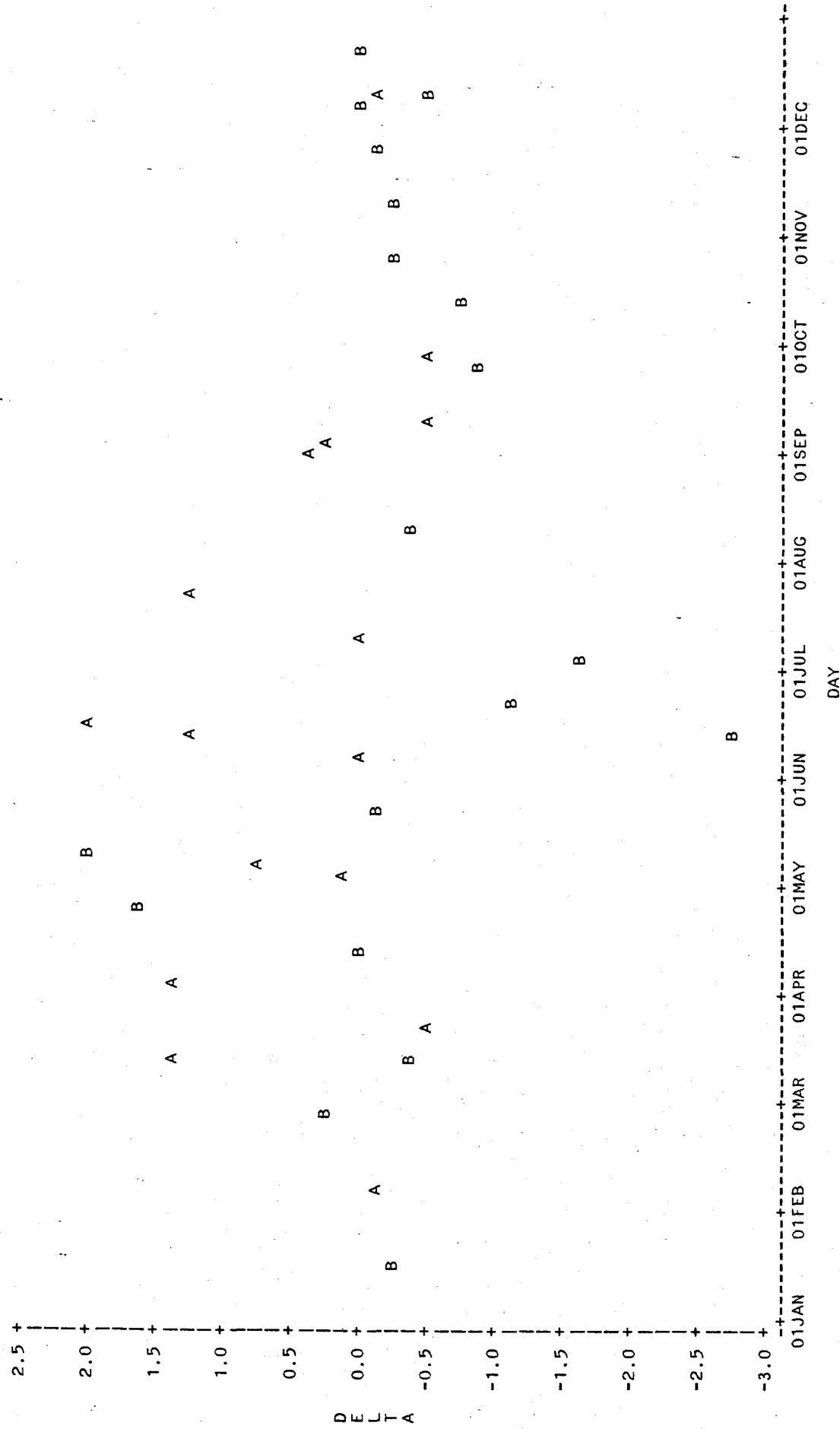
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-138. Summary of Test Results for Neomysis kadiakensis,
Immature.

SPCODE=Neomysis kadiakensis STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-139. Plot of preoperational (B) and operational (A) Delta values for *Neomysis kadiakensis* immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

SPCODE=Neomysis kadiakensis STAGE=IMMATURE

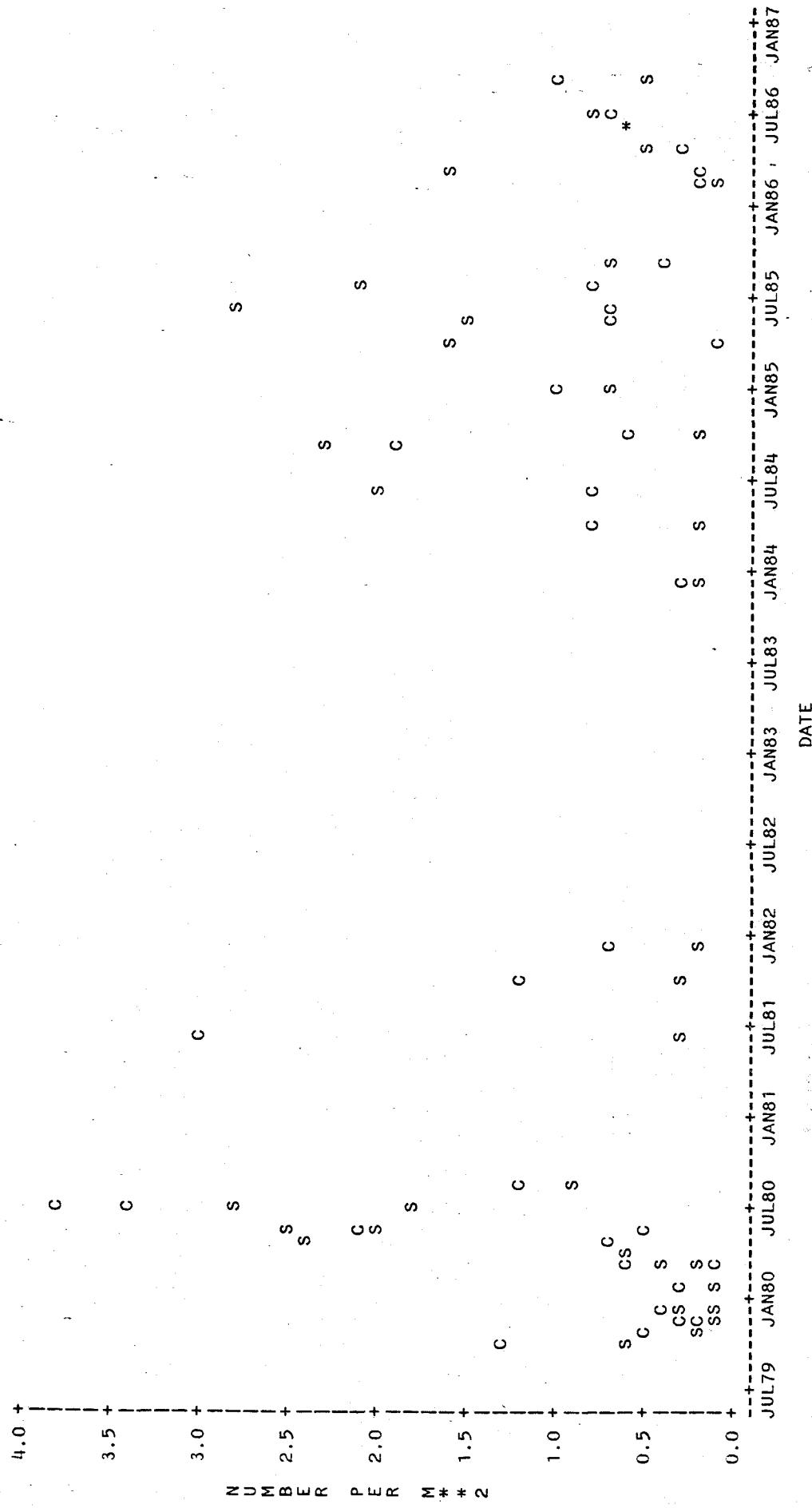


Figure D-140. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis kadiakensis* immatures. Similar abundances at both locations are designated by asterisks.

D-143

Taxon: Neomysis kadiakensis
Stage: Juvenile

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u> <u>Deleted for Additivity</u>
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	B	ns	sig/sig	ns/ns	.10	60.9	9.36/.28
$\log(x+0)$	B	ns	sig/ns	ns/ns	.10	53.8	.24/.19
$\log(x+.1)$	N/A						
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

Transformation 1: N/A
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

Transformation 1: N/A
Transformation 2: N/A

Autoregressive Errors t-test

** Transformation 1: none: ns, first order model
* Transformation 2: $\log(x)$: sig, ($p=.090$) first order model

Binomial: sig

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

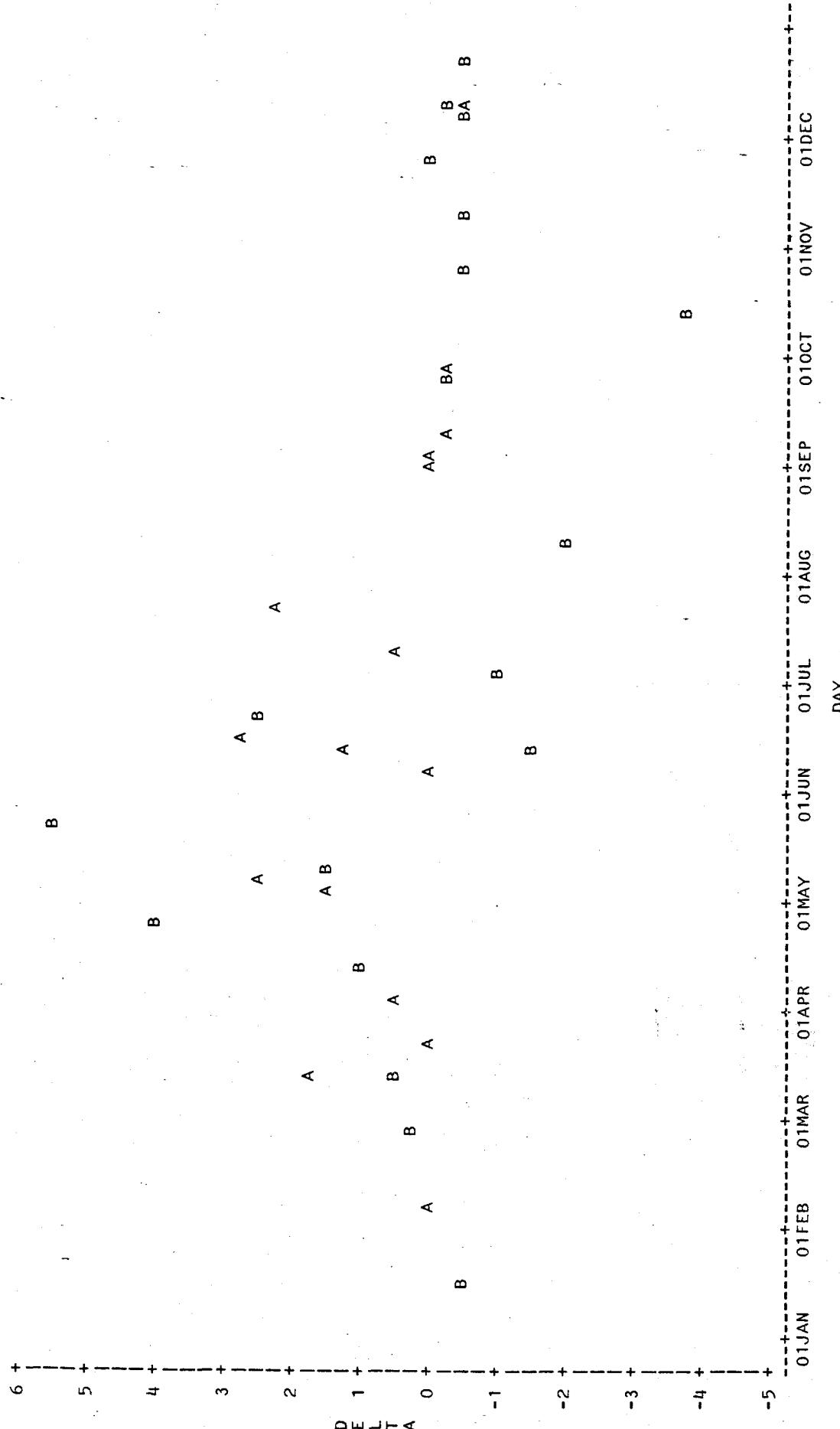
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-141. Summary of Test Results for Neomysis kadiakensis, Juvenile

SPCODE=Neomysis kadiakensis STAGE=JUVENILE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-142. Plot of preoperational (B) and operational (A) Delta values for *Neomysis kadiakensis* juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-145

SPCODE=Neomysis kadiakensis STAGE=JUVENILE

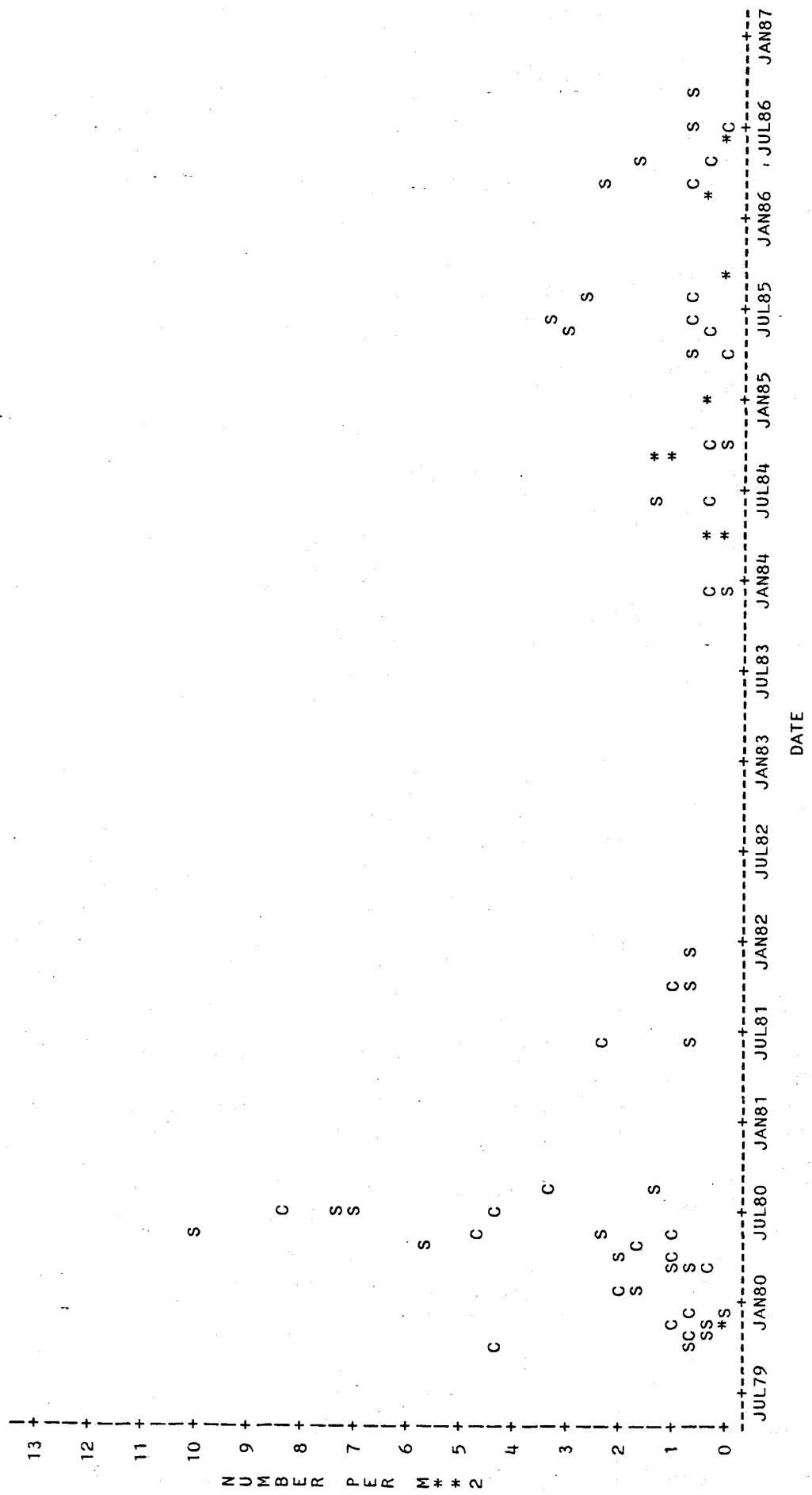


Figure D-143. Abundance values at SONGS (S) and Control (C) plotted through time for *Neomysis kadiakensis* juveniles. Similar abundances at both locations are designated by asterisks.

D-146

Taxon: Acanthomysis nephrophthalma
Stage: All

<u>NUMBER OF OBSERVATIONS</u>	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Before/ Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none	A,D	sig	sig/ns	sig/ns			
$\log(x+0)$		ns	ns/ns	ns/ns	.10	55.2	.21/.24
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	57.8	.15/.09
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

- ** Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

- * Transformation 1: $\log(x)$: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

- Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

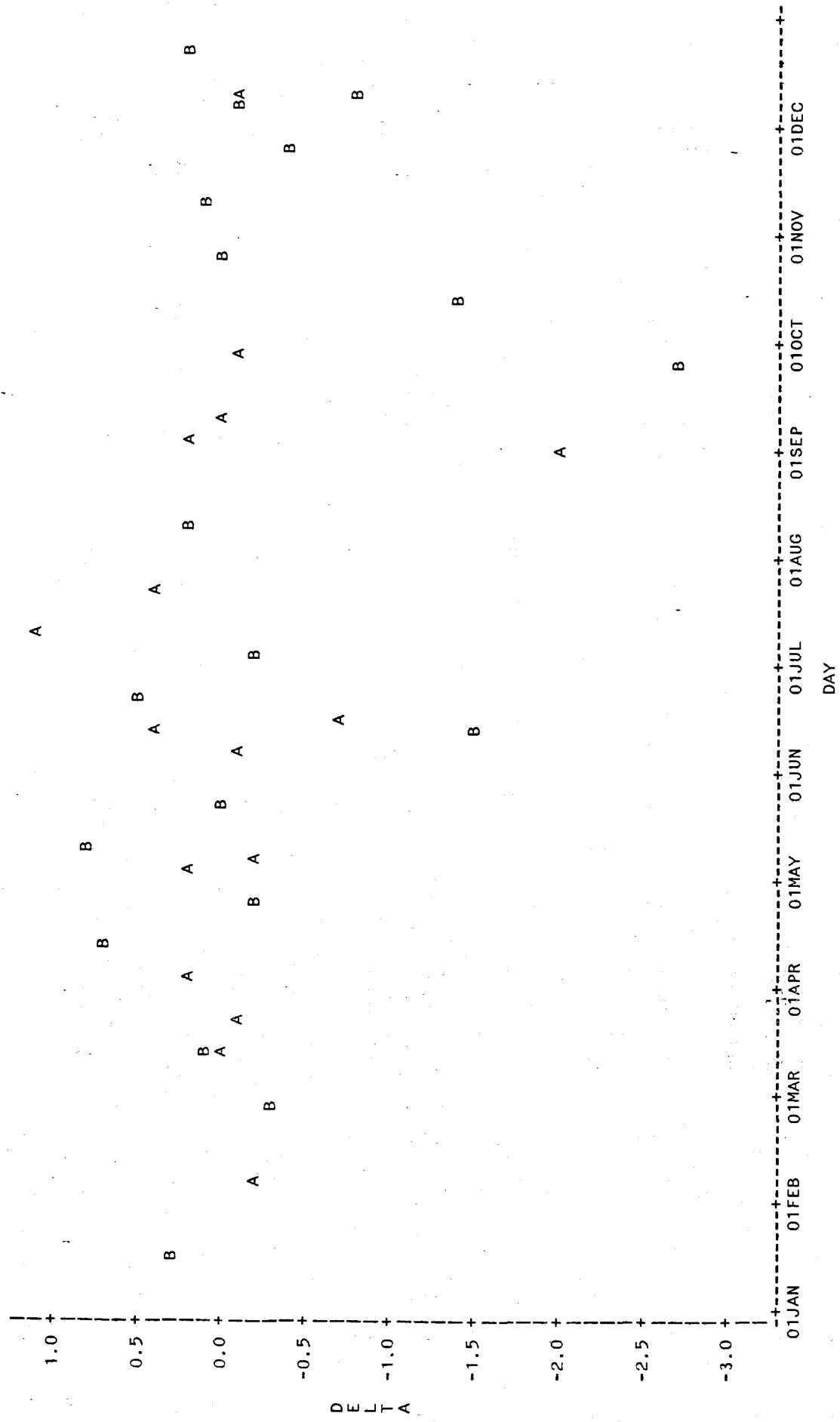
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-144. Summary of Test Results for Acanthomysis nephrophthalma
All Stages Combined.

SPCODE=Acanthomyysis nephrophthallma STAGE=ALL



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-145. Plot of preoperational (B) and operational (A) Delta values for Acanthomyysis nephrophthallma all stages. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-148

SPCODE=Acanthomyysis nephrophthaima STAGE=ALL

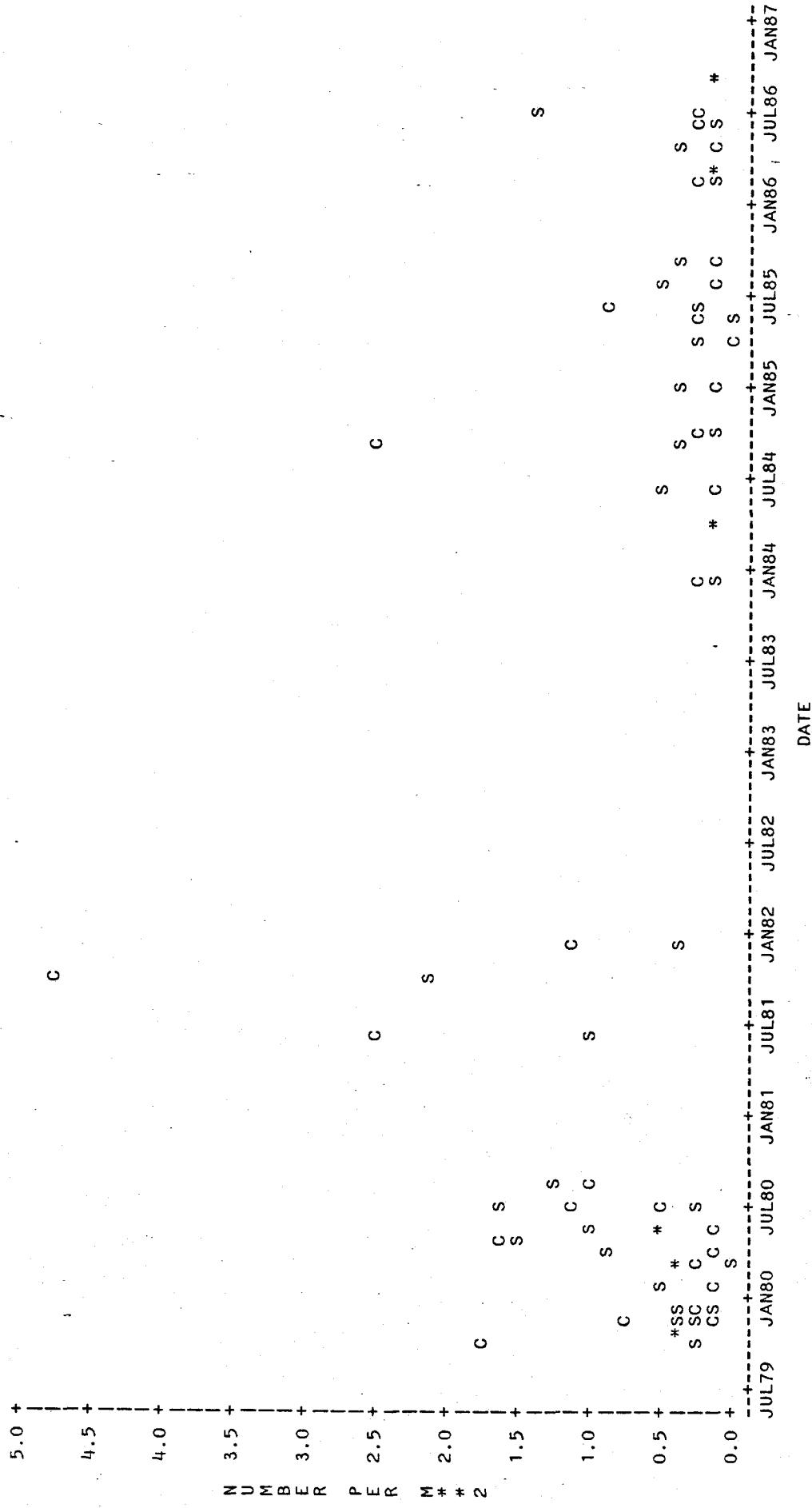


Figure D-146. Abundance values at SONGS (S) and Control (C) plotted through time for Acanthomyysis nephrophthaima all stages. Similar abundances at both locations are designated by asterisks.

D-149

DEVELOPMENTAL STAGE		DEPTH STRATA (m)					
		6-8	8-12	12-15	15-23	23-30	30-37
All Stages	B or C		2.5	2.5	2.8	4.9	5.9
Combined							
p=.03	A-S		2.6	2.8	2.7	4.4	5.9
Adults	B or C				1.7	2.9	3.8
	A-S				1.8	2.6	3.8
Immatures	B or C				1.7	2.8	3.9
	A-S				1.8	2.7	3.7
Juveniles	B or C		2.6	2.6	2.7	4.7	5.9
	A-S		2.6	2.8	2.7	4.4	5.8

Figure D-147. Cross-shelf distributional patterns for *Acanthomysis nephrophthalma*. The value given for each stratum is the mean abundance rank. Highest ranks indicate highest abundance. Outlining denotes strata grouping of highest similar ranks based on Bonferroni t-test. Only strata in which mysids occurred were tested. Mysids at SONGS in the operational period (A-S) were ranked separately from mysids at Control in the operational period plus mysids at both locations in the preoperational period (B or C). P values are shown for patterns showing significant differences between B or C and A-S based on MANOVA testing of the ranks.

Taxon: Acanthomysis nephrophthalma
Stage: Adult

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	18	17	23 Sep 81
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note: Before/After	Trends Before/ After	α	Power % at α	Delta Variance	Delta Abun/Sprse
none		ns	ns/ns	ns/ns	.10	38.7	.02/.002
$\log(x+0)$	A	sig	ns/ns	ns/ns			
$\log(x+.1)$		ns	ns/ns	ns/ns	.10	55.1	.05/.02
$\log(x+1)$	N/A						

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x+.1)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x+.1)$: ns

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

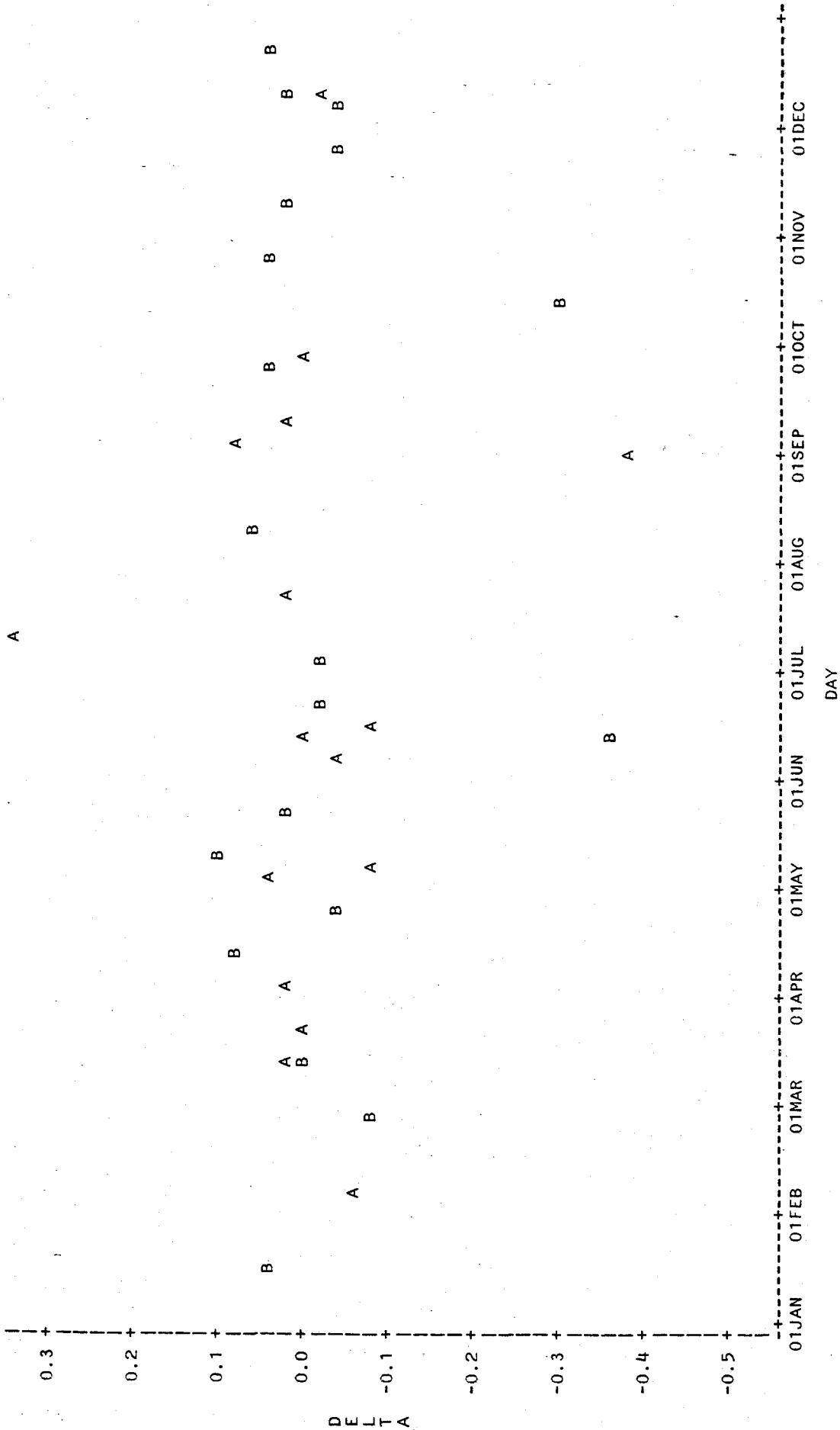
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-148. Summary of Test Results for Acanthomysis nephrophthalma,
Adult.

SPCODE=Acanthomyysis nephrophthalma STAGE=ADULT



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-149. Plot of preoperational (B) and operational (A) Delta values for Acanthomyysis nephrophthalma adults. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-152

SPCODE=Acanthomysis nephrophthalma STAGE=ADULT

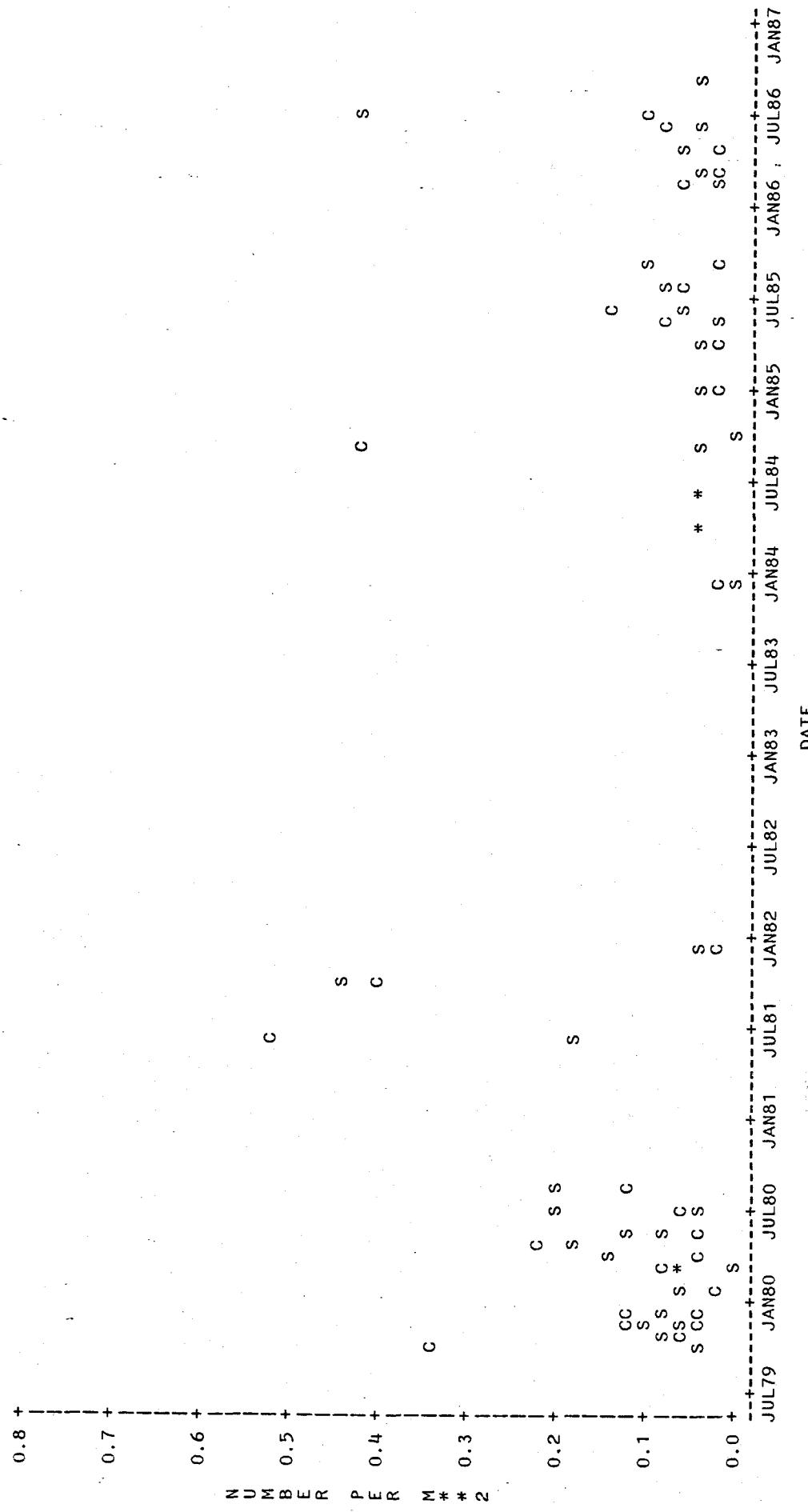


Figure D-150. Abundance values at SONGS (S) and Control (C) plotted through time for Acanthomysis nephrophthalma adults. Similar abundances at both locations are designated by asterisks.

D-153

Taxon: Acanthomysis nephrophthalma
Stage: Immature

<u>NUMBER OF OBSERVATIONS</u>	Before	After	<u>Influence Dates</u>	
			<u>Deleted</u>	<u>for Additivity</u>
Untransformed	19	17		
$\log(x+0)$	19	16		
$\log(x+\text{constant})$	19	17		

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key	Serial Correlation Note:	Trends Before/ Before/After	α	Power % at α	Delta Variance Abun/Sprse
none	ns	ns/ns	ns/ns	.10	49.6	.16/.008
$\log(x+0)$	ns	ns/ns	ns/ns	.10	40.9	.36/.34
$\log(x+.1)$	N/A					
$\log(x+1)$	N/A					

Chi Square; H_0 : even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: none: ns
Transformation 2: $\log(x)$: ns

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: none: ns
Transformation 2: $\log(x)$: ns

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

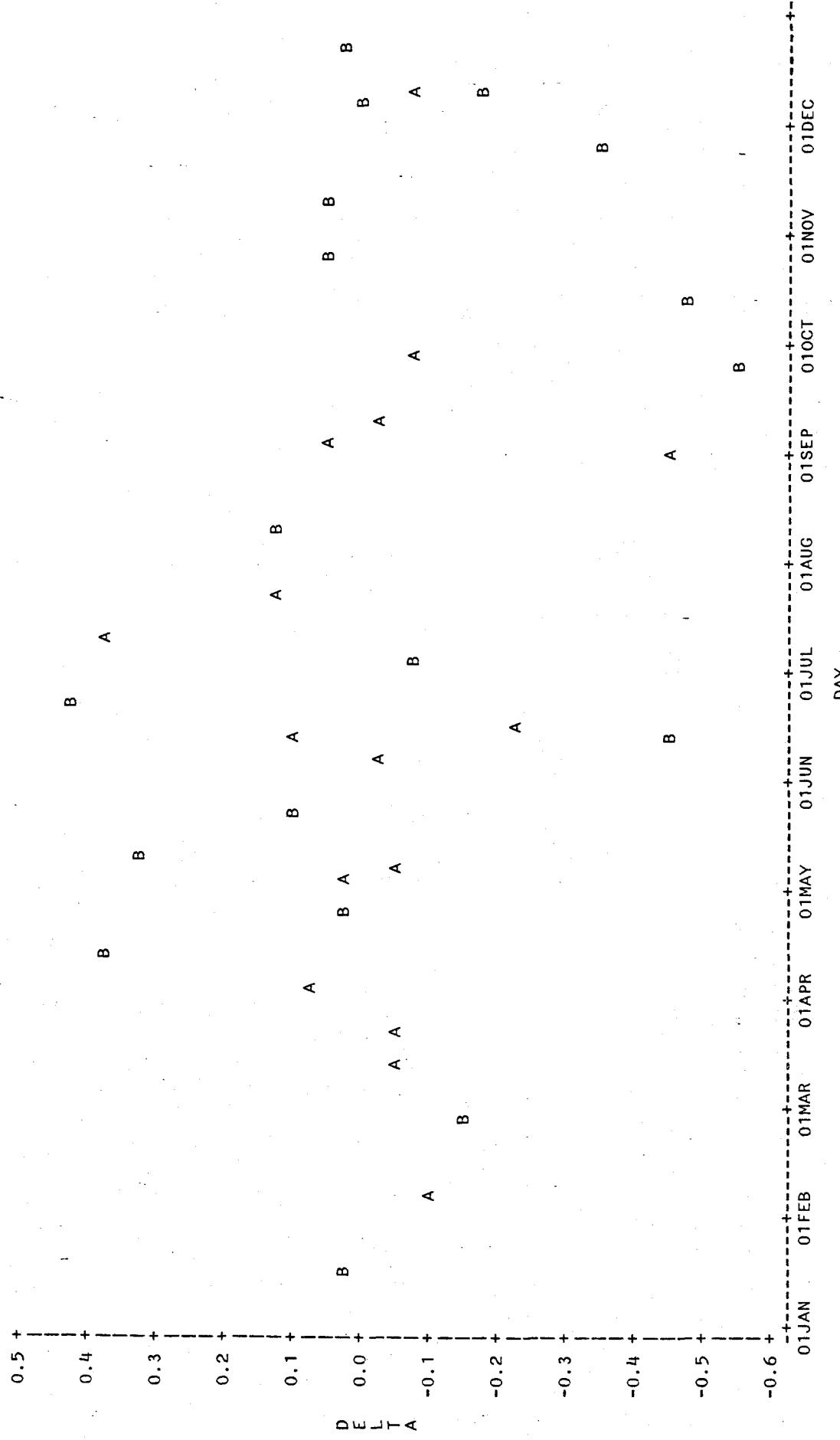
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-151. Summary of Test Results for Acanthomysis nephrophthalma, Immature.

SPCODE=Acanthomysis nephrophtha lma STAGE=IMMATURE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

1 OBS HIDDEN

Figure D-152. Plot of preoperational (B) and operational (A) Delta values for Acanthomysis nephrophtha lma immatures. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-155

SPCODE=Acanthomysis nephrophtalmia STAGE=IMMATURE

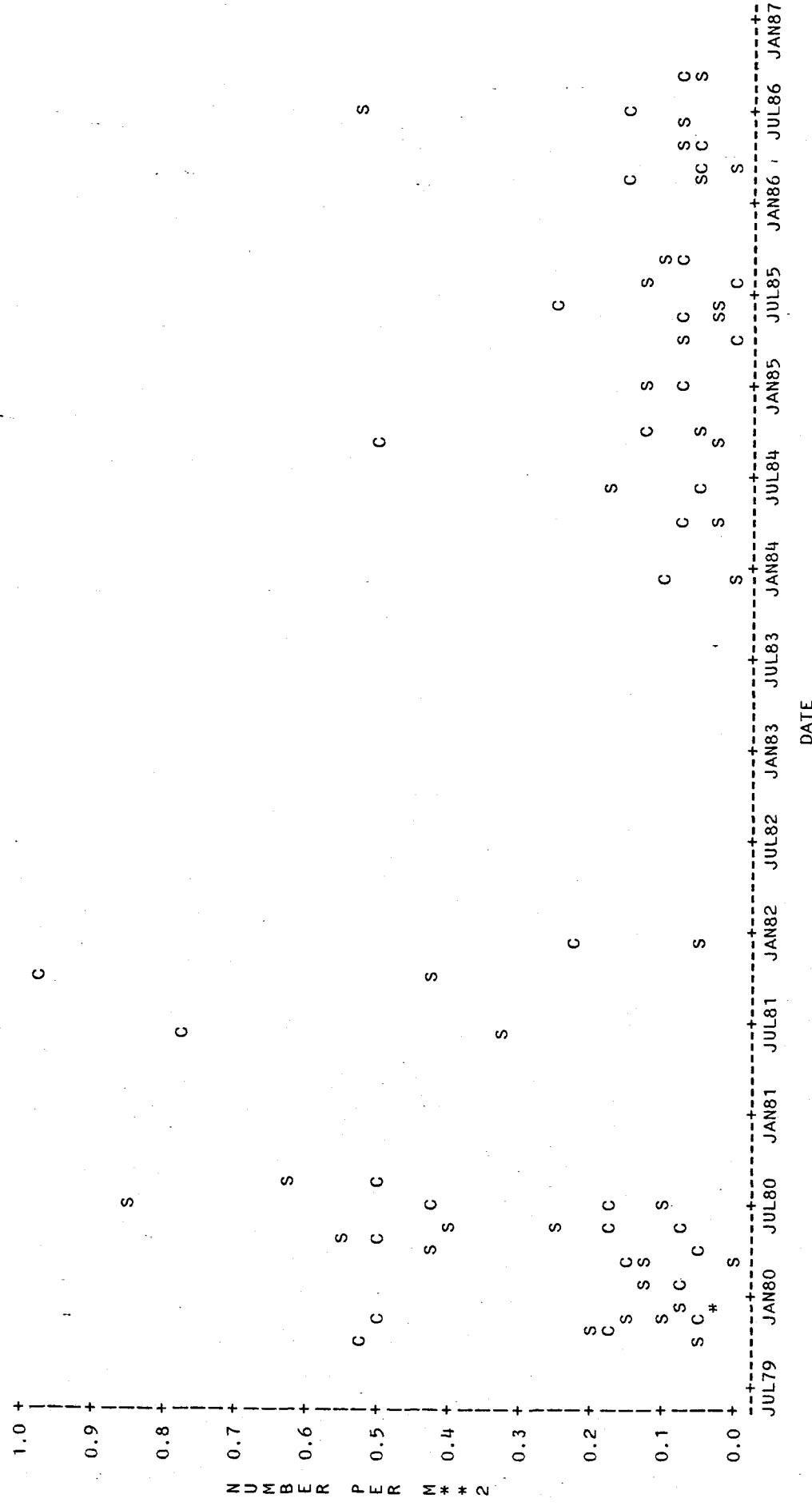


Figure D-153. Abundance values at SONGS (S) and Control (C) plotted through time for *Acanthomysis nephrophtalmia* immatures. Similar abundances at both locations are designated by asterisks.

D-156

TAXON: Acanthomysis nephrophthalma
Stage: Juvenile

NUMBER OF OBSERVATIONS	Before	After	Influence Dates Deleted for Additivity
Untransformed	19	17	
$\log(x+0)$	19	17	
$\log(x+\text{constant})$	19	17	

ASSUMPTION TEST RESULTS

Transformation	Additivity See Key Note:	Serial Correlation Before/After	Trends Before/ After	α	Power % at α	Delta Variance Abun/Sprse
none	A,D	sig	sig/ns			
$\log(x+0)$		ns	ns/ns			
$\log(x+.1)$	A	sig	ns/ns			
$\log(x+1)$	A	sig	ns/ns			
$\log(x+10)$	A	sig	ns/ns			

Chi Square; Ho: even distribution of zeroes in BACI cells: ns

TEST RESULTS

See Key Note:

BACI t-test

** Transformation 1: $\log(x)$: ns
Transformation 2: N/A

Nonparametric (Wilcoxon Rank Sums test)

* Transformation 1: $\log(x)$: ns
Transformation 2: N/A

Autoregressive Errors t-test

Transformation 1: N/A
Transformation 2: N/A

Binomial: ns

Regression (SONGS vs Control Abundances):
One straight line, intercept = 0

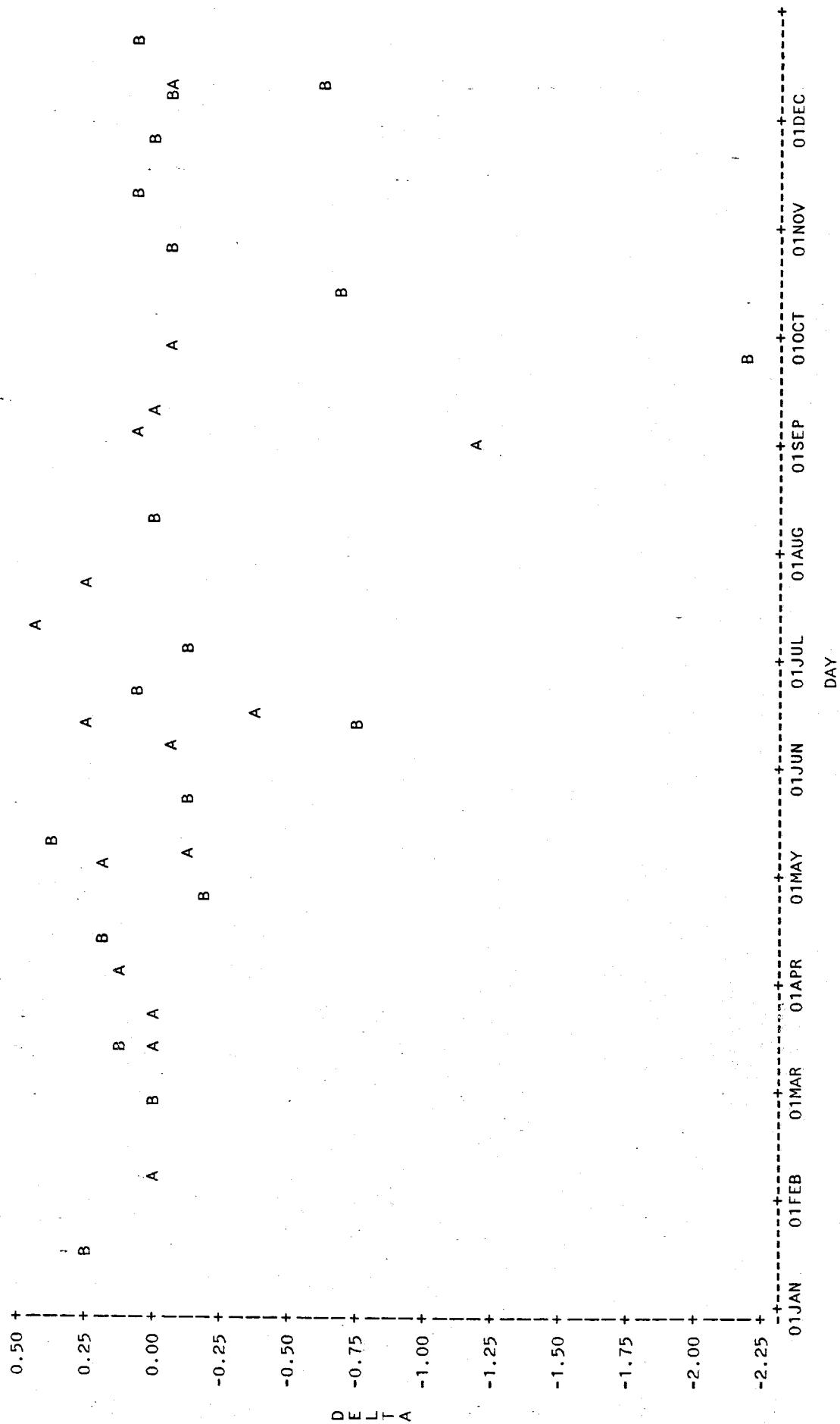
**Primary test results

* Corroborative results

+ Indicates deletion of abundance=0 to attain additivity

Figure D-154. Summary of Test Results for Acanthomysis nephrophthalma, Juvenile.

SPCODE=Acanthomysis nephrophthalma STAGE=JUVENILE



NOTE: 1 OBS HAD MISSING VALUES OR WERE OUT OF RANGE

Figure D-155. Plot of preoperational (A) and operational (B) Delta values for Acanthomysis nephrophthalma juveniles. Values are shown on a seasonal time scale without regard to year to provide a concise comparison between levels of Before and After Deltas.

D-158

SPCODE=Acanthomysis nephrophthalma STAGE=JUVENILE

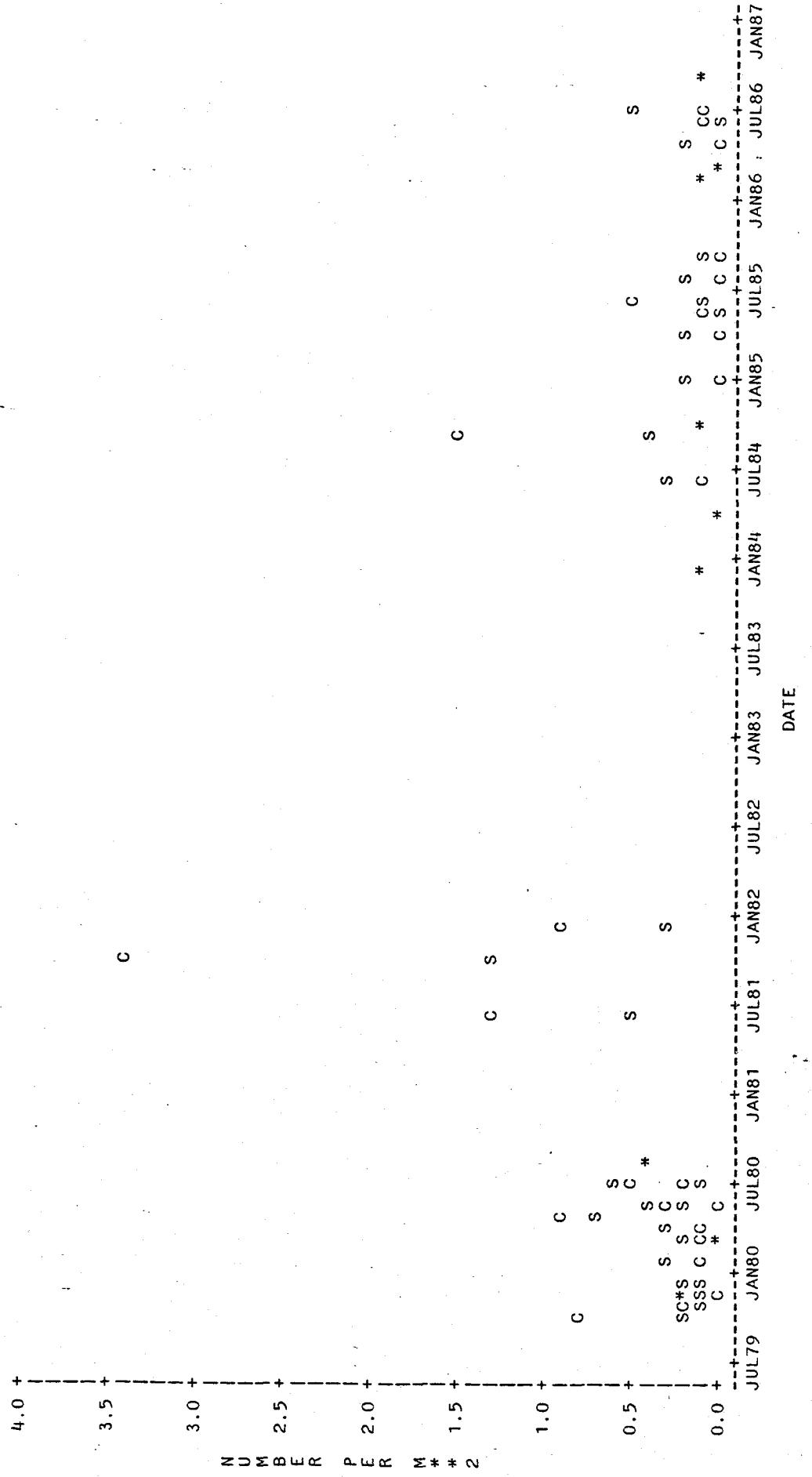


Figure D-156. Abundance values at SONGS (S) and Control (C) plotted through time for *Acanthomysis nephrophthalma* juveniles. Similar abundances at both locations are designated by asterisks.

D-159