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tera
ENVIRONMENTAL
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Ministry of Environment, Lands and Parks
2930 Trans Canada Highway
Victoria, BC
V9E 1K3

April 17, 2001
Our File: 1500
By Courier

Attention: Chris Kissinger
Resource Officer
South Vancouver Island District

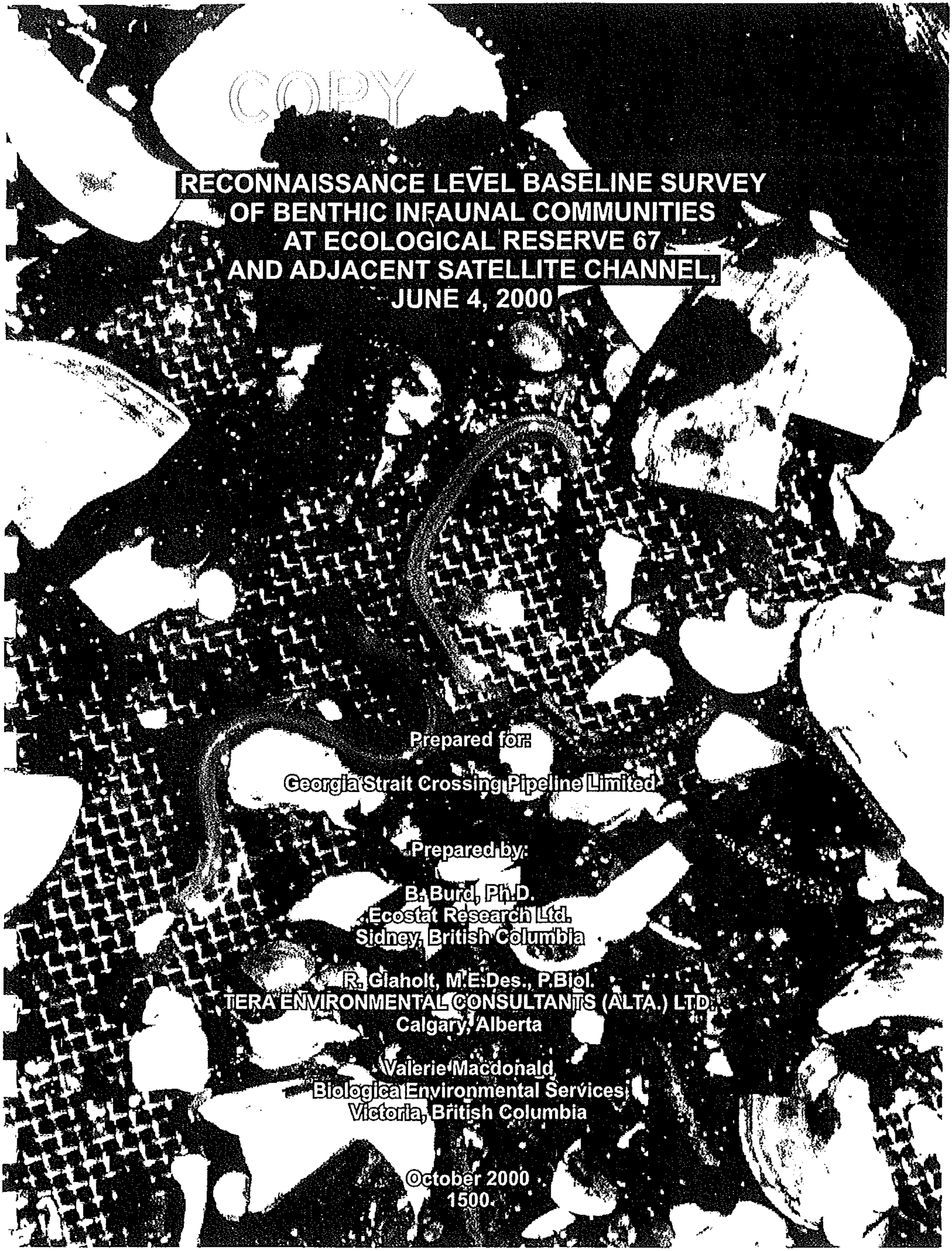
Re: Supplementary GSX PL Report on Benthic Communities at ER67

Accompanying this letter is a copy of a report titled "Reconnaissance Level Baseline Survey of Benthic Communities at Ecological Reserve 67 and Adjacent Satellite Channel". I had sent you previous field data for two benthic grab samples obtained from ER67. The accompanying report includes that data as well as additional data from the surrounding area. The intent is to provide some further environmental context for our assessment titled " Environmental Assessment of the Ecological Significance of Installing a Natural Gas Pipeline Around or Through ER67" which we understand is undergoing MELP review. On a related matter, Ken Farquharson of BC Hydro has passed on to me your request for some supplemental mapping of morphological units and substrate types referred to in the assessment. This map is in preparation and should be forwarded to you in the very near future.

Sincerely,
TERA Environmental Consultants (Alta) Ltd.

Randal Glaholt P.Biol.
Professional Associate

cc. Ken Farquharson, BC. Hydro
Kirt Rhoads, Williams Gas Pipeline



RECONNAISSANCE LEVEL BASELINE SURVEY OF BENTHIC INFAUNAL COMMUNITIES AT ECOLOGICAL RESERVE 67 AND ADJACENT SATELLITE CHANNEL, JUNE 4, 2000

Prepared for:

Georgia Strait Crossing Pipeline Limited

Prepared by:

B. Burd, Ph.D.
Ecostat Research Ltd.
Sidney, British Columbia

R. Glaholt, M.E.Des., P.Biol.
TERA ENVIRONMENTAL CONSULTANTS (ALTA.) LTD.
Calgary, Alberta

Valerie Macdonald
Biologica Environmental Services
Victoria, British Columbia

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1.0 INTRODUCTION

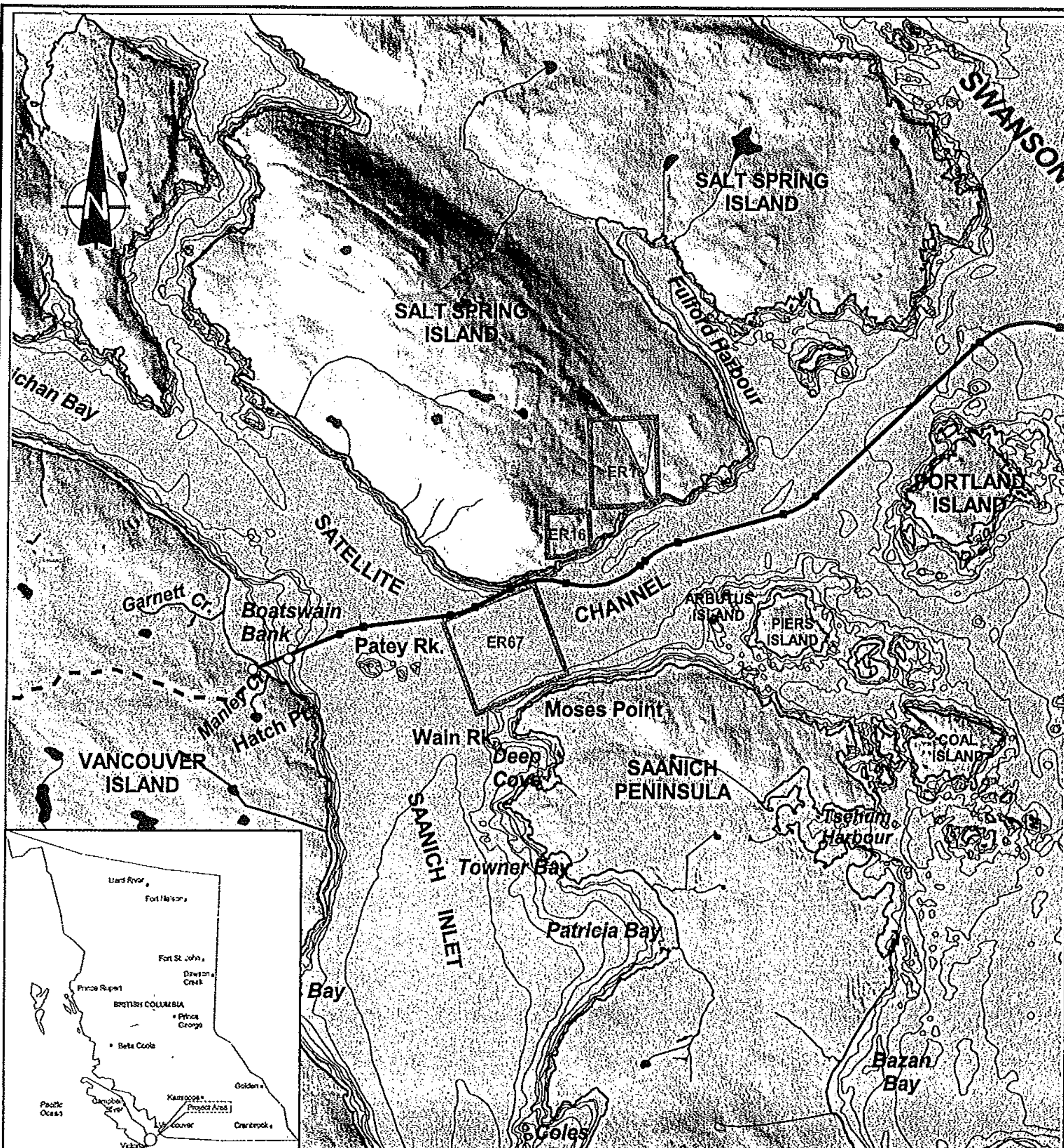
A reconnaissance level baseline survey of benthic infaunal communities was carried out in Ecological Reserve 67 (ER67) and adjacent Satellite Channel, British Columbia as part of a marine studies program being undertaken on behalf of Georgia Strait Crossing Pipeline Ltd. for its Georgia Strait Crossing Project. Sampling was conducted on June 4, 2000 (Figure 1). The purpose of this work was to provide an indication of benthic infaunal species abundance and diversity in the area. This data allows comparison with previous historical benthic infaunal collections for the area and also provides a reference for monitoring potential change to benthic communities that could result from the installation of a proposed gas pipeline along the northern border of ER67.

1.1 Methods

A total of seven sites were sampled, two in ER67 and five in adjacent Satellite Channel on June 4, 2000 (Figure 2). Paired replicate samples were collected at each site using a $0.1m^2$ Smith McIntyre clamshell grab (Plates 1 and 2). Samples were rinsed through 1.0 mm and 0.5 mm sieves immediately after collection (Plates 3 and 4). All samples were sieved, labelled and preserved (Plates 5 and 6). Detailed qualitative and quantitative taxonomic analysis was performed on one replicate from each paired sample. A 1.0 mm sieve was used to provide comparison with previous historical data collection while a 0.5 mm sieve was used to capture a more inclusive and representative sample of the macrobenthos. All taxonomic work was carried out by Biologica Environmental Services of Victoria, BC.

Proportions of major taxonomic groups for each sample were calculated to compare with historical data from the area, and to show any gross differences in overall faunal composition between samples.

Community analyses used a break down based on species, size fraction (0.5 mm and 1.0 mm), adult and juvenile counts, abundance and biomass values. The final two analyses are for total abundance from each grab and total biomass from each grab. Statistical analysis was performed using a Bray-Curtis similarity measure (Bray and Curtis 1957) with unweighted pair group average sort (Sneath and Sokal 1973). Biomass analyses did not include the few very large megafauna measured because these would have seriously skewed results and provided no real information about the biomass of the rest of the community.



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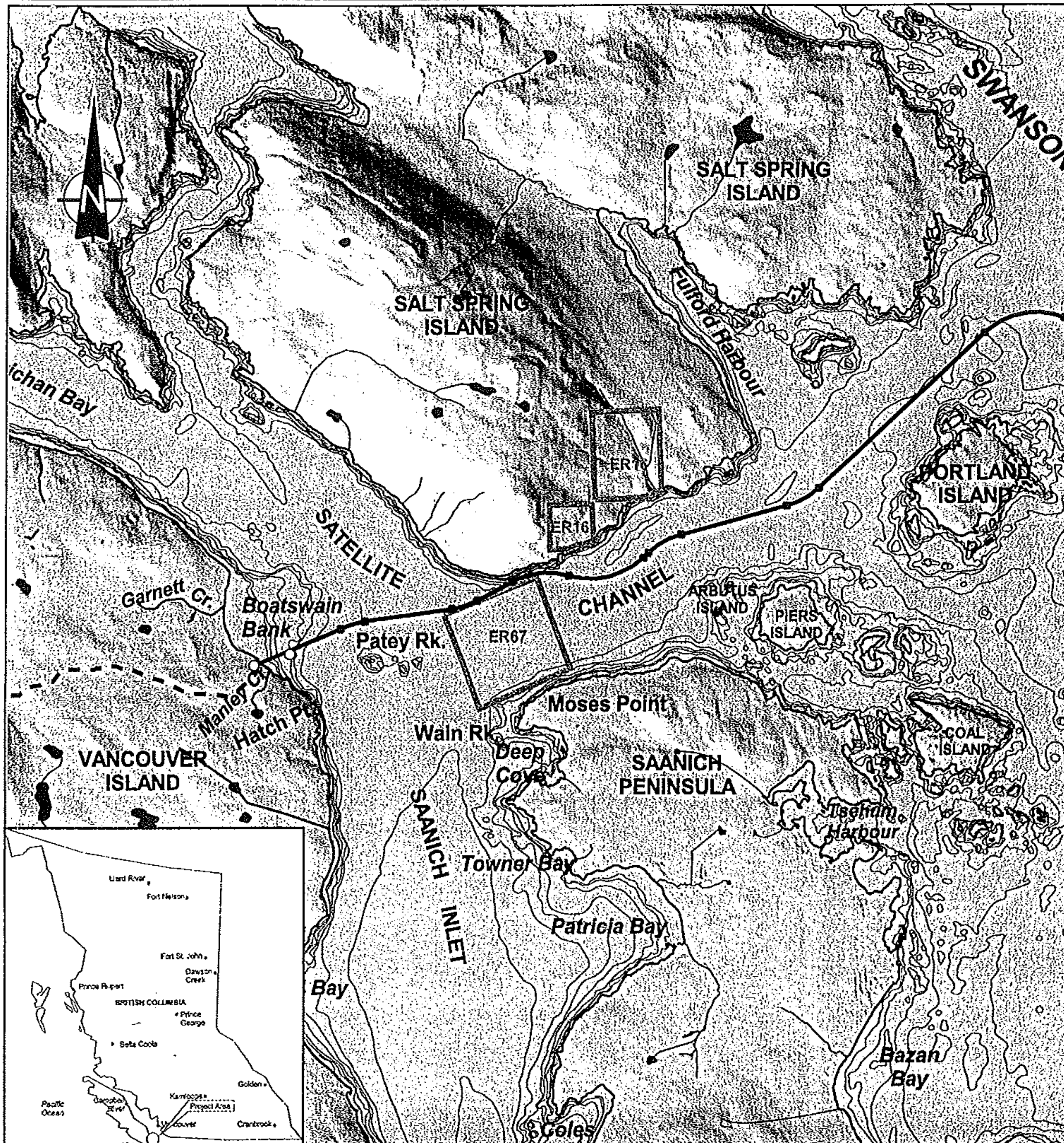
1 0 1 2 Kilometers

Legend

- Marine Portion of Proposed Route
- Terrestrial Portion of Proposed Route
- Proposed Directional Drill Entry and Exit Points
- Shoreline
- Depth Contours
- Ecological Reserve Boundaries

REGIONAL LOCATION OF STUDY AREA

1500	September 2000	FIGURE 1



BIOTECHNICS INTERNATIONAL LTD.	**Legend**	**REGIONAL LOCATION OF STUDY AREA**		
1 0 1 2 Kilometers	Marine Portion of Proposed Route Terrestrial Portion of Proposed Route Proposed Directional Drill Entry and Exit Points Shoreline Depth Contours Ecological Reserve Boundaries	1500	September 2000	FIGURE 1

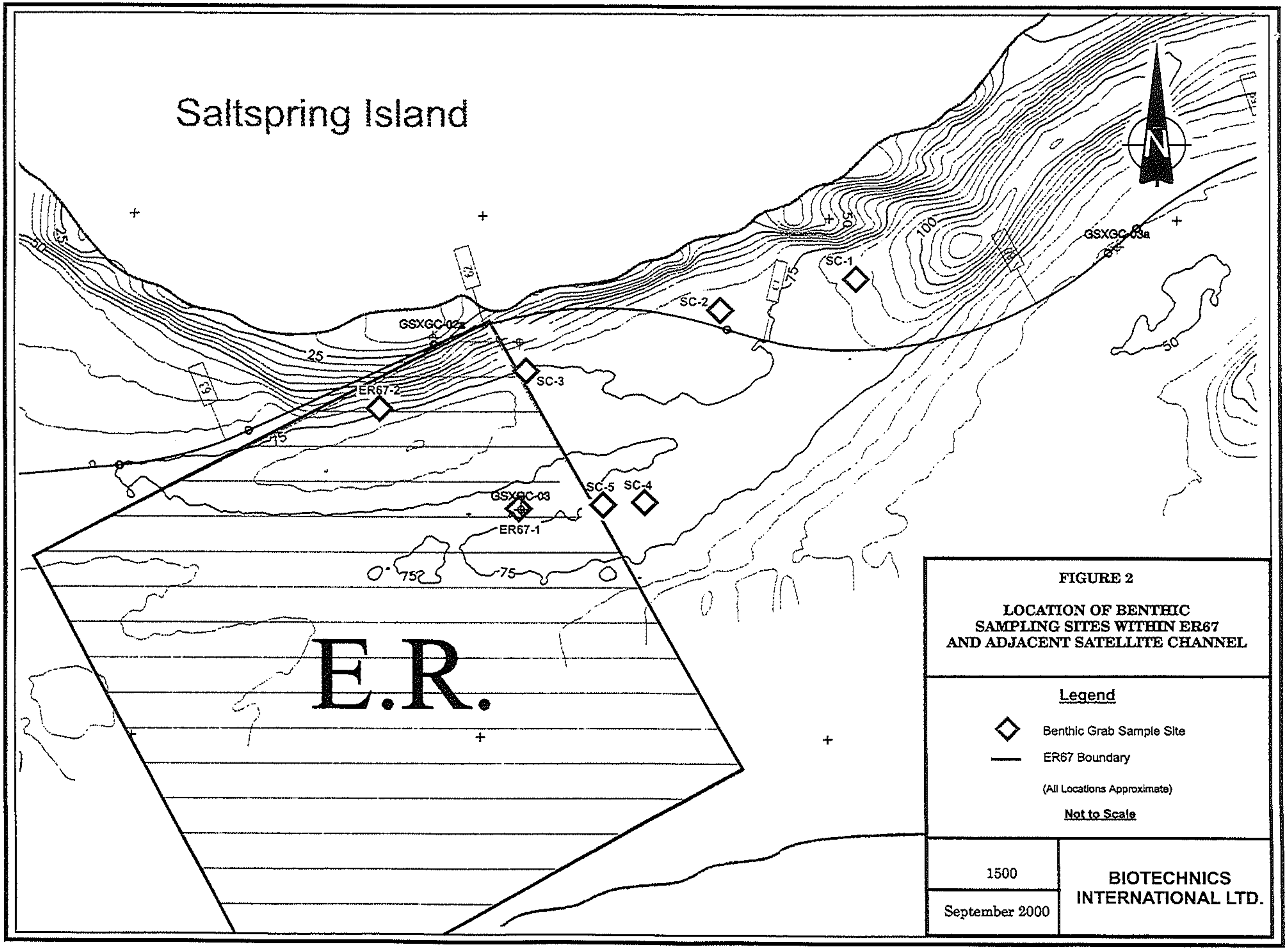


FIGURE 2

LOCATION OF BENTHIC SAMPLING SITES WITHIN ER67 AND ADJACENT SATELLITE CHANNEL

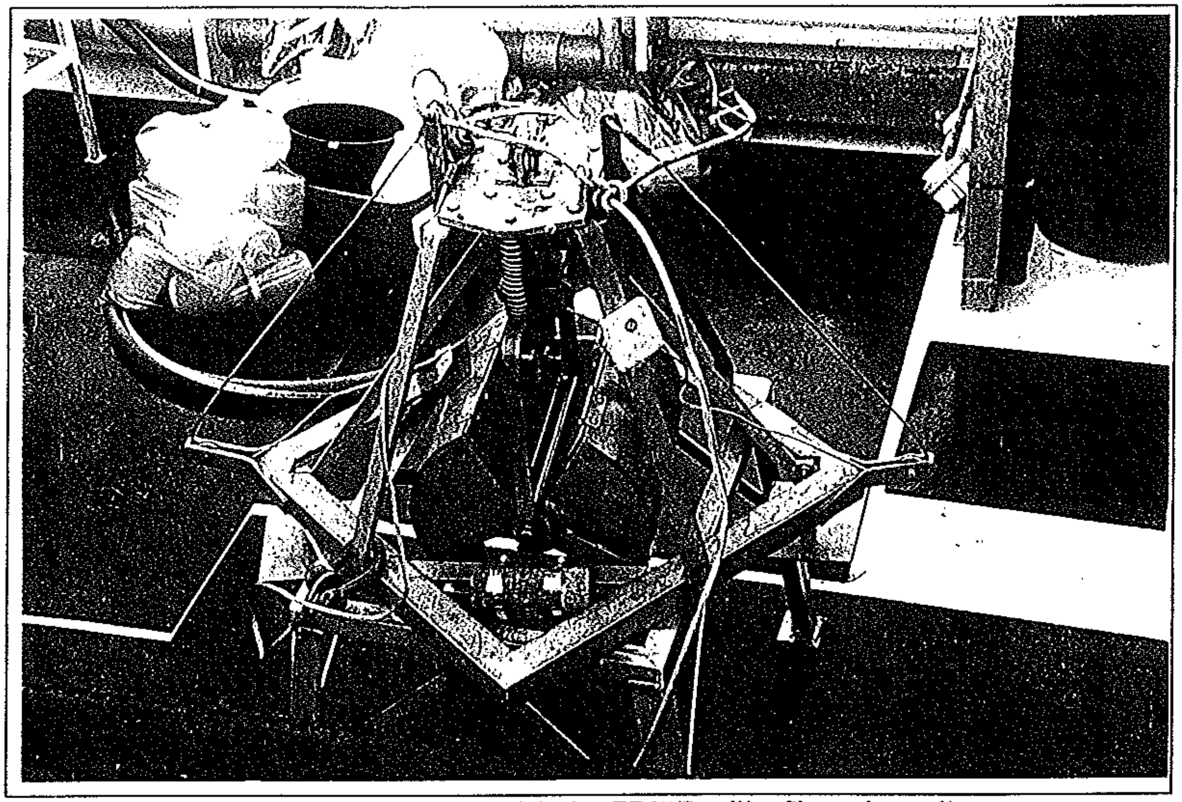


Plate 1 Smith McIntyre clamshell grab used during ER67/Satellite Channel sampling program (June 4, 2000).

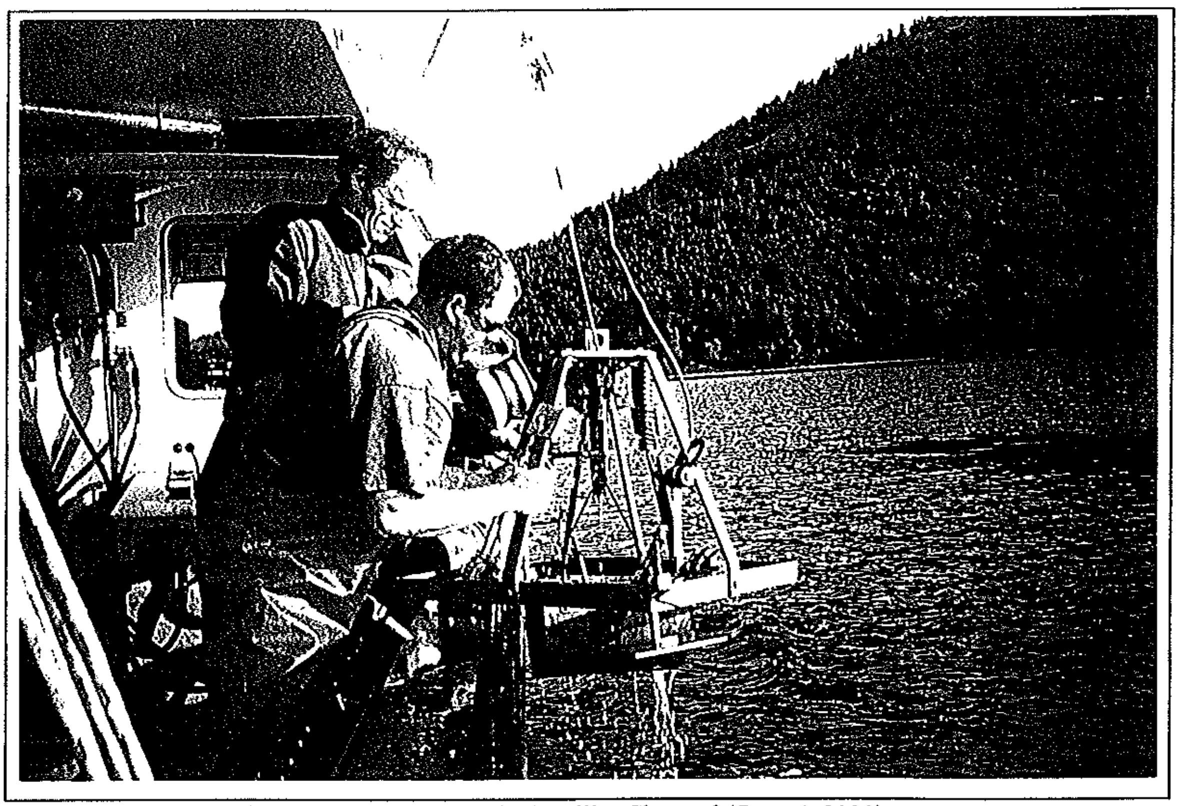


Plate 2 Retrieval of benthic grab samples in Satellite Channel (June 4, 2000).

Plate 3 Low velocity preliminary rinse of grab samples from Satellite Channel.

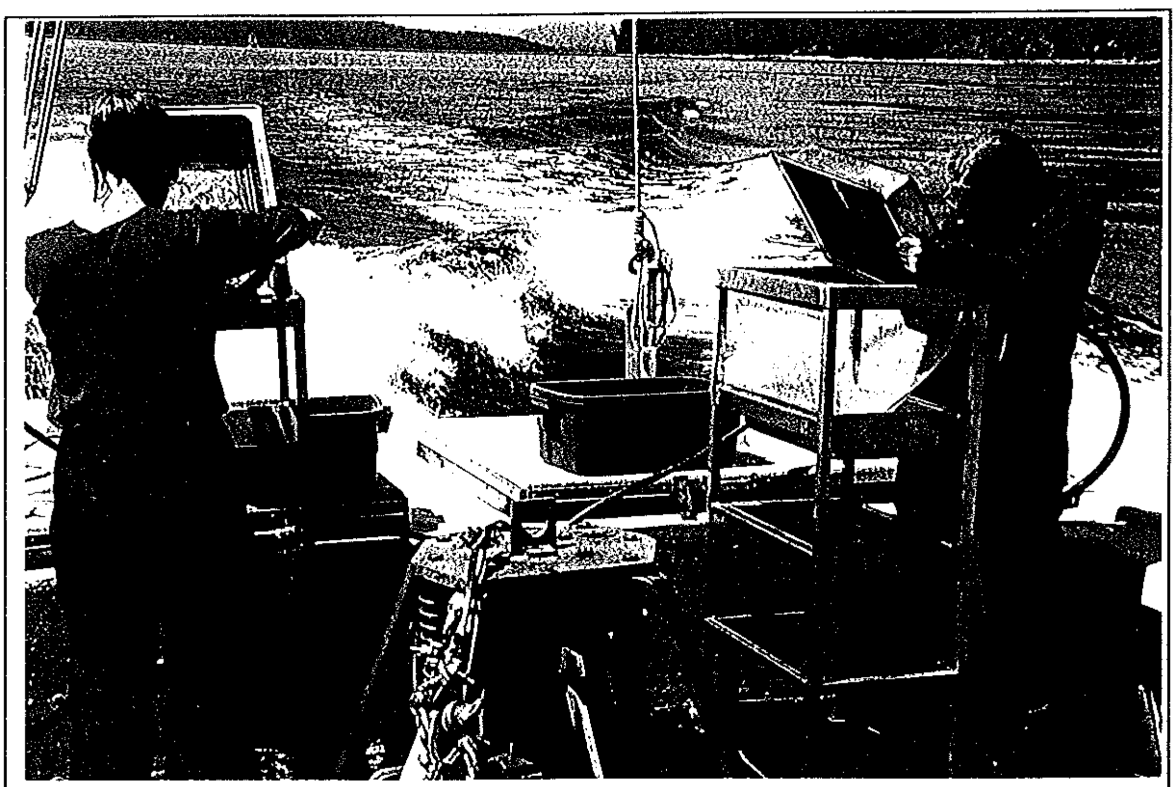


Plate 4 1.0 mm and 0.5 mm sieve racks used during ER67/Satellite Channel sampling program (June 4, 2000).

Plate 5 Rinsed benthic sample from ER67 (June 4, 2000).

Plate 6 Onboard sorting and presentation of fresh specimens from ER67/Satellite Channel area (June 4, 2000).

1.2 Results and Discussion

A complete list of fauna identified at the seven sampling sites is provided in Appendix 1. A data summary illustrating the general characteristics of the community is presented in Table 1. These include sample abundance and biomass values for adults and juveniles, and species richness for each size fraction as well as the entire sample. Values are independent counts for each sieve size, with totals for the entire sample calculated as the sum of these independent counts. The total values are equivalent to processing the entire sample using a 0.5 mm sieve. Precision estimates (Elliott 1977) are listed in Table 2 for total sample abundance. Proportions of major taxonomic groups for each sample are listed in Table 3. Community analyses are included in Appendix 2.

TABLE 1

SUMMARY DATA FROM SATELLITE CHANNEL STATIONS, 2000.

Station	Sieve	Group[1]	Abundance	Abundance per Sieve	Abundance per Grab	Taxa per Sieve	Taxa per Grab	Abundance/m²	Biomass (g)	Biomass per Grab	Biomass + Megafauna
ER67-1	1.0 mm	A	445						9.1		
ER67-1		J	555	1000		72		8475	1.3		
ER67-1	0.5 mm	A	200						0.1		
ER67-1		J	285	485	1485	55	102	4110	1.6	12.6	27.1
ER67-2	1.0 mm	A	493						7.1		
ER67-2		J	276	769		63		6517	1.0		
ER67-2	0.5 mm	A	100						0.2		
ER67-2		J	196	296	1065	49	91	2508	1.6	9.8	9.8
SC-1	1.0 mm	A	262						8.2		
SC-1		J	299	561		70		4754	1.2		
SC-1	0.5 mm	A	270						0.3		
SC-1		J	309	579	1140	58	98	4907	1.4	11.2	11.2
SC-2	1.0 mm	A	334						8.2		
SC-2		J	397	731		60		6195	1.7		
SC-2	0.5 mm	A	241						0.2		
SC-2		J	335	576	1307	52	85	4881	2.1	12.2	31.3
SC-3	1.0 mm	A	745						12.3		
SC-3		J	455	1200		82		10169	1.9		
SC-3	0.5 mm	A	194						0.1		
SC-3		J	266	460	1660	42	102	3898	2.1	16.5	35.6
SC-4	1.0 mm	A	558						12.2		
SC-4		J	396	954		67		8085	2.2		
SC-4	0.5 mm	A	177						0.2		
SC-4		J	306	483	1437	55	105	4093	2.5	17.1	36.2
SC-5	1.0 mm	A	255						6.3		
SC-5		J	457	712		68		6034	0.9		
SC-5	0.5 mm	A	161						0.7		
SC-5		J	329	490	1202	69	118	4153	1.3	9.1	28.2

1 A = Adult / J = Juvenile

The summary data from Table 1 shows a moderate range in values for abundance and biomass. Total abundance values ranges from just under 1,100 to 1,660 units per grab, whereas biomass also ranged from 9 to 17 g/grab without megafauna, and 16.5 to 31 g/grab with megafauna. Because of the inherently high variability in such biomass measurements, a range within one order of magnitude is not unusual.

Station SC-3 had the highest abundance and the lowest biomass. When the megafauna were added, the biomass values were more consistent between samples. Considering the seven sample sites, species richness per grab, ranging from 85 to 118 taxa, was relatively high for this type of habitat and sampling methodology, (c.f. Burd 1993, Burd, submitted). In comparison, 1.0 mm sieve samples of the same grab size from the eastern part of Georgia Basin show richness values over a 10 year survey period averaged around 40-60 taxa per grab, had abundance values averaging about 300 to 600 per grab and total wet weight biomass (with megafauna) averaging around 20 to 70 g per grab (2WE 1999, EVS 1991, 1995)[1]. In addition, the reference ranges developed over many years for different sediment types for habitats less than 46 m in Puget Sound (Striplin 1996) include abundances ranging from 156 to 983 per 0.1 m^2 grab and richness ranging from 24 to 90 taxa per grab.

Data collected during the June 4, 2000 ER67/Satellite Channel survey show a relatively homogeneous set of samples, which will make a reliable baseline reference data set for future comparisons. Partly, the faunal consistency is related to the fact that the substrate type and depth seem to be relatively homogeneous (sandy-silt, 73 to 86 m deep) through the sample locations.

A limitation to data analysis is that with only one replicate analyzed per station, there is no way to determine the sampling precision of the summary values. However, some aposteriori estimates are possible by simply grouping random samples in pairs and measuring variance and therefore sampling precision as per the method of Elliott (1977), using standard error as a percentage of the mean. Analysis of total abundance and species richness on a subset of possible combinations, including the lowest and highest values, identified that total abundance, biomass (excluding megafauna), and species richness all have less than 20% standard error as a proportion of the mean for any combination of pairs which represents an acceptable level of sampling precision (Table 2). In most cases, the precision values indicate that only two replicates would be required (estimated n) to achieve a precision of <0.2. The highest replicate number required was 2.5 for the combination of the lowest and highest abundance sample pair. This may also be an indication that there are not patchy "gaps" in fauna from disturbance as they would show up as high variability (and therefore precision >0.2) between and amongst sites. If the selected combinations of 3 and 2 samples shown in Table 2 were actually replicates, sampling precision would be acceptable (precision <0.2). This illustrates that the total faunal abundances were relatively homogeneous for all stations. The same test was used for total biomass (without megafauna) and richness, also showing precisions less than 0.2 (not shown).

1 *Although the quoted values are from stations well-away from the outfall, these stations are in the region of the IONA outfall, where a variety of natural and anthropogenic factors may be affecting benthic infauna.*

TABLE 2

SELECTED COMBINATIONS OF 3 AND 2 SAMPLES TO SHOW VARIATION BETWEEN STATIONS

AKA	Abundance per Grab	Combinations	Mean	Variance	Precision* SE/mean	Estimated n (Elliott 1977)
ER67-2	1065	67-2,SC1,SC5	1136	4706	0.03	1.3
SC1	1140	SC1,SC5,SC2	1216	7126	0.03	1.3
SC5	1202	SC5,SC2,SC4	1315	13858	0.04	1.4
SC2	1307	SC2,SC4,67-1	1410	8481	0.03	1.3
SC4	1437	SC4,67-1,SC3	1527	13776	0.04	1.4
ER67-1	1485	67-1,SC3,67-2	1403	93508	0.11	2.1
SC3	1660	SC3,67-2,SC1	1288	105008	0.13	2.3
		67-2,SC5,SC4	1235	35396	0.08	1.8
		SC5,SC4,SC3	1433	52453	0.08	1.8
		67-2,SC1	1103	2813	0.02	1.2
		SC1,SC5	1171	1922	0.02	1.2
		SC5,SC2	1255	5513	0.03	1.3
		SC2,SC4	1372	8450	0.03	1.3
		SC4,67-1	1461	1152	0.01	1.1
		67-1,SC3	1573	15313	0.04	1.4
		SC3,67-2	1363	177013	0.15	2.5

Testing for significant differences in summary factors between the stations would require that the replicates for each station be processed. However, based on the results in Table 2, it is highly unlikely that there would be any significant ($P<0.05$) differences between stations.

The proportion of major taxonomic groups (Table 3) also shows relatively consistent distributions amongst stations. The only unusual feature is the very low proportion of cnidaria in station SC-1 (particularly *Monobrachium parasitum*) compared with the remaining stations. There is no obvious reason for this disproportionate number.

Abundance was dominated by bivalves, whereas both bivalves and polychaetes contributed substantially to biomass. This is consistent with the substrate type. Also, hydrozoans were very common in most samples, indicative of sandy substrates. Echinoderms, although present, were not abundance dominants. Echinoderms were also not biomass dominants, except for one large specimen of *Brisaster latifrons*.

If the community composition turns out to be as consistent as the summary factors, then it is possible to consider all seven samples to be replicates of each other for the purposes of comparisons with future surveys. Unfortunately, we cannot statistically test for the homogeneity of overall community composition with only one replicate per station. Formal testing of homogeneity among the samples would require use of the bootstrap method of Nemec and Brinkhurst (1988) and two replicates per station.

TABLE 3

SUMMARY OF MAJOR TAXONOMIC GROUP PROPORTIONS (% OF TOTAL) FOR SATELLITE CHANNEL, 2000

Station	Sieve	Group[1]	Cnidaria	Bivalves	Crustaceans	Echinoderms	Gastropods	Errantiate Polychaetes	Sedentariate Polychaetes	Varia
ER67-1	1.0 mm	A	47	12	15	3	2	3	19	0
ER67-1		J	0	39	2	5	0	2	51	0
ER67-1	0.5 mm	A	22	0	67	0	0	6	5	2
ER67-1		J	0	22	45	1	1	4	26	1
ER67-2	1.0 mm	A	56	12	9	0	2	4	15	1
ER67-2		J	6	72	3	1	0	0	16	2
ER67-2	0.5 mm	A	0	0	24	0	0	20	53	3
ER67-2		J	0	38	23	2	1	8	27	1
SC-1	1.0 mm	A	11	32	27	1	0	10	16	3
SC-1		J	0	74	3	5	0	2	14	1
SC-1	0.5 mm	A	0	0	46	0	0	16	37	1
SC-1		J	0	36	37	4	0	3	19	1
SC-2	1.0 mm	A	43	27	11	0	3	3	14	0
SC-2		J	0	89	0	1	1	0	8	0
SC-2	0.5 mm	A	43	0	34	0	0	5	15	2
SC-2		J	0	38	36	2	1	3	18	1
SC-3	1.0 mm	A	54	13	8	1	1	4	13	7
SC-3		J	0	71	1	4	0	7	16	0
SC-3	0.5 mm	A	59	2	30	0	0	2	7	0
SC-3		J	0	29	48	0	0	6	16	0
SC-4	1.0 mm	A	57	15	8	1	4	5	10	0
SC-4		J	0	89	1	1	0	1	8	0
SC-4	0.5 mm	A	19	0	56	0	0	8	16	0
SC-4		J	0	20	16	3	0	2	57	0
SC-5	1.0 mm	A	40	13	5	5	0	16	19	1
SC-5		J	0	20	1	4	0	2	73	0
SC-5	0.5 mm	A	29	0	38	0	1	10	19	3
SC-5		J	0	34	41	1	1	8	17	0

1 A = Adult / J = Juvenile

Based on an inspection of the cluster patterns, there are no striking differences in faunal composition between stations. Station SC-5 is slightly unusual in terms of adult abundance, due mainly to the comparative absence of the most abundant taxon, the hydrozoan *M. parasitum*. This taxon was also relatively rare in station SC-1. Otherwise the patterns do not show obvious differences between samples.

1.3 Comparison With Previous Studies

Satellite Channel in the vicinity of ER67 and elsewhere was subject to multi-year sampling of benthic infaunal communities by Dr. Derek Ellis of the University of Victoria (Ellis 1968, 1970, 1975). Since that time, ER67 and Satellite Channel has been subject to more or less continuous bottom trawling (Figure 2). Bottom trawling has been shown to have substantial impacts on certain benthic communities (Watling and Norse 1998, Engel and Kvitek 1998). It is anticipated that benthic communities have changed markedly since that time as a result of fish removal, bottom disturbance and other long-term biophysical processes and trends.

Effects from bottom trawling would be most evident in the sessile megafauna, which our grabs sampled poorly because of the patchy distribution of these larger taxa. The infauna which were sampled generally recolonize disturbed patches fairly quickly by larval settlement and immigration from surrounding areas. Thus, it is difficult to clearly identify "trawled" areas without more extensive before and after sampling. A combined program of bottom trawling along with grab samples, carefully positioned using video transects would be required to appreciate any potential effects from trawling. This would have to be continued over a reasonable time frame to measure rates of recolonization and recovery as well as to identify the most vulnerable members of the infaunal community.

Determining to what extent communities may have changed since the late 1960s is difficult due to inconsistencies in sampling effort (sieve size), the level of taxonomic precision, as well as changes in taxonomic nomenclature over the years. Also, the original raw data counts for the earlier work are not available. The range in total abundance and species richness documented in the older studies shows richness for the same screen size comparable and abundance about 2 to 4 times lower in the older surveys (Ellis 1975, unpublished). Also, in the early studies, amphipods and some polychaetes were not identified to species, and abundances of the very numerous, small polychaetes were coded instead of true counts due to lack of processing resources, so it is not feasible to directly compare either set of values with the current data. In addition, it is not clear whether some groups, such as cnidarians, were counted at all. Conversely, biomass estimates from the current study are considerably lower than Dr. Ellis's estimates. However, the method of determination used in the older studies was different (weighing total sample for wet weight in older surveys and using mean reference specimen weights in current studies). The difference appears to be about 2 to 4 times. If the difference is still evident once each entire sample is weighed for the current survey, then the difference may be important and/or related to trawling. However, the sampling design and differences between studies make it impossible to be certain.

Abundance and biomass dominants show a few similarities (Table 4), particularly in the larger bivalves and echinoderms. *Compsomyax subdiaphana*, *Macoma carlottensis* and *M. elimata*, *Yoldia* spp., *Brisaster latifrons* were predominant in both the early and the current studies. Unlike the Ellis studies, the current study did not show echinoderms to be abundant, biomass dominants or importance in terms of overall proportions. Whether this is related to historic trawling is unknown. Trawling does appear to reduce habitat complexity and biodiversity but may also enhance productivity of certain opportunistic species (Engel and Kvitek 1998). Some polychaete dominants are similar between current and older surveys, including high abundances of the predaceous *Nepthys* (ubiquitous throughout the BC coast) and the smaller *Prionospio*. Since many polychaetes were not counted or identified in the previous studies, the polychaete dominances are not readily comparable. Note that cnidarians can be colonial or clonal, so counts are not exact. *M. parasitum* was, however, counted as individuals attached to *Axinopsida serricata* shells.

TABLE 4

DOMINANT TAXA FROM SATELLITE CHANNEL BENTHOS, 2000

Taxon	Group[1]	Abundance per Survey	Taxon	Group[1]	Total Abundance of Biomass Dominants
Monobrachium parasitum	cn	1444	Compsomyax subdiaphana	b	4
Axinopsida serricata	b	1362	Macoma elimata	b	43
Spiophanes berkeleyorum	p	817	Praxillella pacifica	p	36
Euphilomedes producta	c	702	Axinopsida serricata	b	1362
Levinsenia gracilis	p	299	Brisaster latifrons	e	1
Eunnucula tenuis	b	237	Glycera americana	p	4
Leptognathia gracilis	c	223	Macoma carlottensis	b	176
Parvilucina tenuisculpta	b	206	Pectinaria granulata	p	33
Yoldia sp.	b	187	Eunnucula tenuis	b	237
Macoma sp.	b	183	Parvilucina tenuisculpta	b	206
Acila castrensis	b	182	Phyllodoce groenlandica	p	9
Macoma carlottensis	b	176	Notomastus tenuis	p	71
Lafoea sp.	cn	175	Sternaspis fossor	p	98
Rhabdus rectius	s	175	Onuphis iridescens	p	12
Pholis parvidons	c	158	Travisia pupa	p	1
Prionospio lighti	p	144	Goniada brunnea	p	6
Eudorella pacifica	c	118	Diopatra ornata	p	4
Nephtys cornuta	p	117	Nitidella gouldii	b	13
Obelia sp.	cn	116	Acila castrensis	b	182

1 b = bivalves, p = polychaetes; c = crustaceans; cn = cnidarian; e = echinoderms; s = scaphopods

There are a few striking differences between the older studies and the current survey. The most abundant taxon, the hydroid *M. parasitum* (which was not colonial, and tended to be attached to many of the small bivalve *A. serricata* shells) in the current study was not even included in species lists for the older studies. This may have been a deliberate oversight of a taxa group often ignored in benthic infaunal studies. In the current study, there were no holothurians identified. This is unusual, but may be coincidental, since holothurians tend to be larger and infrequently spaced, and may also migrate. *Molpadia intermedia* is a common species throughout the BC coast. Also, one of the characterizing community taxa Dr. Ellis described, which was consistently present and abundant (the small sedentariate polychaete *Maldane glebifex*), was entirely absent from the current samples. Dr. Ellis (2000) described this species as occurring in a "matted network at and near the sediment surface", however, this species is not known to form mats or occur in such high abundances elsewhere in British Columbia. Therefore, it could be a misidentification of several similar polychaetes which do form mats, including *Galathowenia oculata* and *Owenia fusiformis*, both of which were found in only moderate abundance in the current survey. However, the high numbers of polychaetes counted in these surface mats in the late 1960s and 1970s were not evident in the current study, and could possibly have been disrupted by long-term chronic trawling. Similar mats of small tubicolous polychaetes have been noted in nearby Saanich Inlet during student educational surveys using bottom grabs. Since there is no bottom trawling in Saanich Inlet, it might be illuminating to collect some grab samples from inside the sill or Patricia Bay for comparison with the Satellite Channel samples.

1.4 Conclusions

The current survey shows that the benthic infaunal community in central Satellite Channel has a relatively "normal" abundance and species richness compared to similar areas in the Strait of Georgia and Puget Sound. In addition, the samples taken from the seven different locations are fairly homogeneous in terms of the variance in abundance, species richness and biomass. Total faunal complement cannot be tested for homogeneity without replicate data. However, there are a few striking differences in taxa and biomass between the older surveys and the current ones. At present, there is insufficient data to determine if this is related to trawling, or long-term natural cycles in the community.

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APPENDICES

APPENDIX 1

BENTHIC INFAUNAL SPECIES DIVERSITY AND ABUNDANCE SAMPLE IN ER67 AND ADJACENT SATELLITE CHANNEL

June 4, 2000

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
CNIDARIA																												
Hydrozoa																												
Clytia sp.													34	0			4	0			34	0						
Lafoea sp.	37	0			23	0											113	0									2	0
Monobrachium parasitum	169	0	43	0	250	15			28	0			108	0	104	0	272	0	114	0	272	0	34	0			35	0
Obelia sp.																	6	0							100	0	10	0
Tubularia marina									1	0													0	1				
Anthozoa																												
Edwardsia sipunculoides																									1	0		
Pachycerianthus fimbriatus					1	0																						
PLATYHELMINTHES																												
Leptoplana sp.					1	0																						
NEMERTEA																												
Cerebratulus californiensis					0	1			0	2	0	1					1	0			1	0						
Nemertea indet.																									0	1		
Tubulanus polymorphus									0	1	0	1																
NEMATODA																												
Nematoda indet.			3				3		6		4				4		1										5	
ANNELIDA																												
Polychaeta Errantia																												
Antinoella macrolepida									2	1							1	3										
Diopatra ornata									2	0							1	0							1	0		
Drilonereis falcata minor											1	0			1	0									2	0	0	1
Errano bicirrata																	1	0			1	0			1	0		
Eteone californica																									1	0		
Eteone longa complex	0	1																							1	1		
Eteone spilotus																											2	0
Eumida longicornuta																					1	0						
Eunoe sp.	0	1																										
Exogone dwisula																											0	1
Exogone molesta					1	0									1	0			1	0								
Gattyana cirrosa											1	2													4	3	0	1

	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
TAXON	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Glycera americana	1	0							1	0							1	0										
Glycera nana	2	0			3	0			1	1			2	0	0	1	2	1			5	0			2	1		
Glycera tesselata													1	0														
Glycinde armigera							1	1			0	2									1	0	0	1				
Goniada brunnea									1	0							1	1			3	0						
Hesperonoe complanata																							0	3				
Lumbrineris cruzensis	3	2	0	2									2	0	0	1	3	1			5	0	4	0	15	2	2	1
Lumbrineris latreilli									3	0	6	1																
Malmgreniella scriptoria	1	2	0	3					1	0																		
Micropthalmus sp.																	0	1										
Nephtys cornuta			4	4	4	0	15	3	1	0	17	3			4	5	14	3	3	10	2	0	4	2			5	14
Nephtys ferruginea	0	1	0	1	1	0	1	1	2	0	0	1	0	1	0	2	0	4			1	2			2	0		
Nephtys sp.							0	1																				
Nereis procera																											0	1
Onuphis iridescens	0	2	0	1					1	1							1	2			1	0			1	0	1	1
Pholoe glabra	2	0	7	0	2	1	2	7	3	0	18	1	3	0	6	2	2	11	0	5	4	0	7	1	2	0	4	0
Phyllodoce groenlandica	1	2											1	0			1	1							2	0	1	0
Phyllodoce sp.							0	1																				
Pilargis berkeleyae							1	1									0	1										
Podarkeopsis glabra	1	0	1	0													1	0			1	0			1	0		
Polynoidae indet.									0	1																		
Scoletoma luti	1	2			7	0			7	0			1	0			4	2	0	1	4	0			5	0		
Sphaerodoropsis sphaerulifer									0	1																	1	3
Sphaerosyllis sp.																											0	2
Polychaeta Sedentaria																												
Ampharete acutifrons	0	1																			1	0			1	1	0	1
Aphelochaeta monilaris	1	1			1	1											1	0			1	0	0	1	1	0		
Aphelochaeta multifilis									0	1	0	1	1	0			1	0							0	2		
Aphelochaeta sp.																							0	2				
Aricidea catherinae	4	0	1	1	3	0	4	3	1	0	6	0	3	0	2	2	4	0			2	0	0	5	1	0	1	1
Aricidea ramosa	1	0	0	1							1	0					1	0					3	0			1	0
Artacama conifera	1	0																							1	0		
Asabellides sibirica			0	1																								
Barantolla americana					1	2							2	1			6	3			0	2						
Boccardia basilaria																					1	0						
Brada villosa	2	0			0	1	0	1	1	0	0	2	2	0	1	0	2	3			4	0						
Capitella capitata complex																	0	2										

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Chaetozone acuta	1	0	0	1	6	2	2	1			0	6	0	4	2	0	0	6	0	1			4	0	1	0	0	1
Chone mollis	3	0									1	0	1	0	0	1	0	1							1	0	0	1
Chone sp.																							0	1				
Cossura modica			1	0																								
Cossura pygodactylata					7	1	1	4	3	0	4	1	1	0	3	0	1	0	0	3			1	0			2	0
Decamastus gracilis					1	1	0	1																				
Dipolydora socialis	3	0																			1	0	0	1	1	0		
Euclymeninae indet.	0	1	0	1																								
Galathowenia oculata	3	4	0	3	11	2	0	7	13	2	0	2	6	0			22	1							6	11	0	2
Heteromastus filobranchus							0	1	3	2	1	1	3	0											3	1		
Laonice cirrata																									1	0		
Levinsenia gracilis	18	0	1	27	11	7	29	5	6	3	62	19	1	1	14	20	9	3	8	10	7	4	0	5			11	18
Leitoscolopos pugettensis	0	3			4	1	0	1	1	0	0	2	2	0	0	4	7	6			7	1			0	1	2	3
Magelona longicornis	0	1											1	0											1	0		
Mediomastus ambiseta	6	3	0	1	4	0	2	9	1	0	5	6					3	6	2	13			17	1	16	7	1	4
Mediomastus sp.													0	1	0	2												
Melinna elisabethae	2	0											1	0														
Mesochaetopterus taylori																									2	0		
Notomastus tenuis	17	8			3	0			3	3	0	1	3	4	0	1	16	3			5	2			1	1		
Ophelina acuminata											0	1																
Owenia fusiformis					3	0																						
Paraprionospio pinnata	4	0			3	0			1	1											3	0	0	1			1	0
Pectinaria granulata	1	0			9	1	0	1	3	0			5	1			3	0			7	0			2	0		
Pectinaria sp.																											0	1
Polycirrus californica													1	0											1	1		
Polycirrus sp. complex																	0	1										
Polydora brachycephala																									1	0		
Praxillella pacifica	2	2			0	2			0	3			3	1			4	7	0	2	5	5						
Praxillella praetermissa	3	2							0	1			0	2											0	5		
Praxillella sp.	0	1											0	1											1	2		
Prionospio lighti	4	0	6	1	6	5	15	4	3	2	20	3	4	0	15	16	6	1	3	2	8	2	0	2	3	0	12	1
Prionospio steenstrupi			0	2	1	0	0	2	1	0			3	0	0	1	1	1					3	0	1	0		
Pseudopolydora kempi japonica																							0	5				
Spio cirrifera							0	1																			0	1
Spiochaetopterus costarum																	1	0			1	0						
Spionidae indet.							0	3																				
Spiophanes berkeleyorum	0	244	0	31	0	7	0	8	0	23	0	15	0	1	0	10	0	8	0	10	0	4	0	143	0	295	0	18

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Sternaspis fossor	9	5	0	3	0	10			2	1			2	13	0	1	4	16	0	2	1	11	0	7	5	6		
Terebellides californica																	1	1					0	1			0	2
Terebellides reishi			0	1									1	0	0	2	0	1										
Travisia pupa																					1	0						
Oligochaeta																												
Tubificidae indet.					0	1	0	1																				
Hirudinea																												
Piscicolidae indet.									1	0																		
SIPUNCULA																												
Golfingia pugettensis					0	2							1	0	0	1	1	0							1	0		
Phascolosoma agassizii																	1	0										
MOLLUSCA																												
Aplacophora																												
Chaetoderma argenteum									1	0													0	1				
Gastropoda																												
Alvania compacta					2	0							1	0	1	0	1	0							1	0	1	1
Bittium attenuatum	4	0	0	1	7	0			1	0			6	2	0	3	3	2			9	0						
Bullidae indet.							0	1																				
Cylichna attonsa	0	1							0	1			1	0														
Euspira pallida																					1	0						
Haminoea vesicula					1	0									0	1					1	0						
Nitidella gouldii	3	0															1	0			9	0						
Odostomia quadrae					1	1																						
Odostomia sp.	0	1	0	1																	0	1					0	1
Ophiodermella cancellata																					1	0						
Philine sp.	1	0																										
Turbonilla sp.	2	0					0	1					1	0							1	0						
Bivalvia																												
Acila castrensis	0	7	0	3	2	8	0	12	1	20	0	26	2	8	0	22	0	9	0	16	1	4	0	8	3	14	0	16
Axinopsida serricata	35	152	0	17	25	97	0	2	44	107	0	3	50	205	0	15	57	197	0	15	49	219	0	9	16	35	0	13
Bankia setacea	1	0																										
Compsomyax subdiaphana	0	9	0	1	1	2			0	2			1	7			1	8			1	2	0	2			0	2
Crenella decussata																							0	1				
Cyclocardia ventricosa																					0	1	0	1			0	5
Eunnucula tenuis	1	1	0	3	22	22	0	14	10	15	0	7	16	32	0	18	14	20	0	5	8	13	0	2	1	2	0	11

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Hiatella arctica									0	2													0	17	2	9		
Lucinoma annulatum	0	1			0	2					0	2	0	2	0	4	0	1	0	1	0	4					0	2
Lyonsia bracteata	1	0			1	1											1	1			0	3						
Macoma brota																	0	2							0	1		
Macoma calcarea					0	1			0	4			0	3														
Macoma carlottensis	9	14			3	7			24	19			15	7			10	11			14	25			7	11		
Macoma elimata	3	2			2	8			2	0			1	2			1	11			0	6			2	3		
Macoma sp.	0	6	0	16	0	12	0	5	0	27	0	22	0	20	0	26	0	13	0	11	0	3	0	4			0	18
Megacrenella columbiana																									1	0		
Musculus niger	0	2											1	0			0	1			0	1						
Mysella tumida			0	5	1	0	0	3	1	1	0	10	2	2	0	2	1	3	4	2			0	2	2	0	0	2
Mytilidae indet.																							0	1			0	1
Nemocardium centifilosum																					1	0						
Nuculana minuta					1	1							0	6	0	2	1	0	0	1	3	1					0	3
Pandora filosa																					1	0						
Parvilucina tenuisculpta	0	9	0	1	1	17	0	26	0	16	0	2	0	30	0	9	6	24	0	3	2	45	0	1	0	9	0	5
Psephidia lordi	1	1																										
Thyasira gouldii			0	1					0	1																		
Yoldia ensifera																					0	1			0	1		
Yoldia martyria					0	1							0	1							0	1						
Yoldia scissurata	0	1			0	1			1	0			0	1	0	1											0	1
Yoldia sp.	0	1	0	16	0	8	0	11	0	7	0	38	1	2	0	26	0	6	0	23	0	3	0	13	0	4	0	28
Scaphopoda																												
Rhabdus rectius	2	18	0	1	7	14	0	4	0	2	0	1	0	30	1	9	9	23			20	22	0	1	0	2	0	9
ARTHROPODA																												
CRUSTACEA																												
Cirripedia																												
Balanus glandula																	1	0										
Copepoda																												
Harpacticoida indet.			1	1																								
Ostracoda																												
Acanthocythereis sp.							1	0																				
Euphilomedes producta	38	0	11	55	30	1	4	34	49	0	16	65	29	1	24	102	38	0	8	74	25	1	6	3	1	0	13	74
Ostracoda indet.											0	1																
Postasterope sp.			2	0			2	0			2	0			1	1			6	0							1	5
Rutiderma lomae							0	1			1	1							0	1			1	0				

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Leptostraca																												
Nebalia pugettensis															0	1												
Cumacea																												
Campylaspis biplicata			1	0																								
Diastylis bidentata	1	0							2	0																		
Diastylis dalli					1	0							1	0														
Diastylis paraspinulosa																									1	0		
Diastylis sp.																											0	1
Eudorella pacifica	5	0	14	9	3	1	0	4	4	4	17	11	2	0	9	2	0	1	5	3	3	0	1	4	1	0	7	8
Eudorellopsis longirostris									1	0	0	1			1	0	0	1	0	1			1	0	1	0		
Leucon subnasica			5	0			1	0			17	0			5	0			5	1			5	1			5	0
Tanaidacea																												
Leptochelia savignyi																							0	1			0	1
Leptognathia gracilis			39	2	1	0	0	3			19	6			18	8	3	0	18	8			64	9			11	14
Isopoda																												
Haliophasma geminatum											0	1									1	0						
Munnogonium cf. *tillerae*			5	0							2	2											3	0				
Pleurogonium rubicundum							2	0											2	0							2	1
Amphipoda																												
Americhelidium shoemakeri	1	0	3	0			1	0	1	0	10	3			2	1	0	1	1	1			2	4			9	0
Ampelisca unsocalae	2	6	0	5	2	4	0	1	2	4	0	2	1	0							1	1	0	2	3	0	0	2
Amplelisca sp.																			0	1								
Aoroides intermedius																									2	1	0	2
Aoroides sp.															0	1							0	4				
Bathymedon pumilus																			1	0								
Bathymedon sp.									1	0	2	0																
Caprella laeviuscula																	1	0										
Cheirimedela zotea																							0	5				
Dyopedos sp.	2	0	5	0			2	0	3	0	1	3			1	0							2	0			1	0
Foxiphalus similis																	1	0										
Gammaridea indet.									0	1															1	0	1	0
Guernea reduncans			10	0			1	0			1	1							1	1			9	2			1	2
Heterophoxus affinis					1	1	0	1	1	0	2	6	1	0			1	0					5	3				
Heterophoxus ellisi																									1	0		
Heterophoxus sp.			0	2															0	2					0	4	0	3
Lepidepecreum garthi																			0	1							0	1
Metaphoxis frequens																											1	0

	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
TAXON	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Microjassa sp.																											1	0
Orchomene cf. *pinguis*											1	0																
Pachynus cf. *barnardi*			7	4	1	0	6	0			10	0			6	0			4	1			1	0			5	0
Parametopella sp.											1	0																
Photis brevipes											20	7																
Photis parvidons	9	2	29	42			4	1	4	0			2	0	13	2	11	0	8	23					1	0	2	5
Photis sp.																			0	1	3	0	0	10			0	5
Phoxocephalidae indet.			1	0																								
Pleustidae indet.			0	1																								
Prachynella lobo																											1	0
Protomedeia grandimana	5	3	0	4																								
Protomedeia sp.									1	0	0	1							0	1								
Rhepoxynius barnardi	2	0	0	2	3	0			2	0	1	1			2	0	2	0	0	8	7	0	0	2	1	0	0	6
Westwoodilla caecula	1	0							0	1	0	1									0	1			0	1		
Decapoda																												
Crangon dalli					1	0																						
Pinnixa occidentalis																					1	0						
PHORONIDA																												
Phoronis sp.	0	2			4	0													0	1					1	0		
ENTOPROCTA																												
Barentsia sp.																	4											
BRYOZOA																												
Bowerbankia gracilis																	47											
ECHINODERMATA																												
Ophiuroidea																												
Amphiodia periercta	3	22			2	3			3	12			1	5			2	18			3	3			8	16		
Amphiodia urtica	9	2							0	1							3	1							5	2		
Amphiodia sp.																			0	1	0	2						
Ophiura sarsia	0	2							0	1																		
Ophiuroidea indet.	0	1	0	3			0	4	0	1	0	13			0	6							0	10	0	1	0	2
Echinoidea																												
Brisaster latifrons	1	0																										

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
UROCHORDATA																												
Ascidiacea																												
Ascidiacea indet.			0	4											0	1												
HEMICHORDATA																												
Saccoglossus sp.																					1	0						
Total Number of Adults and Juveniles	445	555	200	285	493	276	100	196	262	299	270	309	334	397	241	335	745	455	194	266	558	396	177	306	255	457	161	329
Total Number of Organisms		1000		485		769		296		561		579		731		576		1200		460		954		483		712		490
Total Number of Taxa		72		55		63		49		70		58		60		52		82		42		67		55		68		69
Organisms per m²		8475		4110		6517		2508		4754		4907		6195		4881		10169		3898		8085		4093		6034		4153
MEMO																												
Amphipoda indet. (larval)																			1									
Aranae indet. (Spider)			1																									
Autolytus fasciatus																									2			
Balanus sp. nauplius					1																							
Brachyura indet. zoea	1						1		1								1				1							
Calanoida indet.			1				1										1						1					
Calanoida indet. copepodite							1																					
Calanoida indet. nauplius							2																					
Caridea indet. zoea																							1					
Cirripedia indet. cypris larvae									1																			
Corycaeus sp.							3																					
Crinoidea indet. (fragment)			1																									
Cumacea indet. (larval)			6												1													
Eucalanus bungii					1																							
Euphausia pacifica					1																							
Euphausiacea indet. furcilia																			2									
Euphausiacea indet. nauplius							1																					
Fish egg													2															
Gammaridae indet. (larval)	1																											
Gastropod egg case	17				6		1		17				1														1	
Gastropteron pacificum	1																											
Hydroida indet. medusae																											1	
Invertebrate egg			95		1		34		6		27				30				1								17	

TAXON	GSX ER67-1				GSX ER67-2				GSX SC-1				GSX SC-2				GSX SC-3				GSX SC-4				GSX SC-5			
	1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm		1.0 mm		0.5 mm	
	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A	J	A
Invertebrate egg case																											1	
Invertebrate egg sac																			1									
Mollusca egg case					1																7							
Mysidacea indet.	1								1								1											
Neocalanus sp.					1																							
Ostracoda indet. (larval)															2													
Parathemisto pacifica					1																							
Tanaidacea indet. (larval)			1																									
Thysanoessa raschii					3																							

NOTES

GSX ER67-1: Some gravid *Photis parvidons.*

GSX ER67-1: Phoxocephalidae indet. - head only.

GSX ER67-2: Spionidae indet. are larvae

GSX ER67-2: Gravid *Leptognathia gracilis*

APPENDIX 2

CLUSTER ANALYSES FOR SATELLITE CHANNEL SAMPLES, INCLUDING ADULT, JUVENILE 0.5 mm AND 1.0 mm SAMPLES

Satellite Channel Adult cluster analyses

Data matrix read from file: adabun_5.prn
No. of objects = 7
No. of variables = 158

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.63327	.00000					
SC-2	.27213	.60931	.00000				
SC-1	.53571	.56780	.47197	.00000			
SC-3	.37389	.71322	.38064	.62022	.00000		
SC-4	.37455	.67979	.30575	.62569	.36019	.00000	
ER67-2	.35166	.65174	.30420	.51736	.37574	.36762	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	ER67-1	SC-2	.27213
2	ER67-1	ER67-2	.32793
3	ER67-1	SC-4	.34931
4	ER67-1	SC-3	.37261
5	ER67-1	SC-1	.55419
6	ER67-1	SC-5	.64252

```
                                                   ********************ER67-1
                                                ****
                                              ***  ********************SC-2
                                              * *
                                            *** ***********************ER67-2
                                            * *
                                ************* *************************SC-4
                                *           *
                          *******           ***************************SC3
                          *     *
                          *     ***************************************SC-1
                          *
                          *********************************************SC-5

|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0
                                DISTANCE
                          Scale Factor =  .1E+01
```

```
Data matrix read from file: adabun1.prn
No. of objects   =    7
No. of variables =  158
```

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.78479	.00000					
SC-2	.42234	.77474	.00000				
SC-1	.54391	.72710	.43529	.00000			
SC-3	.36824	.83855	.49860	.61600	.00000		
SC-4	.40681	.85093	.36415	.60197	.31269	.00000	
ER67-2	.34258	.82796	.44068	.58300	.30950	.26699	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	SC-4	ER67-2	.26699
2	SC-3	SC-4	.31110
3	ER67-1	SC-3	.37255
4	ER67-1	SC-2	.43144
5	ER67-1	SC-1	.55603
6	ER67-1	SC-5	.80068

```
                                        ****************************ER67-1
                                    *****
                                    *   *    ***********************SC-3
                                    *   ******
                           *********         *  ********************SC-4
                           *        *        ****
                           *        *           ********************ER67-2
        *********************       *
        *                  *        *********************************SC-2
        *                  *
        *                  *****************************************SC-1
        *
        *************************************************************SC-5

|-------------|-------------|-------------|-------------|-------------|
1            .8            .6            .4            .2             0

                              DISTANCE
                        Scale Factor =  .1E+01
```

```
 Data matrix read from file: adbio_5.prn
 No. of objects    =    7
 No. of variables =  158

Distance Matrix (Scale Fact=  .1E+01)

        ER67-1     SC-5      SC-2      SC-1      SC-3      SC-4      ER67-2
 ER67-1.00000
 SC-5   .69319    .00000
 SC-2   .65141    .58677    .00000
 SC-1   .66352    .44653    .48206    .00000
 SC-3   .59389    .61709    .33135    .47663    .00000
 SC-4   .75439    .78218    .43711    .65729    .42663    .00000
 ER67-2.72140    .50386    .46989    .44321    .59510    .65503    .00000

           Linkage    Clusters Linked        Distance  (Scale Factor =  .1E+01)

               1     SC-2    SC-3        .33135
               2     SC-2    SC-4        .43187
               3     SC-1    ER67-2      .44321
               4     SC-5    SC-1        .47520
               5     SC-5    SC-2        .59134
               6     ER67-1  SC-5        .67964

                       *************************************************ER67-1
                       *
                       *             ***********************************SC-5
                       *     *********
                       *     *       * *********************************SC-1
                       *     *       ***
                       *******         *********************************ER67-2
                             *
                             *                 *************************SC-2
                             *          ********
                             ************      *************************SC-3
                                        *
                                        ********************************SC-4

 |-------------|-------------|-------------|-------------|-------------|
 1            .8            .6            .4            .2             0

                                 DISTANCE
                           Scale Factor =  .1E+01
```

```
Data matrix read from file: adbio1.prn
No. of objects   =    7
No. of variables =  158


Cluster Analysis Options:

    (1) Coefficient    = Bray-Curtis Coefficient
    (2) Linkage        = UPGMA
    (3) Linkage scale  = Distance
    (4) COMTRE1 File   = None
    (5) PLOTGRAM File  = None
    (6) VAXPLOT File   = None
    (7) PAUP File      = None
```

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.50571	.00000					
SC-2	.47419	.57797	.00000				
SC-1	.48356	.42885	.47773	.00000			
SC-3	.41895	.61222	.33479	.47498	.00000		
SC-4	.65019	.79410	.44026	.65518	.42523	.00000	
ER67-2	.56331	.49612	.47295	.44425	.59595	.65932	.00000

Linkage	Clusters Linked		Distance	(Scale Factor = .1E+01)
1	SC-2	SC-3	.33479	
2	SC-5	SC-1	.42885	
3	SC-2	SC-4	.43274	
4	SC-5	ER67-2	.47018	
5	ER67-1	SC-2	.51444	
6	ER67-1	SC-5	.57275	

```
                                   *************************************ER67-1
                                   *
                               *****            ************************SC-2
                               *   *     ********
                               *   *******      ************************SC-3
                               *         *
                               *         *******************************SC-4
                               *
                               *         *******************************SC-5
                               *       ***
                               ********* *******************************SC-1
                                       *
                                       *********************************ER67-2

|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0

                              DISTANCE
                        Scale Factor =  .1E+01
```

```
Data matrix read from file: juvabun_5.prn
No. of objects   =    7
No. of variables =  148

Cluster Analysis Options:

    (1) Coefficient    = Bray-Curtis Coefficient
    (2) Linkage        = UPGMA
    (3) Linkage scale  = Distance
    (4) COMTRE1 File   = None
    (5) PLOTGRAM File  = None
    (6) VAXPLOT File   = None
    (7) PAUP File      = None

                                Distance Matrix (Scale Fact=  .1E+01)

         ER67-1   SC-5     SC-2      SC-1      SC-3       SC-4     ER67-2
ER67-1 .00000
SC-5   .30602    .00000
SC-2   .48191    .56713    .00000
SC-1   .47765    .47864    .37178    .00000
SC-3   .41269    .50338    .24382    .37028    .00000
SC-4   .40265    .51199    .40831    .52031    .40160    .00000
ER67-2 .53365    .56479    .37113    .36832    .36419    .47069    .00000

           Linkage    Clusters Linked        Distance  (Scale Factor =  .1E+01)

               1    SC-2         SC3         .24382
               2    ER67-1       SC-5        .30602
               3    SC-2         ER67-2      .36766
               4    SC-2         SC-1        .37013
               5    SC-2         SC-4        .45023
               6    ER67-1       SC-2        .49345

                                                 **********************ER67-1
                                    **************
                                    *            **********************SC-5
                                    *
                                    *                ******************SC-2
                                    *        *********
                                    *        *       ******************SC-3
                                    *        *
                                    *  ********************************ER67-2
                                    *  *     *
                                    ****     **************************SC-1
                                       *
                                       ********************************SC-4

|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0

                               DISTANCE
                         Scale Factor =  .1E+01
```

Q Type Cluster Analysis

Data matrix read from file: juvabun1.prn
No. of objects   =   7
No. of variables =   96

Cluster Analysis Options:

(1) Coefficient   = Bray-Curtis Coefficient
(2) Linkage   = UPGMA
(3) Linkage scale = Distance
(4) COMTRE1 File   = None
(5) PLOTGRAM File = None
(6) VAXPLOT File   = None
(7) PAUP File   = None

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.30600	.00000					
SC-2	.51340	.81557	.00000				
SC-1	.52663	.66801	.42647	.00000			
SC-3	.46653	.74775	.20828	.40518	.00000		
SC-4	.52248	.80861	.20676	.44787	.24331	.00000	
ER67-2	.58000	.76353	.37008	.29799	.36628	.39937	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	SC-2	SC-4	.20676
2	SC-2	SC-3	.22580
3	SC-1	ER67-2	.29799
4	ER67-1	SC-5	.30600
5	SC-2	SC-1	.40254
6	ER67-1	SC-2	.64125

```
                                                  **********************ER67-1
                          ************************
                          *                       **********************SC-5
                          *
                          *                              ***************SC-2
                          *                             **
                          *                *****************************SC-4
                          *                *            *
                          *****************             ****************SC-3
                                           *
                                           *        ********************SC-1
                                           *********
                                                    ********************ER67-2
|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0
                                   DISTANCE
                             Scale Factor =  .1E+01
```

Q Type Cluster Analysis

Data matrix read from file: juvbio_5.prn
No. of objects = 7
No. of variables = 148

Cluster Analysis Options:

(1) Coefficient = Bray-Curtis Coefficient
(2) Linkage = UPGMA
(3) Linkage scale = Distance
(4) COMTRE1 File = None
(5) PLOTGRAM File = None
(6) VAXPLOT File = None
(7) PAUP File = None

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.43062	.00000					
SC-2	.41443	.58062	.00000				
SC-1	.36817	.41457	.40540	.00000			
SC-3	.32392	.49292	.23296	.38241	.00000		
SC-4	.43888	.51373	.25639	.46007	.30252	.00000	
ER67-2	.51355	.52884	.26173	.37471	.35837	.31866	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	SC-2	SC-3	.23296
2	SC-2	SC-4	.27946
3	SC-2	ER67-2	.31292
4	ER67-1	SC-1	.36817
5	ER67-1	SC-2	.41417
6	ER67-1	SC-5	.49355

```
                                             **************************ER67-1
                                          ****
                                          *  **************************SC-1
                                          *
                                    *******           *****************SC-2
                                    *     *        ****
                                    *     *      ***  *****************SC-3
                                    *     *      * *
                                    *     ******** ********************SC-4
                                    *            *
                                    *            **********************ER67-2
                                    *
                                    ***********************************SC-5
|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0
                               DISTANCE
                         Scale Factor =  .1E+01
```

Q Type Cluster Analysis

Data matrix read from file: juvbio1.prn
No. of objects = 7
No. of variables = 148

Cluster Analysis Options:

(1) Coefficient = Bray-Curtis Coefficient
(2) Linkage = UPGMA
(3) Linkage scale = Distance
(4) COMTRE1 File = None
(5) PLOTGRAM File = None
(6) VAXPLOT File = None
(7) PAUP File = None

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.45941	.00000					
SC-2	.39289	.68269	.00000				
SC-1	.34920	.52098	.38825	.00000			
SC-3	.32934	.61491	.22751	.39215	.00000		
SC-4	.45037	.63867	.24177	.44796	.28922	.00000	
ER67-2	.42668	.56036	.33528	.26985	.36241	.43872	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	SC-2	SC-3	.22751
2	SC-2	SC-4	.26550
3	SC-1	ER67-2	.26985
4	ER67-1	SC-1	.38794
5	ER67-1	SC-2	.39304
6	ER67-1	SC-5	.57950

```
                                           ****************************ER67-1
                                           *
                                           *        *******************SC-1
                                           **********
                              **************        *******************ER67-2
                              *            *
                              *            *           ****************SC-2
                              *            *        ****
                              *            **********  ****************SC-3
                              *                     *
                              *                     *******************SC-4
                              *
                              *****************************************SC-5

|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0
                               DISTANCE
                         Scale Factor =  .1E+01
```

Q Type Cluster Analysis

Data matrix read from file: Satellite Channel total abundance (adults, juveniles, all sieves)
No. of objects = 7
No. of variables = 214

Cluster Analysis Options:

(1) Coefficient = Bray-Curtis Coefficient
(2) Linkage = UPGMA
(3) Linkage scale = Distance
(4) COMTRE1 File = None
(5) PLOTGRAM File = None
(6) VAXPLOT File = None
(7) PAUP File = None

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.38965	.00000					
SC-2	.36605	.56317	.00000				
SC-1	.47048	.47737	.39027	.00000			
SC-3	.36916	.56045	.28008	.47000	.00000		
SC-4	.36140	.54831	.32143	.54366	.33742	.00000	
ER67-2	.41490	.55271	.29680	.43401	.33505	.38449	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	SC-2	SC-3	.28008
2	SC-2	ER67-2	.31592
3	SC-2	SC-4	.34778
4	ER67-1	SC-2	.37788
5	ER67-1	SC-1	.46168
6	ER67-1	SC-5	.51528

```
                                            ***************************ER67-1
                                            *
                                            *      ********************SC-2
                                      *******   ****
                                      *     * ***  ********************SC-3
                                      *     * * *
                                  *****     *** ***********************ER67-2
                                  *   *       *
                                  *   *       *************************SC-4
                                  *   *
                                  *   *********************************SC-1
                                  *
                                  *************************************SC-5
|-------------|-------------|-------------|-------------|-------------|
1            .8            .6            .4            .2             0
                                DISTANCE
                          Scale Factor =  .1E+01
```

Q Type Cluster Analysis

Data matrix read from file: Data matrix read from file: Satellite Channel total biomass (adults, juveniles, all sieves)
No. of objects = 7
No. of variables = 214

•

Cluster Analysis Options:

•

•

(1) Coefficient = Bray-Curtis Coefficient

•

(2) Linkage = UPGMA

•

(3) Linkage scale = Distance
(4) COMTRE1 File = None
(5) PLOTGRAM File = None
(6) VAXPLOT File = None
(7) PAUP File = None

Distance Matrix (Scale Fact= .1E+01)

	ER67-1	SC-5	SC-2	SC-1	SC-3	SC-4	ER67-2
ER67-1	.00000						
SC-5	.48775	.00000					
SC-2	.44444	.57716	.00000				
SC-1	.44043	.43823	.46119	.00000			
SC-3	.38926	.58025	.30206	.44572	.00000		
SC-4	.59670	.72860	.38288	.61011	.39050	.00000	
ER67-2	.54370	.49994	.41148	.42817	.54821	.59339	.00000

Linkage	Clusters Linked		Distance (Scale Factor = .1E+01)
1	SC-2	SC-3	.30206
2	SC-2	SC-4	.38669
3	SC-1	ER67-2	.42817
4	SC-5	SC-1	.46909
5	ER67-1	SC-2	.47680
6	ER67-1	SC-5	.53567

```
    *********************************ER67-1
    *
*****           *********************SC-2
*   *     *******
*   *******     *********************SC-3
*         *
*         ***************************SC-4
*
*    ********************************SC-5
******
     *  *****************************SC-1
     ****
        *****************************ER67-2

|-------------|-------------|-------------|-------------|-------------|
1             .8            .6            .4            .2            0
```

DISTANCE
Scale Factor = .1E+01