Appendix E:
Column Sampling and the Archaeology of Small Fish at Ts'ishaa

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Introduction

Archaeologists working on the Northwest Coast have periodically employed the use of core and column sampling (Casteel 1970, 1976a) to describe the taxonomic composition of fish recovered from small volumes of fine-screened archaeological deposit (Cannon 2000; Casteel 1976a; Coupland 1991; Fawcett 1991; Hanson 1991; Monks 1977; Moss 1989; Wigen and Eldon 1987). Although the controlled recovery and laboratory processing of these fine-screened (<6 mm) matrix samples is known to be an effective way to describe the composition of fish in a shell midden deposit, this type of analysis is rarely conducted in more than a single area of a site, and the results are not often explicitly compared to fauna identified from adjacent excavation units (but *see* Cannon 2000; Wigen and Eldon 1987). As a result, taxonomic frequencies of fine-screened fish remains are often not included in the spatial, temporal, and quantitative investigation of prehistoric subsistence practices on the Northwest Coast, despite the fact that fish are often the most numerous and ubiquitous vertebrate taxa present in shell midden deposits (e.g., Calvert 1980; Heulsbeck 1994; Wigen and Stucki 1988).

In this paper, I describe fish remains recovered from five fine-screened (<6 mm) column samples and compare this with the large assemblage of fish remains identified from excavation units at Ts'ishaa (Frederick and Crockford, this vol.). My purpose in doing so is to provide a broader assessment of the context and significance of the fauna recovered from the site as a whole. My column sample analysis is based an assemblage of 20,245 fine-screened fish remains and is compared to an assemblage of 45,333 fish specimens examined from ¼" excavation units, where fish account for the overwhelming majority of the fauna identified (66–98% NISP, Frederick and Crockford, this vol.).

Before comparing fauna from the units and columns, I first describe the methods I used to identify and quantify the column sample assemblage. I then explore how sample size affects the richness of fish taxa found in both the unit and column assemblages and how this variation is expressed among the different recovery methods. I show that large numbers of herring and anchovy are present throughout the examined deposits and this affects the composition of species throughout the entire faunal assemblage. I then demonstrate how the average body-size of the two most abundant fish species in the unit assemblage (e.g., rockfish and greenling) is smaller and recovered in different relative proportions in the fine-screened columns. I also quantify the temporal rate of midden accumulation and examine how shell and bone frequency vary within deposits. Collectively, the analysis of the fauna recovered from the fine-screened column samples reveals a fundamentally important aspect of the prehistoric Nuu-chah-nulth fishery in the Broken Group Islands of Pacific Rim National Park Reserve.

Methods

The site of Ts'ishaa is a large cultural shell midden deposit extending roughly 300 m across the northeast shoreline of Benson Island in Barkley Sound. Ethnographically documented as the location of two distinct village communities of the Tseshaht First Nation (Ts'ishaa, DfSi-16 and Himayis, DfSi-17), extensive excavation at the site sampled approximately 219 m^3 of cultural deposit from 35 excavation units (2x2 m) spanning between ca. 5000–250 years before present (cal yr BP, McMillan and St. Claire, this vol.). Vertebrate fauna was recovered using ¼" mesh screens in the field and fauna has been identified for five excavation units (*see* Frederick and Crockford, this vol.). The fine-screened fauna (≤6 mm) reported in this paper was collected from 'columns' of archaeological matrix sampled from within unit quadrants or directly adjacent to excavated units (e.g., Casteel 1976a). Column matrix samples consisted of bulk sediments removed in ten-centimetre levels of known volume (Table 1). The deposits containing identified fauna fall within the two chronological periods archaeologically documented at Ts'ishaa; 1) the 'back terrace' component which dates to between ca.

Table 1. Archaeological context of the ≥ 2 mm column sample fauna.

Column Sample	Approx. age range (cal yr BP)[a]	Column Dimensions	Screen Size (mm)	Examined Levels [n lvls.]	Layers	Depth (m)	Volume per level (litres) [b]	Total Vol. (litres)	NSP[c]	NISP[d]	NSP/ litre
N2-4/ W102-104	250–1500	20x20x10cm	3 & 6	1, 3, 5, 9, 13, 15, 17, 19, 23, 27, 31 [n=10]	A-E [n=6]	3.1	4.0	40	**6,267**	**2,876**	156.7
S14-16/ W25-27	250–1800	25x25x10cm	3 & 6	3, 7, 11, 15, 17, 19, 21, 25, 28, 31, 33, 35 [n=12]	A, B, C, E, F, G [n=5]	3.5	6.25	75	**4,874**	**1,956**	65.0
S5-7/ W11-13	250–1000	2 litres (bulk)	2	1-23, odd lvls. [n=12]	A-C [n=3]	2.3	2.0	24	**3,403**	**565**	141.8
S56-57/ W50-52	3000–5000	10x10x10cm	3 & 6	1-25, odd lvs. [n=13]	A, B [n=2]	2.5	1.0	13	**1,854**	**942**	142.6
S62-64/ W62064	3000–5000	20x20x10cm	3 & 6	1-9, odd lvs. [n=5]	A-D [n=4]	0.9	4.0	20	**1,557**	**704**	77.9
Totals				[n=52]				172	**17,955**	**7,043**	104.4

[a] Age range based on one or more calibrated radiocarbon dates from the adjacent excavation unit (Table 7).
[b] Volume calculated by dimensions of individual matrix sample (i.e., before excavation).
[c] Number of identified specimens positively identified to genus or above (e.g., rockfish, herring, etc.).
[d] The total number of examined skeletal specimens (including unidentified specimens).

Table 2. Archaeological context of the 1.5 mm column sample fauna.

Column Sample[a]	Approx. age range (cal yr BP)[b]	Screen size (mm)	Examined Levels [n levels.]	Volume per level (litres)[c]	Total Volume (litres)	NISP[d]	NSP[e]	NSP/ litre
N2-4/W102-104	300–1500	1.5	1,3,5,9,13,15,17, 19,23,27,31[n=10]	0.25	2.50	**465**	**2,057**	822.8
S56-57/W50-52	3000–5000	1.5	5, 15, 25 [n=3]	0.25	0.75	**68**	**234**	312.0
S62-64/W62-64	3000–5000	1.5	1, 5, 9, [n=5]	0.25	0.75	**77**	**318**	424.0
Totals			[n=16]		4.00	**610**	**2,609**	652.3

[a] Columns S14-16/W25-27 and S5-7/W11-13 were previously processed and did not retain 1.5mm specimens.
[b] Age range based on one or more calibrated radiocarbon dates from the adjacent excavation unit (Table 7).
[c] Volume calculated by dividing the screened matrix into portions representing 250cc of the original excavated volume.
[d] Number of identified specimens positively identified to genus or above (e.g., rockfish, herring, etc.).
[e] The total number of examined skeletal specimens (including unidentified specimens).

5000 and 3000 years before present and 2) the 'main village' component which dates to between ca. 1800 and 250 years ago (cal yr BP).

Three of the five column samples described in this paper were recovered from areas directly adjacent to excavation units with identified 6 mm fauna (Columns S62-64/W62-64 [back terrace]; S14-16/W25-27 [main village]; N2-4/W102-104 [main village]). Fauna from the two other column samples are from areas of the site that do not contain identified unit fauna (Column S5-7/W11-13 [Himayis]; S56-57/W50-52 [back terrace]). Although the column samples are from dispersed areas of this large site (see site map in McMillan and St. Claire, this vol.), the three columns from the main village are broadly contemporaneous with each other as are the two columns from the back terrace (Tables 1–4).

Bulk matrix from the column samples was wet-screened through nested geological sieves at the Parks Canada Laboratory (Victoria, BC). Due to the large number of skeletal elements encountered during this process, a limited number of individual column levels was selected for identification (Tables 1 and 2). Individual lev-

els were selected to maximize the temporal and spatial coverage of the site and to ensure the stratigraphic independence of individual level assemblages (i.e., ≥10cm separated each examined level). Every odd level was identified for three of the five column samples (Columns S56-57/W50-52, S5-7/W11-13, S62-64/W62-64, Table 1). In the remaining two column samples (Columns N2-4/W102-104 and S14-16/W25-27), only select levels from stratigraphic layers defined in the adjacent excavation unit were analysed (Table 1). Faunal recovery from 1.5 mm mesh was limited to three column samples and fauna from these samples was further subdivided into portions representing 250 cc of the original excavated volume (Table 2).

Identification

I identified vertebrate fauna with the aid of a binocular dissecting microscope (6.3–40x) and the use of the extensive comparative fish collection at the University of Victoria Zooarchaeology Laboratory (Victoria, BC). Identification data was recorded by skeletal element in a *Paradox 35* database which noted relevant modification and provenience information. The completed database was converted to an *Excel* spreadsheet that was then imported into *SPSS* for statistical analyses. With the exception of fish spines, branchials, scales, and gill-rakers, identification was attempted for all skeletal elements recognizable to species or genus level. Confidence codes were assigned to each examined specimen to indicate the certainty of identification (for criteria, see Frederick and Crockford, this vol.). Using the same comparative collection, Rebecca Wigen conducted a review and verification of all identifications. Considerable effort was taken to employ the same procedures followed during the identification of the unit fauna (i.e., Frederick and Crockford, this vol.).

Quantification

Faunal remains described in this paper are quantified according to the number of individual specimens attributable to species/taxon (NISP, e.g., rockfish, herring, etc.) or the number of specimens identifiable to class (NSP, e.g., mammal, fish, etc.). Relative abundance refers to the percentage of skeletal specimens attributable to a particular taxon in relation to the total number of identified taxa (i.e., %NISP). Although the use of relative abundance is an imperfect measure of species frequency, it is the most widespread method of describing abundance in archaeological faunal assemblages (Grayson 1984). Clearly, significant differences exist in the number and durability of skeletal elements found in different fish taxa and calculating the specimen abundance will cause some species to be under or over-represented in a given assemblage (e.g., Rick et al. 2002). Some researchers attempt to compensate for this uncertainty by choosing to identify a limited number of skeletal elements from fish species (e.g., Leach 1997; Vale and Gargett 2002), but this strategy neglects to include a number of identifiable elements and does not easily facilitate comparisons with analyses which do not utilize this approach. In contrast, identifying the greatest possible number of elements and specimens most completely documents a given assemblage and can be subsequently modified to accommodate alternative approaches to quantification. The latter identification strategy was used during this analysis, principally in order to establish a comparable dataset with the larger unit assemblage

Results

The examined column sample assemblage contains 20,564 skeletal specimens from 52 discrete 10 cm levels representing an excavated volume of 172 litres (Tables 1–4). Fish comprise the overwhelming majority of skeletal specimens (NSP=20,245, 98.45%) In contrast, small numbers of specimens were identifiable as mammal (NSP=303, 1.47%) and bird (NSP=9, 0.04%). Fish specimens were found in every one of the 52 examined column sample level assemblages and vastly outnumber mammal and bird specimens. From the initial total, 6979 fish specimens were identified to species or genus (i.e., NISP) from 3 and 2 mm mesh (Tables 1 and 3). An additional 610 fish specimens (NISP) were identified to species from 1.5 mm mesh (Tables 2 and 4). However, since the 1.5 mm assemblage represents fauna identified from sub-sampled portions of individual levels and do not include specimens from the larger mesh sizes (Table 2), these data are evaluated and discussed separately. The low abundance and taxonomic richness of bird and mammal remains recovered from the column sample assemblage demonstrates the infrequent distribution of these animals in the deposits but also precludes the use of these data for evaluating species composition.

Table 3. Frequency and relative abundance (%NISP fish) of faunal specimens from fine-screen column sample deposits (Table 1). Species are grouped by class and listed in order of overall abundance.

		Column Sample											
		N2-4/ W102-104		S14-16/ W25-27		S5-7/ W11-13		S56-57/ W50-52		S62-64/ W62-64		Total	NISP
Species	**Common Name**	**NISP**	**%**	**NISP**	**%**	**NISP**	**%**	**NISP**	**%**	**NISP**	**%**	**NISP[a]**	**Fish %[b]**
Clupea pallasi	Pacific herring	1,404	49	1,096	57	449	48	300	54	473	68	**3,722**	53.33
Engraulis mordax	Anchovy	769	27	175	9	246	26	19	3	34	5	**1,243**	17.81
Sebastes sp.	Rockfish sp.	338	12	335	17	64	7	18	3	15	2	**770**	11.03
Hexagrammos sp.	Greenling sp.	121	4	129	7	88	9	149	27	137	20	**624**	8.94
Oncorhynchus sp.	Salmon	57	2	43	2	65	7	15	3	1	*	**181**	2.59
Embiotocidae	Perch sp.	58	2	44	2	8	1	26	5	23	3	**159**	2.28
Squalus acanthias	Dogfish shark	25	1	20	1	3	*	15	3			**63**	0.90
Ophiodon elongatus	Lingcod	14	*	11	1	2	*	11	2	3	*	**41**	0.59
Merluccius productus	Hake	25	1	6	*	6	1					**37**	0.53
Porichthys notatus	Plainfin midshipman	3	*	18	1					4	1	**25**	0.36
Hippoglossus stenolepis	Halibut	4	*	14	1	2	*	3	1	1	*	**24**	0.34
Anoplopoma fimbria	Sablefish	8	*	14	1					1	*	**23**	0.33
Pleuronectiformes	Flatfish sp.	7	*	3	*	1	*			1	*	**12**	0.17
Hemilepidotus hemilepidotus	Red Irish lord	3	*	7	*	2	*					**12**	0.17
Scorpaenichthys marmoratus	Cabezon	6	*	2	*	3	*					**11**	0.16
Hydrolagus colliei	Ratfish	3	*	5	*			1	*			**9**	0.13
Damalichthys vacca	Pile perch	7	*	1	*							**8**	0.11
Platichthys stellatus	Starry flounder	2	*					1	*			**3**	0.04
Eopsetta jordani	Petrale sole	1	*	2	*							**3**	0.04
Raja sp.	Skate sp.			1	*					1	*	**2**	0.03
Cymatogaster gracilis	Shiner perch	1	*							1	*	**2**	0.03
Cottidae	Sculpin sp.			1	*	1	*					**2**	0.03
Embiotica lateralis	Striped seaperch					1	*					**1**	0.01
Lepidopsetta bilineata	Rock sole	1	*									**1**	0.01
Gadus macrocephalus	Pacific cod			1	*							**1**	0.01
Aves	Unidentified bird	2		3								**5**	
Aves (lg)	Unident. Lrg. bird	1										**1**	
Aves (med)	Unident. med. bird	1		1		1						**3**	
Odocoileus sp.	Deer sp.							1				**1**	
Peromyscus sp.	Deer mouse			2						1		**3**	
Mustela vison	Mink							3				**3**	
Mammalia	Undet. Ind mamml.	1										**1**	
Callorhinus ursinus	Fur seal			2				2		3		**7**	
Phocoena phocoena	Harbour porpoise									1		**1**	
Pinnepedia	Pinnepedia, sm	2										**2**	
Delphinidae/Phocoenidae	Porpoise/Dolphin sp.			1								**1**	
Mammalia	Und. sea mamml.					1		1				**2**	
Mammalia	Undet.mammal	41		98		32		100		8		**279**	
Mammalia	Undet.mammal (sm)	1		1								**2**	
Amphibian	salamander sp.			5								**5**	
Unidentified bone	Unident.taxa							2				**2**	
	NSP Non-Fish	49		113		34		109		13		**318**	
	NISP FISH	**2857**		**1,928**		**941**		**558**		**695**		**6,979**	
	Unid. Fish	3361		2,833		2,428		1,187		849		**10,658**	
	NSP Fish	6218		4,761		3,369		1,745		1,544		**17,637**	
	TOTAL NSP	**6267**		**4,874**		**3,403**		**1,854**		**1,557**		**17,955**	
	Approx. age (cal yr BP)[c]	250–1500		250–1800		250–1000		3000–5000		3000–5000			
	Examined Volume (litres)	40 L		75 L		24 L		13 L		20 L		172 L	

* Less than 1% of identified fish (NISP).

[a] NISP = Number of identified specimens.

[b] % NISP = relative abundance of identified fish

[c] Age range based on one or more calibrated radiocarbon dates from the adjacent excavation unit (see Table 7).

Table 4. Frequency and relative abundance of faunal specimens from examined 1.5mm column sample deposits.*

		Column Sample							
		N2-4/W102-104		S56-57/W50-52		S62-64/W62-64		Total	NISP
Species	Common name	NISP	%	NISP	%	NISP	%	NISP[a]	Fish %[b]
Engraulis mordax	Anchovy	385	82.8	7	10.3	26	33.8	**418**	68.52
Clupea pallasi	Pacific herring	61	13.1	56	82.4	45	58.4	**162**	26.56
Embiotocidae	Perch sp.	5	1.1			3	3.9	**8**	1.31
Hexagrammos sp.	Greenling sp.	4	0.9	3	4.4			**7**	1.15
Oncorhynchus sp.	Salmon	5	1.1			1	1.3	**6**	0.98
Sebastes sp.	Rockfish sp.	3	0.6	1	1.5			**4**	0.66
Ophiodon elongatus	Lingcod			1	1.5			**1**	0.16
Gadidae	Gadid sp.					1	1.3	**1**	0.16
Stichaeidae	Prickleback sp.					1	1.3	**1**	0.16
Hemilepidotus hemilepidotus	Red Irish lord	1	0.2					**1**	0.16
Squalus acanthias	Dogfish shark	1	0.2					**1**	0.16
	Undet. Mammal	1						**1**	
	NISP Fish	465		68		77		**610**	
	Unid fish	1,591		166		241		**1,998**	
	NSP fish	2,056		234		318		**2,608**	
Approx. age range (cal yr BP) [c]		250–1500		3000–5000		3000–5000			
Examined Volume (Litres)		2.50L		0.75L		0.75L		4.00L	

*1.5mm estimates reported here should be considered highly tentative due to sampling effort that was disproportionately focused on column N2-4/W102-104, the small examined volume (4L), and sub-sampling that prevented the inclusion of specimens that were recovered in larger mesh sizes (Table 2).

[a] NISP = Number of identified specimens.

[b] % NISP = relative abundance of identified fish

[c] Age range based on one or more calibrated radiocarbon dates from the adjacent excavation unit (Table 7).

Assessing Sample Size and Sample Richness

A perennial question in faunal analysis is whether assemblages are large enough to adequately assess differences between them without these comparisons being unduly influenced by differences in sample size (e.g., Grayson 1984). To evaluate whether insufficient sample size (NISP) is a factor that prevents an effective comparison of the unit and column assemblages, I generated cumulative frequency curves illustrating the relationship between taxonomic richness and sample size in both assemblages (Figure 1). This was accomplished by cumulatively adding the identified fish specimens from individual level assemblages and recording the sample size at which new fish taxa are added to the assemblage (e.g., Lepofsky et al. 1996). This relationship was plotted according to the addition of identified specimens (NISP) recovered from each individual level assemblage (Figure 1a) as well as by adding numbers of individual level samples (Figure 1b). In order to equably compare taxonomic richness between the two assemblages, certain taxa identified beyond a genus level were collapsed into taxon-specific categories (Irish lords – *Hemilepidotus* sp.; perches – Embiotocidae; greenlings - *Hexagrammos* sp.; and salmon - *Onchorhynchus* sp.). Specimens not identified to genus level were not considered taxa (e.g., flatfish) with the exception of perch (Embiotocidae) and sculpins (Cottidae).

The result of this analysis illustrates that taxonomic richness in both assemblages appears to similarly plateau after reaching twenty taxa, indicating that a degree of sampling redundancy has been achieved (Reitz and Wing 1999:107). It also shows that species richness is numerically equivalent in both assemblages (n=21 fish taxa) despite the presence of many more identified specimens in the unit assemblage (NISP=22,100) than in the column assemblage (NISP=6,979). Moreover, even the comparatively tiny assemblage

(NISP=817) recovered exclusively from the 6 mm fraction of the column samples reaches 20 taxa and plateaus after the analysis of 22 individual level assemblages (Figure 1b).

Thus, after an initially dramatic increase in species richness, the rate at which new fish taxa are discovered becomes considerably reduced until the addition of more samples and specimens appears less likely to influence the richness of the assemblage. This is not to say that taxonomic richness has reached its theoretical maximum nor does it mean that the unit assemblage is more diverse than the column assemblage or vice-versa. For as Figure 1a suggests, richness can increase even after many thousands of specimens have been examined (e.g., ≈17,000 NISP). Another important aspect of the comparing the two assemblages is the observation that two taxa in each assemblage were not present in the other assemblage, effectively cancelling out the cumulative richness of both assemblages (n=23 fish taxa, Figure 1*). Nevertheless, despite considerable differences in recovery technique and sample size, this analysis indicates that the two assemblages contain a sufficiently large enough sample to reliably evaluate the taxonomic composition in each assemblage without those differences being the result of differences in sample size.

Assessing Relative Abundance and Ubiquity

The multitude of spatially and temporally distinct contexts represented by the column sample fauna and their proximity to units containing identified fauna provides an opportunity to evaluate the taxonomic composition of fish remains for the site as a whole. In the following discussion, I use these data to describe some of the basic characteristics of the fish assemblage and contrast this with the fish identified from the excavation units.

A considerable variety of fish taxa are present in both the unit and column assemblages, but only a limited number of these taxa have relative

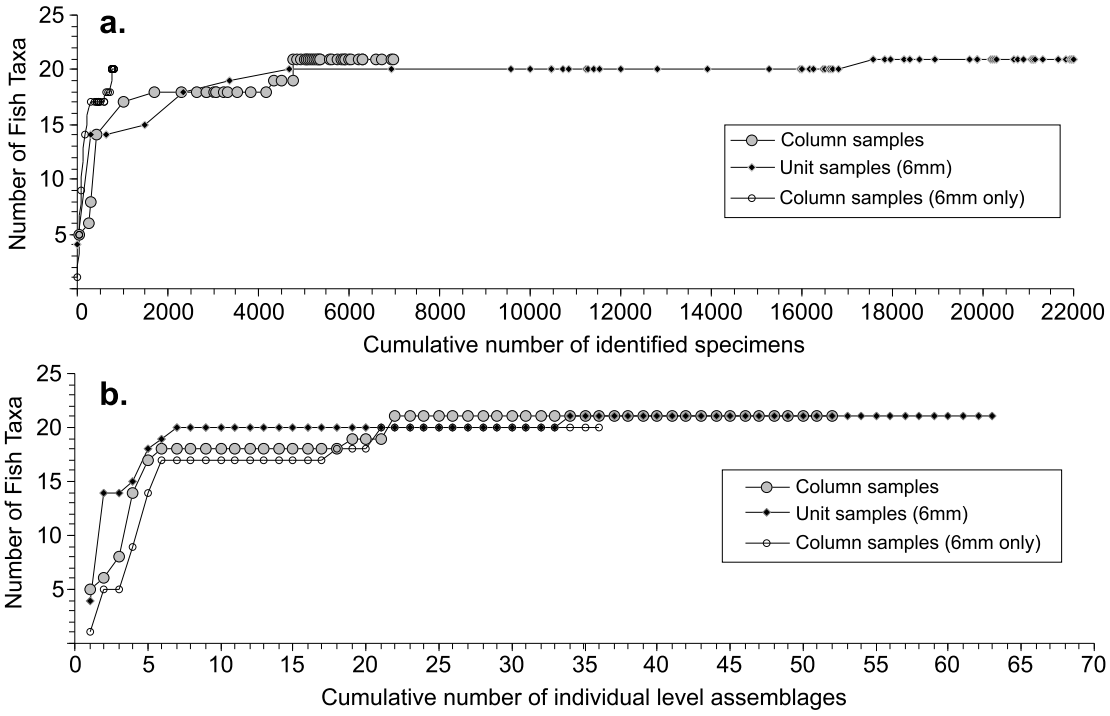

Figure 1. Cumulative frequency graphs showing the number of fish taxa* in relation to (a) the cumulative number of identified specimens grouped according to individual level assemblages and (b) the cumulative number of individual level assemblages (the same data but shown in different presentation formats). The separate lines represent fauna from the unit (6 mm), column assemblages (6+3 and 2 mm), and column sample fauna recovered exclusively from the 6 mm fraction (6 mm only). *Sablefish *(Anoplopoma fimbria)* and Starry flounder *(Platichthys stellatus)* were recovered in the column but not the unit assemblage. Conversely, Bluefin tuna *(Thunnus thynunus)* and English Sole *(Parophrys vetulus)*, were found in the unit assemblage but not in the column assemblage (Frederick and Crockford, this vol.).

abundance values of greater than 1% (Table 3, Frederick and Crockford, this vol.). For instance, the six most abundant taxa in the unit assemblage account for more than 88% (NISP) of the identified fish specimens (Frederick and Crockford, this vol.). In the column assemblage, the six most abundant taxa account for more than 95% (NISP) of the identified fish specimens (Table 3). This suggests that the bulk of the fishing activity at Ts'ishaa was focused on a relatively narrow range of taxa. As discussed below however, some of the taxa representing large proportions of the unit assemblage are not present in similar quantities in the column sample assemblage.

The six most abundant fish taxa recovered from the column samples are herring, anchovy, rockfish, greenling, salmon and perch respectively (Figure 2). These same taxa are also the six most abundant in each of the five individual column sample assemblages, though not all in the same rank order (Tables 3 and 4). The relative abundance of fish specimens in the column samples differs substantially from the unit assemblage (Figure 2). The latter is dominated by rockfish (65%, NISP) and followed distantly by greenling (8%), lingcod (7%), perch (4%), petrale sole (3%) and hake (2%) (Frederick and Crockford, this vol.).

Herring is by far the most abundant (53% NISP) and frequently occuring (98% ubiquity) fish taxa in column sample assemblage (Figures 2 and 3). It represents an average of approximately half (mean %NISP= 49±28) of the identified specimens from the 52 column sample level assemblages. Herring is also the most abundant of the identified specimens in each of the five column samples (mean %NISP = 55.2±8, Table 3). Thus, herring account for at least half of all the fish remains throughout the deposits at Ts'ishaa. The consistently dominant abundance and widespread use of this species suggests that herring was central to the subsistence practices of the residents of Ts'ishaa for the duration of human occupation of this site.

Anchovy is the second most abundant taxa in the column sample assemblage and is less ubiquitous and abundant than herring in all five columns (Table 3). However, in the 1.5 mm sub-sampled assemblage, anchovy is more abundant than herring which indicates that this small fish (<20 cm, Hart 1973) is recovered more readily in screen sizes smaller than 3 mm (Tables 4 and 5). In spite of this, it is difficult to evaluate the rank order abundance of anchovy in the 1.5 mm assemblage because; 1) sampling effort was disproportionately focused on a single column sample (N2-4/W102-104), 2) the sub-sampling procedure prevented the inclusion of specimens recovered from larger screen sizes and 3) collectively, these data only represent 4 litres of examined deposit (Tables 2 and 4). Irrespective of the inadequacies of the 1.5 mm assemblage however, the fact that anchovy is less abundant than herring in both the 1.5 mm and 3 mm fractions from the two back terrace columns samples provides evidence to suggest that anchovy were less abundant than herring between ca. 5000–3000 cal yr BP (Tables 3 and 4).

Rockfish dominate the assemblage of fauna

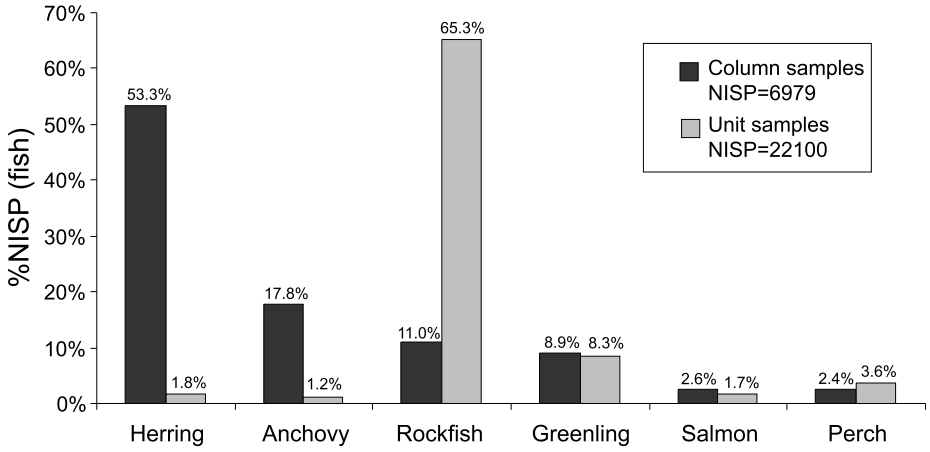

Figure 2. Relative abundance of the six most abundant fish taxa from the column samples (Table 3) compared with the same taxa identified from the excavation unit assemblage (Frederick and Crockford, this vol.). Rockfish, greenling, salmon, and perch represent pooled taxonomic categories (i.e., combined genus, species or family level identifications).

recovered from the excavation units (65% NISP) but are much less abundant in the column sample assemblage (11% NISP). This striking contrast is partially explained by the fact that 82% (NISP=11,863) of the rockfish in the unit assemblage was identified from two adjacent excavation units in the main village (Units N2-4/W102-104 and N4-6/W102-104). Thus, the high number of rockfish specimens recovered from this one area of the site produces a spatially uneven sampling distribution which is further compounded by the biasing effects of 6 mm mesh recovery. In the column sample assemblage, rockfish abundance is only marginally greater than the relative abundance of greenling (Figure 3).

Greenling represents a slightly higher relative percentage in the column assemblage (8.93%) than the unit assemblage (8.35%) despite the large increases in the abundance of herring and anchovy (Table 3). Greenling is also the second most frequently occurring taxon in the 52 individual column level assemblages (Figure 3) suggesting that it is consistently found in small volumes of deposit throughout the site.

Salmon is also found in an incrementally greater proportion of the column sample assemblage than in the unit assemblage and is present in 62% of the examined column sample levels (Figures 2 and 3). One of the reasons for the increased abundance may be the increased recovery of fragmented but highly identifiable salmon vertebrae (e.g., Wigen and Stucki 1988:108). For instance, vertebra in the column assemblage represents 83% (NISP=151) of the identified salmon specimens and 66% of these have intact vertebral centra (NISP=99). In the unit assemblage, 88% (NISP=295) of salmon vertebrae are intact suggesting that fragmentation partially explains the increased recovery for this taxon, a difference that amounts to a three fold increase in fragmented vertebrae. In spite of this taphonomic factor however, the abundance and ubiquity of salmon is only slightly exceeded when specimens from the 15 remaining taxa are combined and compared to salmon (Figure 3).

Perch is also a consistently low percentage of both the unit and column assemblages (Figures 2 and 3). Perch and salmon exhibit similar abundance values but perch is slightly more ubiquitous than salmon (Figure 3b). The recovery of perch in low frequencies suggests it was regularly utilized but did not represent a large percentage of the fish consumed at the site.

Some of the taxa that are abundant in the unit assemblage are prominently absent from the list of top six taxa in the column assemblage (Table 3; Frederick and Crockford, this vol.). In particular,

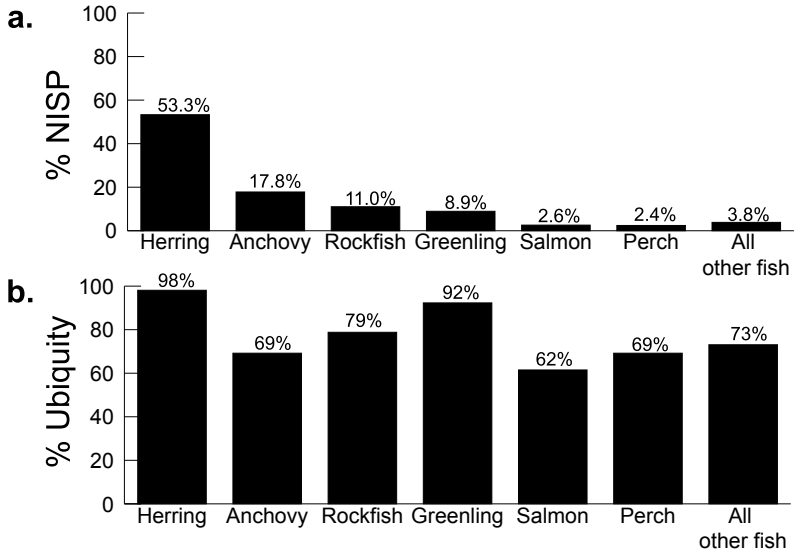

Figure 3. Relative abundance (a) and ubiquity (b) of the six most abundant fish taxa from the column samples (Table 3) Ubiquity measures the presence/absence of species in the 52 column sample levels. 'All other fish' refers to the combined percentage of the remaining 15 taxa in the column sample assemblage. Greenling, salmon and perch represent pooled taxonomic categories (i.e., combined genus, species or family level identifications).

the conspicuously low abundance of taxa such as lingcod, petrale sole, and hake suggests that a combination of increased body size, skeletal robusticity, visibility during field recovery, and low overall density (NSP/litre) contributed to the disproportionately high recovery and rank order abundance of these fish in the unit assemblage. There is a notable absence of sardine or 'pilchard' (*Sardinops sagax*) elements in both the unit and column assemblages. This is surprising given the unique skeletal morphology of this species, its historically documented presence along the southwest coast of British Columbia (e.g., Hart 1973:102; McFarlane and Beamish 2001), and the 5000 year record of human fishing activity represented at Ts'ishaa.

Assessing Recovery in Bones per Litre

The analysis of the fine-screened column samples indicates that a much higher density of fish specimens was recovered from the 3 mm mesh than from the 6 mm mesh. Estimating the magnitude of this difference is important because it helps to clarify the amount of faunal data missing from the excavation unit assemblage and provides a reference point from which to evaluate how separate rates of recovery affect the relative abundance of fish taxa. To characterize differences in recovery, I used the number of fish specimens per litre in each assemblage (calculated as the amount of excavated volume divided by the number of specimens) to compare the unit and column assemblages (Table 5).

Comparisons of the different mesh sizes provide evidence to suggest that a large proportion of the fish remains are absent from the unit assemblage (Table 5). For instance, among the four column samples that utilized nested 6 and 3 mm mesh, 88% of the fish specimens (NSP) and 86% of the *identified* fish specimens (NISP) were recovered in the 3 mm screens (Table 5). Thus, notwithstanding comparisons to the fauna collected directly from the excavation units, this estimate indicates that fewer than 15% of the fish remains are recovered during the use of 6 mm mesh. The considerable loss of fauna is similar to the differences observed for fish remains recovered from ¼" mesh in other archaeological contexts (e.g., Casteel 1972; Gordon 1993; Hanson 1991:158; James 1997; Stein et al. 1992:102).

Table 5. Estimates for numbers of fish specimens per litre recovered from the column and unit assemblages.*

Quantification	Unit samples (6 mm only) [a]	Column samples (6 mm only)	Column samples (3 + 6 mm)[b]	2 mm column samples [c]	1.5 mm column sub-samples*	Column/unit ratio [d]
Total NSP/litre	1.828	12.04	96.41	140.3	652.0	**52.7**
Total NISP/litre	0.887	5.52	40.8	39.2	152.5	**45.9**
Herring/litre	0.016	0.87	22.11	18.71	40.5	**1,367.7**
Anchovy/litre	0.013	0.13	6.74	10.25	104.5	**509.3**
Rockfish/litre	0.580	2.67	4.77	2.67	1.0	**8.2**
Greenling/litre	0.074	0.74	3.62	3.67	1.75	**48.8**
Perch/litre	0.032	0.28	1.09	0.34	2.0	**33.9**
Salmon/litre	0.015	0.13	0.78	2.71	1.5	**53.3**
Examined volume (litres)	24,800	148	148	24	4	
Total NISP fish	22,100	817	6,038	941	610	
Total NSP fish	45,333	1,782	14,268	3,369	2,608	
Id rate (NISP/NSP)	46%	45%	42%	27%	22%	

*1.5mm estimates should be considered highly tentative due to sampling effort that was disproportionately focused on column N2-4/W102-104, the small examined volume (4L), and sub-sampling that prevented the inclusion of specimens that were recovered in larger mesh sizes (Tables 2 and 4).

[a] Data from Frederick and Crockford (this vol.).

[b] Excluding 2mm fauna from column S5-7/W11-13.

[c] Fauna recovered exclusively from column S5-7/W11-13 (Table 1).

[d] 3 and 6mm column fauna divided by 6mm unit fauna.

An even greater proportion of the fish remains appears to be absent from the excavation unit assemblage (Table 5). Corrected for volume, the total number of fish specimens (NISP and NSP) recovered from the 3 mm column samples is approximately 45 to 55 times greater than the 6 mm excavation samples (Table 5). Moreover, a greater number of fish specimens was recovered from the 6 mm column samples screens than in the 6 mm field screens (Table 5), indicating that differences in recovery extend beyond the differences in screen size. This latter result suggests that faunal recovery is considerably higher when sorting is conducted in controlled laboratory settings where it is possible to take greater care to sort small bones from the matrix. This roughly six fold increase is considerably larger than the differences observed between wet and dry screening at other sites on the Northwest Coast (i.e., Cannon 1991:6; Huelsbeck 1994:56).

At the species level, differences in the recovery of individual fish taxa are more variable but depict how particular taxa are differentially represented in both assemblages and in relation to each other (Table 5). Specifically, herring and anchovy exhibit the greatest disparity in recovery between the column and unit samples whereas rockfish exhibits the least. This result helps to account for the over-representation of rockfish and the under-representation of herring and anchovy in the unit assemblage. Greenling, perch and salmon are also recovered in much greater quantities in the 3 mm screen sizes than in the 6 mm screens. Despite the sheer scale of the increased recovery of fauna in the column sample assemblage relative to the unit assemblage, it is surprising that herring and anchovy appear to be the only two taxa to significantly increase in relative abundance in the column sample assemblage.

Correlating Recovery in the Unit and Column Levels

Although the quantification of column sample fauna is generally assumed to reflect the abundance and density of taxa in the surrounding matrix (e.g., Casteel 1976a), this assumption is rarely tested against data obtained from adjacent excavation units (Wigen and Eldon 1987). This notion is critical however, because estimates of the density and taxonomic composition of column sample fauna are often projected from small to large volumes of examined deposit (e.g., Fawcett 1991; Moss 1989). Consequently, extrapolating numbers and proportions of fish remains recovered from different mesh sizes may inaccurately characterize the variable or 'patchy' distribution of these specimens, particularly if this conversion is based on a small number of examined contexts (e.g., Maschner 1997:90; Wigen and Eldon 1987).

As discussed above, the use of multiple measures (abundance, ubiquity, and NSP/litre) and multiple examined deposits (individual level assemblages, column samples, and excavation units) provides a general way to assess the level of variation in the fish assemblage. However, in order to determine whether small scale patterns are similarly expressed in adjacent column and unit assemblages, I further examined the fine-grained association between the adjacent column and unit levels (i.e., arbitrary 10 cm increments). To accomplish this, I investigated whether the number of fish specimens per litre found in individual column sample levels is correlated with the number of fish specimens recovered in the adjacent excavation unit levels (Figure 4a–c).

The result of this analysis indicates that for the three columns adjacent to units with identified fauna (Columns N2-4/W102-104; S14-16/W25-27; and S62-64/W62-64), there is a significant positive relationship between the number of fish specimens present in the total number of comparable levels (Pearson's $R=0.764$, $p<0.01$, $n=23$). This suggests that the overall density of fish remains is similarly expressed between these two sampling strategies. However, on an individual basis, the density (NSP/litre) of fauna in the column and unit levels is significantly correlated in only two of the three cases (Figure 4a,b) The one instance in which there was not a significant relationship between the unit and columns was also the column which had the fewest number of paired levels (n=5, Figure 4c). In this respect, the lack of a significant correlation between the fauna recovered from individual column and unit levels in S14-16/W25-27 is most likely due to the small number of paired levels as opposed to a consistently different density of fish in adjacent arbitrary levels (Figure 4c).

Rockfish and Greenling Length in Different Screen Sizes

Archaeologists have generally observed that the use of smaller mesh sizes recovers smaller-bodied taxa more readily (e.g., Gifford 1916; Gordon 1993; James 1997; Shaffer 1992; Thomas 1969). In the Ts'ishaa column sample assemblage, the increased recovery of herring and anchovy clearly demonstrates an increased abundance for these

small fish taxa (<25 cm, Hart 1973). However, it is difficult to know the size range of some of the other species found in the assemblage because many of these marine fish continue to grow throughout their often lengthy lifetimes (e.g., Munk 2001) and this makes singular estimates of body size a dubious proposition (Casteel 1976b:119). As discussed previously, both rockfish and greenling represent

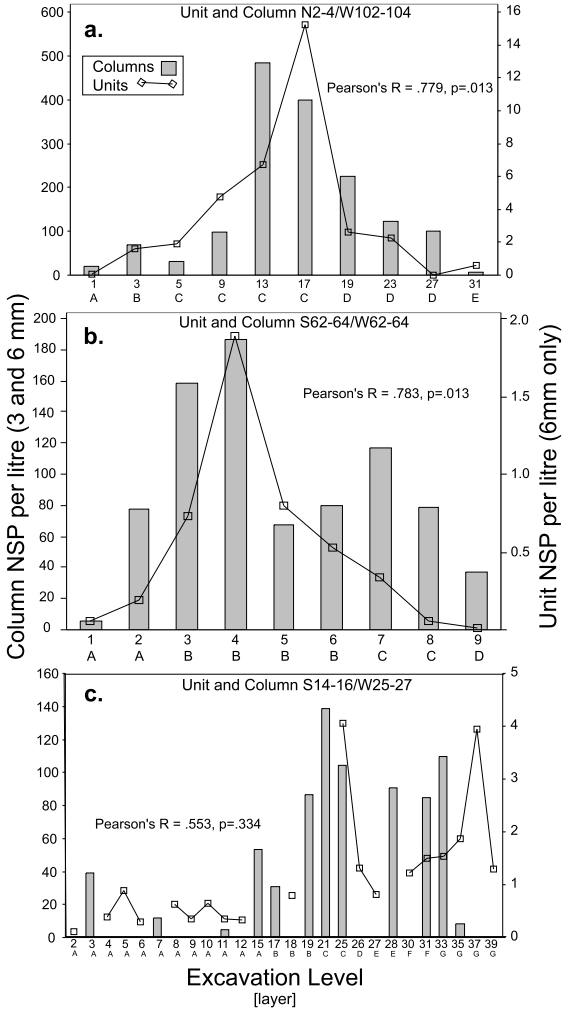

Figure 4. Fish specimen frequency (NSP/litre) in excavation unit and column sample levels for the three columns with associated excavation unit data; (a) N2-4/W102-104; (b) S62-64/W62-64; (c) S14-16/W25-27. Levels without bars or rectangles indicate the absence of quantified data. Excavation level numbers refer to arbitrary 10 cm levels (i.e., higher numbers represent deeper levels). Layers are stratagraphic 'natural layer' designations assigned in the field (McMillan and St. Claire, this vol.).

significant proportions of the unit and column assemblages but the abundance of rockfish is dramatically lower in the column assemblage whereas the abundance of greenling is incrementally larger in the column sample assemblage (Figure 2). To investigate whether these differences are related to the differential recovery of larger or smaller-bodied individuals, I used the allometric regression formulae developed by Orchard (2003), to estimate the lengths of rockfish and greenling by measuring select skeletal elements recovered from different mesh sizes in the column sample assemblage (Figure 5, Table 6).

Briefly, these length estimations are based on skeletal measurements taken from a suite of modern fish specimens where the length of the fish and the size of the skeletal element is known and the relationship is evaluated for a sample of multiple individuals (>10). Linear regression is then used to generate equations capable of predicting total length based on the dimensions of individual skeletal elements (Orchard 2003:43–55). For rockfish and greenling, length estimates with high predictive accuracy are available for 16 skeletal elements (mean rockfish R^2=0.84±0.06; mean greenling R^2=0.96±0.03).

By measuring a total of 77 greenling and 129 rockfish elements which could be used to predict total length (TL), I generated estimates of the distribution of fish length for the different screen sizes throughout the column sample assemblage (Figure 5a–d). The result of these analyses illustrate a consistent difference in the average size-class of both rockfish and greenling, with smaller individuals recovered in smaller screen sizes (Figure 5a–b). This demonstrates that 6 mm mesh does not adequately represent the range of rockfish and greenling size-classes present in the deposits. Moreover, comparisons of mean length demonstrates that the average size of greenling is 5 cm smaller than rockfish, indicating that a substantial portion of the greenling length distribution is smaller than the mean length of rockfish (Figure 5c–d). This is further suggested by the differences in the mean length of greenling and rockfish in the separate screen sizes, where the greatest disparity in fish length is in the 6 mm fraction of the column sample assemblage (Table 6). Conversely, the greatest similarity in rockfish and greenling length is in the 3 mm mesh (Table 6). Combined with the relative abundance and ubiquity data (Figures 2 and 3), these differences indicate that the reason for the greater proportion of rockfish in the excavation unit assemblage is due to the preferential recovery of larger-sized rockfish relative to the smaller-sized greenling.

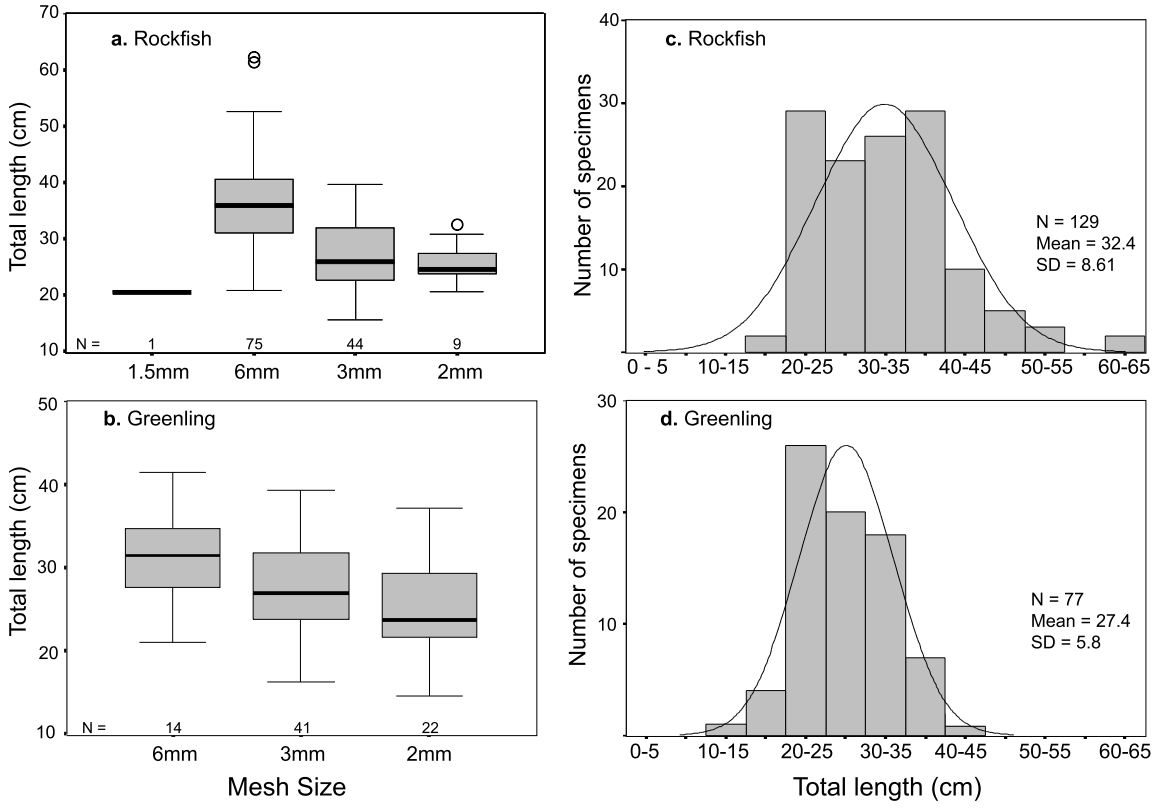

Figure 5. Fish size distribution for measured rockfish (a) and greenling (b) elements from the column sample assemblage recovered separate screen sizes (box-plots show median [line], the middle 50% of cases [box], cases which lie within 1.5 box lengths [wiskers], and outliers which lie beyond 1.5 box lengths [circles]). Rockfish (c) and greenling (d) mortality profiles for measurable specimens from all column screen sizes compared against a derived normal curve (Norusis 2000).

Table 6. Mean total lengths (cm) of rockfish and greenling recovered from different mesh sizes in the column sample assemblage.

		Mesh size				
Taxon	**Length (cm)**	**6 mm**	**3 mm**	**2 mm**	**1.5 mm**	**Total**
Rockfish	Mean	36.4	27.2	26.0	20.6	32.4
Greenling	Mean	30.2	27.9	24.7		27.4
Rockfish	max	62.4	39.6	32.8		62.3
Greenling	max	40.3	39.4	37.1		40.3
Rockfish	min	20.9	15.7	20.6		15.7
Greenling	min	21.0	16.3	14.6		14.6
Rockfish	Std. Dev.	8.2	5.9	4.0		8.6
Greenling	Std. Dev.	5.9	5.6	5.1		5.8
Rockfish	Count	75	44	9	1	129
Greenling	Count	14	41	22		77

Assemblage Formation and Taphonomy

The excavations at Ts'ishaa exposed rich deposits of molluscan and vertebrate fauna, but the archaeological expression of these remains varies among deposits, levels and within stratigraphic layers. Modelling the distribution of these ubiquitous constituents provides a basis for evaluating their formation and potential degradation over time. The following section explores the potential for such taphonomic factors to influence the faunal assemblage.

Exploring the Association Between Bone and Shell

Alkaline conditions created by the abundant presence of shell is considered to be an influential factor that structures the burial environment in shell midden deposits and is conducive to the preservation of bone (Linse 1992; Waselkov 1987:155). However, while the preservation of vertebrate fauna is generally ascribed to the presence of shell (e.g., Ames and Maschner 1999:89; Erlandson 2001:302), the fine-grained association between bone and shell is a rarely reported aspect of shell-midden archaeology. To investigate if the amount of recovered bone is related to the amount of shell in the surrounding matrix, I compared the number of fish specimens per litre (NSP/litre) to the amount of shell (grams/litre) using data collected from the 52 discrete column level samples (unpublished shell data kindly provided by Ian Sumpter). Thus, if there is a positive or negative relationship, this would be indicative of a taphonomic affect. Conversely, if there is not a detectable relationship, this would be suggestive of a random depositional sequence expected for human waste disposal practices (cf. Beck and Hill 2004).

The result of this analysis indicates that the frequency of bone fragments and the weight of shell in individual levels from the five column samples is not linearly related (Figure 6). This lack of a correlation suggests that the sequence of faunal deposition is not the result of chemical or taphonomic degradation, at least among the examined deposits containing identified fauna. Rather, this analysis appears to indicate that the depositional sequence of bone and shell is random. Thus, the patterning in shell and bone density cannot be explained by preservation factors alone. This suggests that human-mediated deposition is primarily responsible for the frequency of bone and shell in individual level assemblages.

The comparison of the amount of bone and

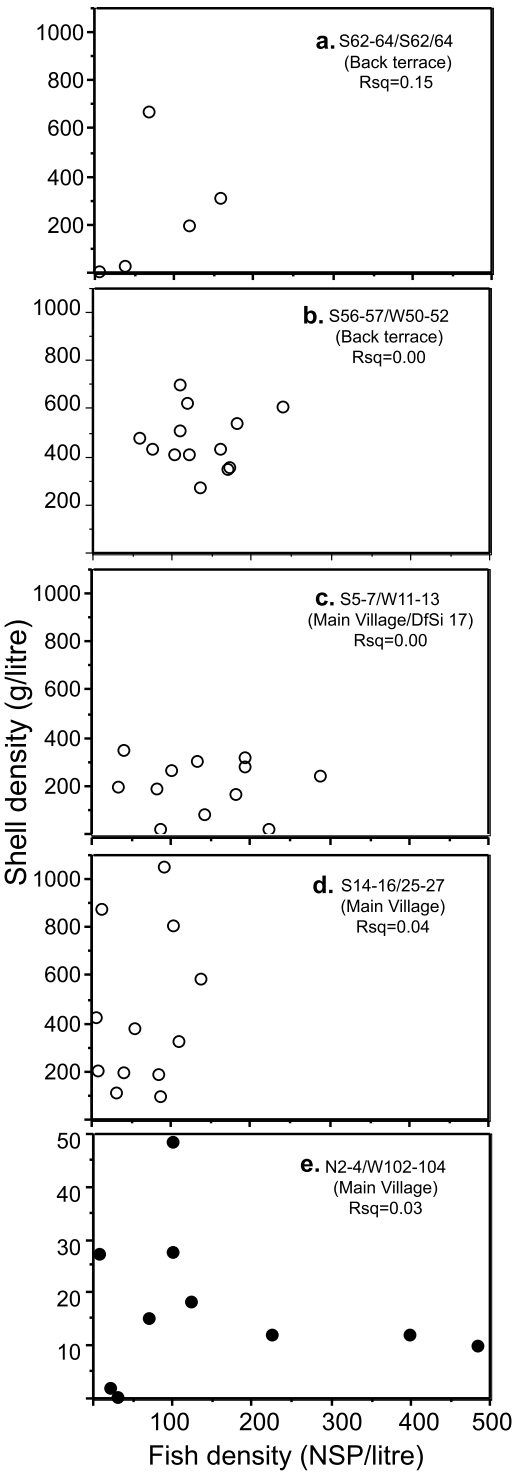

Figure 6. The relationship between shell density (g/litre) and fish density (NSP/litre) for each of the 52 examined levels grouped by individual column sample (Table 1). Note different scale on the y axis of column N2-4/W102-104, where shell data was collected only from the 6mm fraction (filled circles).

shell present in these spatially and temporally distinct areas of the site also provides an opportunity to evaluate whether the preservation of bone and shell in the older back terrace component of the site (ca. 3000–5000 cal yr BP) differs from the younger main village deposits (ca. 250–1800 cal yr BP). Based on a visual assessment of the plots in Figure 6, it is apparent that broadly similar densities of bone and shell are found in both components of the site. This suggests that chronological differences do not have an effect on the density of shell or fish specimens present in the midden deposits. In fact, only in a few of the 52 examined individual column sample levels, do deposits contain both a low density of both bone and shell (i.e., S62-64/W62-64, N2-4/W102-104).

Accumulation Rates and the Formation of the Faunal Assemblage

Comparisons of the age, rate of burial (accumulation) and density of fauna provides an additional way to asses whether human or taphonomic factors are responsible for the fauna preserved in the examined deposits. Rates of accumulation are produced by complex interplay between the regularity of deposition, the *in situ* deterioration of this material and the erosion or physical attrition of the deposits (Kidwell 1986). However, if bones or shells are subject to slower rates of accumulation, they should tend to be present in lower densities relative to younger or more quickly accumulating deposits (cf., Olszewski 1999). In shell midden contexts, several of these processes presumably affect and are affected by the deposition of vertebrate and molluscan fauna (i.e., the regularity of consumption and deposition, the preservational conditions of the burial environment and the human and animal use of the immediate landscape).

To explore how these factors may have affected the preservation and density of the fish assemblage at Ts'ishaa, I first estimated the accumulation rates for the five spatially separate deposits containing identified column sample fauna and subsequently examined whether the density of bone and shell varies with the differing rates of accumulation. To generate estimates of accumulation rates (cm/100 yr), I compared the age (cal yr BP) and depth below surface (cm) using the 26 ^{14}C dates directly associated with the column sample fauna (Table 7, Figure 7). I determined accumulation rates using correlation coefficients on the group of dates from the three columns dating to the main village occupation (S14-16/W25-27; N2-4/W102-104; and S5-7/W11-13) and individually for the two separate column sample deposits from the back terrace (S56-57/W50-52; S62-64/W62-64) (Figure 7). Each of the column deposits is associated with three or more radiocarbon ages with the exception of S5-7/W11-13 which is incorporated into the contemporaneous sample of 15 dates from the main village occupation (i.e., DfSi-17, Table 7).

This analysis indicates that midden accumulation occurred more rapidly over the past 1800 years in the main village (ca. 250–1800 cal yr BP) than in back terrace (ca 3000–5000 cal yr BP, Figure 7). Thus, midden deposits in the highly dispersed (>100 m apart) locations of the main village and Himayis (S5-7/W11-13), appear to have accumulated at similarly consistent rate of approximately 25 cm every 100 years (Figure 7). In contrast, the two columns from the older back terrace deposits accumulated at distinctly slower rates (≈11 cm/100 yr in col. S56-57/W50-52 and ≈1 cm/100 yr in col. S62-64/W62-64).

Despite considerable differences in accumulation rate, fish bone density (NISP/litre) is strik-

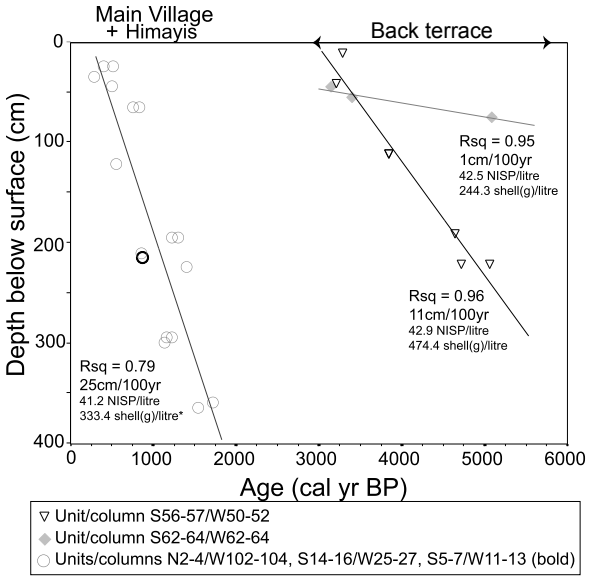

Figure 7. Age of column sample deposits measured against depth below surface based on associated radiocarbon dates (Table 7). Lines represent least squares regression and are shown with the corresponding correlation coefficients (Rsq value). Estimated accumulation rates (cm/100yr) and fish bone density (NISP/litre) are also shown for each group. Asterisk (*) denotes the absence of adequate shell data for column N2-4/W102-104.

ingly similar among these three separate deposits (Figure 7). On the one hand, this similarity provides reason to suspect that *in situ* degradation over time is not a factor influencing the preservation of the faunal assemblage. On the other hand, the differing rates of midden accumulation indicates that fish bone deposition is higher in areas of rapid accumulation. That is, more bones were deposited per unit of time in deposits with higher rates of midden accumulation.

Comparison of the three accumulation rates and the deposition of shellfish indicates that the deposit with the slowest rate of accumulation does have the lowest density of shell (244.3 g/litre, S62-64/W62-64, Figure 7). However, the deposit with the highest density of shell (S56-57/W50-52) does not have the fastest accumulation rate, suggesting that rate of accumulation is more complex than the quantity of shell deposited in a single location.

Another interesting aspect of this analysis is that three separate areas of the main village show a consistent pattern of midden accumulation over the same temporal interval (ca. 250–1800 cal yr BP). This suggests that the consumption and deposition of midden material was occurring relatively rapidly and on a consistently large scale throughout the site. This finding is consistent with a village occupation, where large quantities of food are

Table 7. Radiocarbon dates associated with the column sample deposits and used in the calculation of accumulation rates (Figure 7). Calibration achieved using Calib. 4.3 (Stuiver et al. 1998a–b). Marine samples were calibrated with a ΔR of 250±0 (100% marine), based on discussion in Southon and Fedje (2003).

Lab number	Site area[a]	Unit	Level/ layer	^{14}C age	Material	δ^{13}C**	2 sigma range (cal yr BP)	Midpoint cal yr BP[b]	Depth below surface (cm)	Midpoint depth below surface (cm)
Beta-158744	BT	S56-57/W50-52	4B	3050±70	charcoal	-25	3440–3000	3220	35–45	40
CAMS-97186	BT	S56-57/W50-52	1B*	3100±35	charcoal	-25	3380–3210	3295	5–15	10
CAMS-97177	BT	S56-57/W50-52	11C*	3575±35	charcoal	-25	3980–3730	3855	105–115	110
CAMS-97176	BT	S56-57/W50-52	11C*	3585±40	charcoal	-25	3980–3730	3855	105–115	110
Beta-158747	BT	S56-57/W50-52	17+	4160±70	charcoal	-25	4850–4450	4650	165–235	190
CAMS-97181	BT	S56-57/W50-52	23C*	4210±35	charcoal	-25	4840–4620	4730	225–235	220
CAMS-97182	BT	S56-57/W50-52	23C*	4415±35	charcoal	-25	5260–4870	5065	225–235	220
Beta-158740	BT	S62-64/W62-64	5B	3000±70	charcoal	-25	3360–2950	3155	40–50	45
CAMS-N48305	BT	S62-64/W62-64	6B	3770±35	fur seal	-14.5	3470–3330	3400	50–60	55
Beta-158741	BT	S62-64/W62-64	7/8D	4470±70	charcoal	-25	5320–4870	5095	70–80	75
CAMS-97191	EA2	N2-4/W102-104	3B*	350±45	charcoal	-25	510–300	405	20–30	25
CAMS-97192	EA2	N2-4/W102-104	3B*	475±35	charcoal	-25	550–480	515	20–30	25
CAMS-85651	EA2	N2-4/W102-104	5C	1145±30	fur seal	-14.4	540–470	505	40–50	45
CAMS-85650	EA2	N2-4/W102-104	7C	1545±30	fur seal	-14.6	910–760	835	60–70	65
CAMS-97203	EA2	N2-4/W102-104	20D*	1385±35	charcoal	-25	1350–1260	1305	190–200	195
CAMS-97204	EA2	N2-4/W102-104	20D*	1300±35	charcoal	-25	1290–1170	1230	190–200	195
CAMS-97198	EA2	N2-4/W102-104	30D*	1230±35	charcoal	-25	1260–1060	1160	290–300	295
CAMS-97197	EA2	N2-4/W102-104	30D*	1310±35	charcoal	-25	1290–1170	1230	290–300	295
Beta-147074	EA2	N2-4/W102-104	31E	1230±90	charcoal	-25	1310–950	1130	300	300
CAMS-85649	EA2	N4-6/W102-104	7C	1470±30	fur seal	-14.4	830–680	755	60–70	65
CAMS-85648	EA2	N4-6/W102-104	21D	1595±35	fur seal	-13.4	950–800	875	210–220	215
CAMS-85647	EA1	S14-16/W25-27	4A	895±30	fur seal	-14.1	330–250	290	30–40	35
Beta-134655	EA1	S14-16/W25-27	25C	1490±60	charcoal	-25	1520–1290	1405	220–230	225
CAMS-85646	EA1	S14-16/W25-27	37G	2235±35	fur seal	-15.3	1620–1460	1540	360–370	365
Beta-134656	EA1	S14-16/W25-27	35-37G	1800±60	charcoal	-25	1870–1560	1715	350–370	360
Beta-134657	DfSi-17	S5-7/W11-13	24C	970±60	charcoal	-25	970–740	855	210–213	211

[a] BT=back terrace, EA1=1999 trench excavation, EA2=2000 trench excavation, DfSi-17=Hemayis.

[b] Midpoint of the 2 sigma calibrated range.

*^{14}C sample obtained from within column sample level.

**^{13}C values given without decimal places are the assumed values according to Stuiver and Polach (1977:335).

processed and consumed over a broad spatial area. This is further supported by the ethnographic information describing Ts'ishaa as a large prehistoric village site (Golla 2000; McMillan and St. Claire, this vol; St. Claire 1991).

This analysis has shown that deposits in separate areas of the site represent considerably different scales of temporal resolution (i.e., 10 vertical cm ≈40–1000 yrs). Despite these differences, the rate of accumulation does not appear to reflect the *in situ* degradation of the shell midden deposits but rather the intensity of deposition.

Conclusions

The recovery and analysis of the fine-screen column sample fauna provides significant insight into the taxonomic composition and depositional context of the fish assemblage recovered from the examined shell midden deposits at Ts'ishaa. Through my analyses, I have shown that the overwhelming majority (>85%) of the fish specimens present in the fine-screened (≤3 mm) deposits are absent from conventional ¼" recovery. Despite considerable recovery differences as well as difference in sample size, the assemblage of specimens identified from column and unit samples can be reliably compared and contrasted to assess the relative importance of different fish taxa over time and space. In this respect, the evaluation of the taxonomic composition of the column sample assemblage indicates that six taxa dominate the assemblage in all contexts and chronological periods, implying a focused utilization of fish resources throughout the 5000 year occupation of this site. This is further supported by the examination of the increased species-specific recovery rates as well as an analysis of the biasing effects of larger sized mesh on the recovery of smaller-sized rockfish and greenling. I have also shown that the density of fish remains can be measurably integrated between the small and large volumes of deposits in the column and unit samples. In relation to formation processes and taphonomy, I discovered that there is no apparent relationship between the amount of bone present and the amount of surrounding shell, at least for the deposits containing identified fauna. In addition, the age of the deposits does not appear to affect the density of fish remains recovered from the midden deposits. Thus, human-mediated deposition appears to be the primary factor responsible for the density and taxonomic composition of the fish remains at the site. Together, these data and analyses suggest that human participation in the prehistoric marine ecosystem of Barkley Sound was intensively focused on a narrow range of fish resources which vastly outnumbered all other vertebrates consumed at the site. This knowledge provides a basis for developing further interpretations which are being explored elsewhere (McKechnie, in prep).

In conclusion, this paper documents a vitally important aspect of the cultural and economic practices of the people who inhabited Ts'ishaa for the past 5000 years. In conjunction with the other research contributions in this volume, these conclusions expand our knowledge of the long-term human and ecological history embedded in the landscape of what is now Pacific Rim National Park Reserve.

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