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The distribution of salt marsh foraminifera at Little Dipper Harbour New Brunswick, Canada: implications for development of widely applicable transfer functions in sea-level research

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Abstract

A stepwise linear regression analysis was carried out on both 0–1 and 0–10 cm surface samples from a transect across the marsh at Little Dipper Harbour, New Brunswick. Only the 0–1 cm surface samples produce statistically reliable results ($R^2 = 0.705$; $R'^2 = 0.609$). These results are in sharp contrast to those obtained from British Columbia marshes where infaunal habitat and taphonomic biasing result in 0–10 cm samples producing the best results using stepwise linear regression. The fundamental difference in the apparent preferred habitats of marsh foraminifera in these areas pose difficulties for researchers attempting to develop transfer function training sets that can be applied over wide areas in paleo-sea-level research.

1. Introduction

Intertidal marsh foraminifera have been demonstrated to be excellent tools for the documentation of Holocene relative sea-level change and prehistoric earthquakes (e.g. Guilbault et al., 1996). Since research in this area began (Scott and Medioli, 1978) an inherent assumption in reconstructing past sea-level change using foraminiferal data is that modern assemblages collected at the surface of the marsh are accurate analogues of microfossil assemblages in subsurface sediments. During the last few years, however, there has been considerable discussion as to the impact of infaunal habitat and taphonomic processes on foraminiferal assemblages (e.g. Goldstein and Harben, 1993; Ozarko et al., 1997; Patterson et al., 1999).

Research carried out on Vancouver Island, British Columbia, has indicated that a greater number of elevation-controlled marsh assemblages are recognizable using samples of the uppermost 10 cm of sediment in the marsh than samples of the top centimeter alone (Ozarko et al., 1997; Patterson et al., 1999); the direct result of infaunal habitat and taphonomic biasing processes. Similar results have been obtained in studies carried out at marshes in the southeastern United States (Goldstein and Harben, 1993; Goldstein et al., 1995; Goldstein and Watkins, 1999). Walker and Goldstein (1999) also independently identified the approximate top 10 cm of the marsh as the taphonomic active zone where most preservational biasing occurs.

Determination of the most suitable surface sample thickness for analysis is important for paleo-sea-level researchers as they strive to recognize subtle changes in sea level as well as to discriminate changes produced by earthquakes from those caused by non-seismic processes. To test whether utilizing a 10 cm surface sample for foraminiferal analysis should be universally applied in all areas we collected and analyzed samples for their foraminiferal content at both 0–1 and 0–10 cm from a transect collected across the salt marsh at Little Dipper Harbour, New Brunswick.

2. Methods

2.1. Field and laboratory

On July 22, 1998, 58 samples were collected for foraminiferal analysis at 29 stations along a single

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transect across the marsh at Little Dipper Harbour, on the Bay of Fundy coast of New Brunswick (Fig. 1). The relative elevations of stations were measured with a surveying level and adjusted for surveying closing error. No absolute tidal gauge data was available for Little Dipper Harbour so values were extrapolated from nearby West Dipper Harbour and Lepreau. Due to the short record available for West Dipper Harbour and Lepreau absolute values may differ by as much as 10 cm but relative values between stations are accurate to less than 1 cm (Table 1).

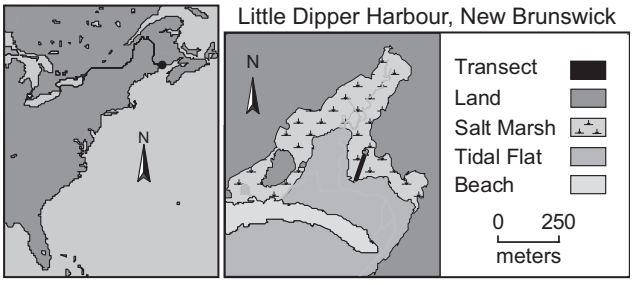

Fig. 1. Map of the Little Dipper Harbour area showing the location of the marsh transect, marsh, tidal flat, and upland environments.

A 10 cm^3 surface sample (0–1 cm) and a 10 cm^3 sample from the top 10 cm were collected for each of the 29 stations (Fig. 2). Samples were stored in Ziploc plastic bags and treated in the field with isopropyl alcohol to prevent microbial decay of living protoplasm. In the laboratory, approximately 10 cm^3 of each sample were washed on a 63 μm sieve. Samples were then fixed in a solution of Rose Bengal stain and buffered formalin and

Table 1
Elevation of sampling stations at Little Dipper Harbour

Station	Chart Datum	CGD	NGVD-1929	HHWLT	MHWS	MHW
TR-1	8.225	4.265	4.535	0.285	0.958	1.369
TR-3	8.081	4.121	4.391	0.141	0.814	1.225
TR-11	7.868	3.908	4.178	−0.072	0.601	1.012
TR-15	7.755	3.795	4.065	−0.185	0.488	0.899
TR-16	7.758	3.798	4.068	−0.182	0.491	0.902
TR-17	7.668	3.708	3.978	−0.272	0.401	0.812
TR-17.5	7.566	3.606	3.876	−0.374	0.299	0.710
TR-18	7.594	3.634	3.904	−0.346	0.327	0.738
TR-23	7.548	3.588	3.858	−0.392	0.281	0.692
TR-26	7.534	3.574	3.844	−0.406	0.267	0.678
TR-30	7.523	3.563	3.833	−0.417	0.256	0.667
TR-33	7.513	3.553	3.823	−0.427	0.246	0.657
TR-36	7.511	3.551	3.821	−0.429	0.244	0.655
TR-40	7.472	3.512	3.782	−0.468	0.205	0.616
TR-44	7.460	3.500	3.770	−0.480	0.193	0.604
TR-46	7.447	3.487	3.757	−0.493	0.180	0.591
TR-48	7.450	3.490	3.760	−0.490	0.183	0.594
TR-50	7.404	3.444	3.714	−0.536	0.137	0.548
TR-52	7.383	3.423	3.693	−0.557	0.116	0.527
TR-54	7.326	3.366	3.636	−0.614	0.059	0.470
TR-56	7.211	3.251	3.521	−0.729	−0.056	0.355
TR-58	7.036	3.076	3.346	−0.904	−0.231	0.180
TR-61	6.749	2.789	3.059	−1.191	−0.518	−0.107
TR-62	6.656	2.696	2.966	−1.284	−0.611	−0.200
TR-63	6.495	2.535	2.805	−1.445	−0.772	−0.361
TR-64	6.337	2.377	2.647	−1.603	−0.930	−0.519
TR-65	6.114	2.154	2.424	−1.826	−1.153	−0.742
TR-66	5.935	1.975	2.245	−2.005	−1.332	−0.921
TR-67	5.689	1.729	1.999	−2.251	−1.578	−1.167
TR-70	5.356	1.396	1.666	−2.584	−1.911	−1.500
TR-72	5.301	1.341	1.611	−2.639	−1.966	−1.555

Determination of the relative sea level data for Little Dipper Harbour was based on curvature of the Earth MSL (mean sea level) in nearby West Dipper Harbour (3.960 m above Canadian Geodetic Datum (CGD) based on a 27-day record in 1983; Canadian Hydrographic Service, pers.comm., 30.09.1998). The CGD is in turn assumed to be 27 cm above the National Geodetic Vertical Datum (NGVD) 29 (1987 adjustment of CGD). The determination of the higher high water large tide (HHWLT) is based on the 19 year average of predictions for the highest high waters in nearby West Dipper Harbour (CHS, pers. comm., 30.09.1998). Values for the highest astronomical tide (HAT), higher high water mean tide (HHWMT), mean higher high water (MHHW), lower low water large tide (LLWLT), low water mean tide (LLWMT) were similarly calculated. For nearby Lepreau Harbour mean tidal range (from tide tables) = 5.791 m; mean spring tidal range = 6.614 m; MTL = 3.962 m above CGD mean high water. Mean high water (MHW) in Little Dipper Harbour is assumed to be 2.896 m above the Geodetic Datum (6.856 m above CGD); half the tidal range of Lepreau Harbour according to tide table. The mean tide level (MTL) in Little Dipper Harbour is therefore assumed to be equal to the Geodetic Datum (3.96 m above CGD) Geodetic Datum, and would be 4.067 m above the CGD if interpolated between St Andrews (3.815 m above CGD, 53 km away) and St. John (4.186 m above CGD, 25 km away).

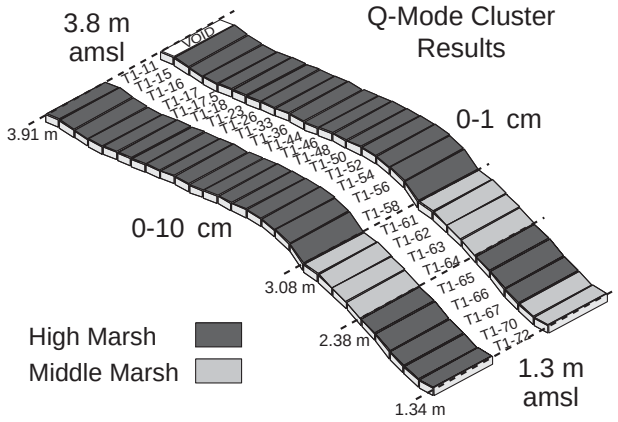

Fig. 2. Marsh transect profile, showing the positions and elevations of the foraminiferal assemblages for both the 0–1 and 0–10 cm marsh surface samples stations.

allowed to sit for several hours. This procedure allows for distinguishing foraminifera that were living at the time of sample collection from those that were dead (Scott and Medioli, 1980a). This procedure is also effective in documenting infaunal marsh foraminiferal microhabitats (see Goldstein et al., 1995, for a discussion). After staining, the samples were washed in tap water and preserved in a 5% isopropyl alcohol solution. They were then washed through a 500 μm screen to remove large plant debris that might inhibit counting. The residue was split using the wet splitter method of Scott and Hermelin (1993) to obtain a fraction of countable size (Patterson and Fishbein, 1989). Wet samples were examined under a binocular microscope generally at around 40 × magnification. Water immersion helped in the identification of marsh species because organic matter found in marsh samples tends to adhere to foraminiferal tests if samples are dried. Of the 58 samples all but five which were collected from elevations above 3.80 m above mean sea level (AMSL) contained statistically significant numbers of foraminifera (Tables 2 and 3; see Patterson and Fishbein, 1989, for background on estimating statistical significance). Separate tallies were made of dead, live and total numbers of specimens (Tables 2 and 3).

2.2. Quantitative analytical procedures

To determine relationships between samples, dead populations were utilized in quantitative analytical procedures as they provide a better estimate than living populations of long-term trends. This is because dead populations more closely reflect the impact of taphonomic time averaging (Horton, 1999; Murray, 2000).

Fifty-three samples, including all but the 5 barren samples (Tables 2 and 3), were found to have statistically significant populations, and were utilized in subsequent multivariate analyses (Patterson and Fishbein, 1989). Although 13 foraminiferal species were observed in this study (Tables 2 and 3), only those species deemed to be present in statistically significant numbers were used to assess relationships between samples. The statistically significant species were subjectively determined to be those that had abundances equal to the standard error +1% at the 95% confidence level in at least one sample. These species, which included *Miliammina fusca* (Brady, 1870), *Jadammina macrescens* (Brady, 1870), *Balticammina pseudomacrescens* (Brönniman et al., 1989), *Trochamminita salsa* (Cushman and Brönniman, 1948), *Pseudothurammina limnetis* (Scott and Medioli, 1980b), *Tiphotrocha comprinata* (Cushman and Brönniman, 1948), *Trochammina inflata* (Montagu, 1808) and *Reophax* sp. were present in statistically significant numbers in either the 0–1 and/or 0–10 cm samples. *Quinqueloculina* sp., and *Haynesina germanica* (Ehrenberg, 1840) were present in statistically insignificant numbers and excluded from cluster analysis in the 0–1 cm samples. *Lepidodeuterammina ochracea* (Williamson, 1858), *Cribroelphidium williamsoni* (Haynes, 1973), and *Haplophragmoides* sp. were present in statistically insignificant numbers and excluded from cluster analysis in the 0–10 cm samples.

2.3. Q-mode cluster analysis

Q-mode cluster analysis was carried out separately on both the 0–1 and 0–10 cm dead foraminifera distributional data to group samples with similar species distributions (Figs. 2 and 3). Samples grouped in this fashion are considered to be representative of a particular environment. The Q-mode clustering of the reduced data set was carried out using the SPSS 10 statistical software package for Apple Macintosh utilizing the Ward's minimum variance method (see Fishbein and Patterson, 1993, for methodology). This methodology simulates a statistically based Error-Weighted Maximum Likelihood (EWML) clustering method fully described in Fishbein and Patterson (1993).

2.4. Shannon diversity index

To assess the relative health of this marsh, an analysis of the faunal diversity and the total abundance of specimens was carried out (Tables 2 and 3). Diversity can be quantified using the Shannon diversity index (SDI) of Sageman and Bina (1997) and is defined as

$$\mathrm{SDI} = -\sum_{i=1}^{S}\left(\frac{X_i}{N_i}\right) ln\left(\frac{X_i}{N_i}\right),$$

Table 2
Total and percent foraminiferal abundances, foraminifera/cm^3, elevational data, assemblage assignment (H = High Marsh; M = Middle Marsh), and SDI values for samples from the 0–1 cm surface sample transect. Samples were quantitatively analyzed and are recorded as fractional abundances

Species/sample	T1-1	T1-3	T1-11	T1-15	T1-16	T1-17	T1-17.5	T1-18	T1-23	T1-26	T1-33	T1-36	T1-44	T1-46	T1-48	T1-50	T1-52	T1-54	T1-56	T1-58	T1-61	T1-62	T1-63	T1-64	T1-65	T1-66	T1-67	T1-70	T1-72
Elevation (m)	4.27	4.12	3.91	3.8	3.8	3.71	3.61	3.63	3.59	3.57	3.55	3.55	3.5	3.49	3.49	3.44	3.42	3.37	3.25	3.08	2.79	2.7	2.54	2.38	2.15	1.98	1.73	1.4	1.34
Sample fraction examined (10 cm^3)	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Total specimens	Void	Void	Void	101	36	111	90	108	127	100	124	158	125	146	126	175	145	124	109	132	80	114	106	88	151	185	181	268	62
Specimens /cm^3				10.1	3.6	11.1	9.0	10.8	12.7	10.0	12.4	15.8	12.5	14.6	12.6	17.5	14.5	12.4	10.9	13.2	8.0	11.4	10.6	8.8	15.1	18.5	18.1	26.8	6.2
Marsh assemblage				H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	M	M	M	M	H	H	H	M	M
Shannon Diversity Index (SDI)				0.879	0.630	1.063	0.868	0.666	0.971	0.959	0.908	0.786	0.685	1.036	0.806	0.796	0.689	0.878	0.680	0.696	0.827	0.803	0.874	0.918	1.226	1.044	0.771	0.160	0.267
M. fusca (total)				0	0	0	3	0	0	7	0	0	2	5	0	0	0	0	0	1	27	60	49	49	20	1	8	9	1
M. fusca (live)				0	0	0	2	0	0	0	0	0	1	2	0	0	0	0	0	0	11	35	6	16	8	0	3	4	1
M. fusca (dead)				0	0	0	1	0	0	7	0	0	1	3	0	0	0	0	0	1	16	25	43	33	12	1	5	5	0
M. fusca (dead) %				0.00	0.00	0.00	1.11	0.00	0.00	7.00	0.00	0.00	0.80	2.05	0.00	0.00	0.00	0.00	0.00	0.76	20.00	21.93	40.57	37.50	7.95	0.54	2.76	1.87	0.00
B. pseudomacrescens (total)				2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
B. pseudomacrescens (live)				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
B. pseudomacrescens (dead)				2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
B. pseudomacrescens (dead) %				1.98	2.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.99	0.00	0.00	0.00	0.00
J. macrescens (total)				34	27	34	58	83	49	59	57	47	105	52	72	107	100	69	68	75	33	45	42	28	68	62	46	1	1
J. macrescens (live)				2	3	6	19	19	9	14	10	5	28	14	11	13	11	12	12	22	11	20	9	8	11	10	0	0	1
J. macrescens (dead)				32	24	28	39	64	40	45	47	42	77	38	61	94	89	57	56	53	22	25	33	20	57	52	46	1	0
J. macrescens (dead) %				31.68	66.67	25.23	43.33	59.26	31.50	45.00	37.90	26.58	61.60	26.03	48.41	53.71	61.38	45.97	51.38	40.15	27.50	21.93	31.13	22.73	37.75	28.11	25.41	0.37	0.00
C. williamsoni (total)				0	0	0	0	0	0	0	2	1	0	6	0	1	0	4	2	29	16	0	14	4	2	39	106	258	58
C. williamsoni (live)				0	0	0	0	0	0	0	2	1	0	6	0	1	0	2	2	29	16	0	11	4	2	38	106	8	5
C. williamsoni (dead)				0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	3	0	0	1	0	250	53
C. williamsoni (dead) %				0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	0.00	0.00	2.83	0.00	0.00	0.54	0.00	93.30	85.50
T. comprimata (total)				61	3	39	16	2	36	22	12	7	8	28	3	5	2	6	0	1	0	1	0	2	33	53	14	0	0
T. comprimata (live)				1	1	3	5	1	15	4	4	4	2	10	1	0	0	2	0	0	0	0	0	1	9	5	0	0	0
T. comprimata (dead)				60	2	36	11	1	21	18	8	3	6	18	2	5	2	4	0	1	0	1	0	1	24	48	14	0	0
T. comprimata (dead) %				59.41	5.56	32.43	12.22	0.93	16.54	18.00	6.45	1.90	4.80	12.33	1.59	2.86	1.38	3.23	0.00	0.76	0.00	0.88	0.00	1.14	15.89	25.95	7.73	0.00	0.00
H. germanica (total)				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
H. germanica (live)				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
H. germanica (dead)				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
H. germanica (dead) %				0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61
Quiqueloculina sp. (total)				0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Quiqueloculina sp. (live)				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Quiqueloculina sp. (dead)				0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Quiqueloculina sp. (dead) %				0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
T. inflata (Total)				4	5	38	13	23	42	12	53	103	10	55	50	62	43	45	39	26	4	8	1	5	24	28	7	0	1
T. inflata (live)				0	4	9	6	3	19	9	14	31	0	18	17	10	12	15	14	10	0	5	0	0	1	1	0	0	0
T. inflata (dead)				4	1	29	7	20	23	3	39	72	10	37	33	52	31	30	25	16	4	3	1	5	23	27	7	0	1
T. inflata (dead) %				3.96	2.78	26.13	7.78	18.52	18.11	3.00	31.45	45.57	8.00	25.34	26.19	29.71	21.38	24.19	22.94	12.12	5.00	2.63	0.94	5.68	15.23	14.59	3.87	0.00	1.61

Table 3
Total and percent foraminiferal abundances, foraminifera/cm^3, elevational data, assemblage assignment (H = high marsh; M = middle marsh), and SDI values for samples from the 0–10 cm surface sample transect. Samples were quantitatively analyzed and are recorded as fractional abundances

Species/sample	T1-1	T1-3	T1-11	T1-15	T1-16	T1-17	T1-17.5	T1-18	T1-23	T1-26	T1-33	T1-36	T1-44	T1-46	T1-48	T1-50	T1-52	T1-54	T1-56	T1-58	T1-61	T1-62	T1-63	T1-64	T1-65	T1-66	T1-67	T1-70	T1-72
Sample fraction examined (10 cm^3)	0.17	0.17	1.00	1.00	1.00	1.00	0.08	0.08	0.08	1.00	0.08	0.17	0.17	0.17	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.17	0.08	0.17	0.07	0.07	1.00	1.00
Elevation (m)	4.27	4.12	3.91	3.80	3.80	3.71	3.61	3.63	3.59	3.57	3.55	3.55	3.50	3.49	3.49	3.44	3.42	3.37	3.25	3.08	2.79	2.70	2.54	2.38	2.15	1.98	1.73	1.40	1.34
Total specimens	Void	Void	57	100	59	110	343	374	349	170	435	233	304	666	376	613	552	419	420	412	272	344	244	238	206	619	406	51	75
Specimens/cm^3	0.017	0.017	0.100	0.100	0.100	0.100	0.008	0.008	0.008	0.100	0.008	0.017	0.017	0.017	0.008	0.008	0.008	0.008	0.008	0.008	0.008	0.008	0.017	0.008	0.017	0.007	0.007	0.100	0.100
Marsh assemblage			H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	M	M	M	M	H	H	H	H	H
Shannon Diversity Index (SDI)			0.383	0.837	0.348	1.058	0.996	0.957	1.037	0.755	1.103	0.722	1.163	1.155	0.846	1.031	0.707	0.857	0.782	0.654	1.019	0.789	0.989	1.421	1.098	1.155	1.278	0.370	1.042
M. fusca (total)			1	3	0	3	10	4	8	3	7	0	14	14	0	0	2	1	1	5	88	245	73	99	12	4	5	1	0
M. fusca (live)			0	0	0	1	0	0	0	0	0	0	3	0	0	0	0	0	0	1	15	7	17	4	6	0	0	0	0
M. fusca (dead)			1	3	0	2	10	4	8	3	7	0	11	14	0	0	2	1	1	4	73	238	56	95	6	4	5	1	0
M. fusca (dead) %			1.8	3.0	0.0	1.8	2.9	1.1	2.3	1.8	1.6	0.0	3.6	2.1	0.0	0.0	0.4	0.2	0.2	1.0	26.8	69.2	23.0	39.9	2.9	0.6	1.2	2.0	0.0
B. pseudomacrescens (total)			1	11	4	14	30	31	138	18	36	47	34	143	48	94	118	106	45	77	19	18	26	52	63	126	66	4	14
B. pseudomacrescens (live)			0	1	0	3	8	6	18	8	2	1	11	15	8	29	22	34	8	30	5	3	5	0	14	3	10	0	0
B. pseudomacrescens (dead)			1	10	4	11	22	25	120	10	34	46	23	128	40	65	96	72	37	47	14	15	21	52	49	123	56	4	14
B. pseudomacrescens (dead) %			1.75	10.00	6.78	10.00	6.41	6.68	34.38	5.88	7.82	19.74	7.57	19.22	10.64	10.60	17.39	17.18	8.81	11.41	5.15	4.36	8.61	21.85	23.79	19.87	13.79	7.84	18.67
J. macrescens (total)			53	77	54	72	249	266	160	137	258	171	204	402	277	391	407	273	320	316	154	75	139	55	112	370	208	46	47
J. macrescens (live)			2	1	1	2	3	35	2	27	13	2	6	9	19	24	14	25	20	15	21	2	17	2	5	2	3	0	0
J. macrescens (dead)			51	76	53	70	246	231	158	110	245	169	198	393	258	367	393	248	300	301	133	73	122	53	107	368	205	46	47
J. macrescens (dead) %			89.47	76.00	89.83	63.64	71.72	61.76	45.27	64.71	56.32	72.53	65.13	59.01	68.62	59.87	71.20	59.19	71.43	73.06	48.90	21.22	50.00	22.27	51.94	59.45	50.49	90.20	62.67
C. williamsoni (total)			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0
C. williamsoni (live)			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
C. williamsoni (dead)			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
C. williamsoni (dead) %			0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.49	0.00	0.00
Haplophragmoides sp. (total)			1	1	0	1	2	2	0	0	0	0	0	1	5	6	0	0	1	0	1	0	4	0	1	0	3	0	0
Haplophragmoides sp. (live)			0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Haplophragmoides sp. (dead)			1	1	0	1	2	1	0	0	0	0	0	1	5	6	0	0	1	0	1	0	3	0	1	0	3	0	0
Haplophragmoides sp. (dead) %			1.75	1.00	0.00	0.91	0.58	0.27	0.00	0.00	0.00	0.00	0.00	0.15	1.33	0.98	0.00	0.00	0.24	0.00	0.37	0.00	1.23	0.00	0.49	0.00	0.74	0.00	0.00
T. comprimata (total)			0	6	1	14	31	2	22	1	9	0	3	44	4	21	0	6	1	1	2	1	0	10	3	68	14	0	11
T. comprimata (live)			0	0	0	2	1	0	19	0	1	0	0	6	1	1	0	2	0	0	0	0	0	0	0	0	1	0	0
T. comprimata (dead)			0	6	1	12	30	2	3	1	8	0	3	38	3	20	0	4	1	1	2	1	0	10	3	68	13	0	11
T. comprimata (dead) %			0.00	6.00	1.69	10.91	8.75	0.53	0.86	0.59	1.84	0.00	0.99	5.71	0.80	3.26	0.00	0.95	0.24	0.24	0.74	0.29	0.00	4.20	1.46	10.99	3.20	0.00	14.67
T. inflata (total)			0	0	0	1	8	37	16	3	102	15	17	51	39	93	25	33	49	12	5	5	2	20	13	43	97	0	1
T. inflata (live)			0	0	0	0	0	11	4	0	15	1	0	3	7	14	0	4	2	0	2	1	0	0	0	0	7	0	0
T. inflata (dead)			0	0	0	1	8	26	12	3	87	14	17	48	32	79	25	29	47	12	3	4	2	20	13	43	90	0	1
T. inflata (dead) %			0.00	0.00	0.00	0.91	2.33	6.95	3.44	1.76	20.00	6.01	5.59	7.21	8.51	12.89	4.53	6.92	11.19	2.91	1.10	1.16	0.82	8.40	6.31	6.95	22.17	0.00	1.33
L. ochracea (total)			0	0	0	0	0	0	4	0	0	0	2	0	0	0	0	0	2	0	0	0	0	0	0	0	3	0	2
L. ochracea (live)			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
L. ochracea (dead)			0	0	0	0	0	0	4	0	0	0	2	0	0	0	0	0	2	0	0	0	0	0	0	0	3	0	2
L. ochracea (dead) %			0.00	0.00	0.00	0.00	0.00	0.00	1.15	0.00	0.00	0.00	0.66	0.00	0.00	0.00	0.00	0.00	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.74	0.00	2.67
T. salsa (total)			0	2	0	0	4	1	0	0	1	0	10	4	2	3	0	0	0	0	2	0	0	1	1	3	0	0	0
T. salsa (live)			0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
T. salsa (dead)			0	2	0	0	4	1	0	0	1	0	10	4	2	3	0	0	0	0	2	0	0	1	1	3	0	0	0
T. salsa (dead) %			0.00	2.00	0.00	0.00	1.17	0.27	0.00	0.00	0.23	0.00	3.29	0.60	0.53	0.49	0.00	0.00	0.00	0.00	0.74	0.00	0.00	0.42	0.49	0.48	0.00	0.00	0.00
Reophax sp. (total)			0	0	0	5	9	31	1	2	0	0	10	6	1	5	0	0	1	1	1	0	0	1	1	5	6	0	0
Reophax sp. (live)			0	0	0	0	0	5	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reophax sp. (dead)			0	0	0	5	9	26	1	1	0	0	9	6	1	5	0	0	1	1	1	0	0	1	1	5	6	0	0
Reophax sp. (dead) %			0.00	0.00	0.00	4.55	2.62	6.95	0.29	0.59	0.00	0.00	2.96	0.90	0.27	0.82	0.00	0.00	0.24	0.24	0.37	0.00	0.00	0.42	0.49	0.81	1.48	0.00	0.00
P. limnetis (total)			1	0	0	0	0	0	0	6	20	0	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P. limnetis (live)			0	0	0	0	0	0	0	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P. limnetis (dead)			1	0	0	0	0	0	0	5	13	0	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
P. limnetis (dead) %			1.75	0.00	0.00	0.00	0.00	0.00	0.00	2.94	2.99	0.00	3.29	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

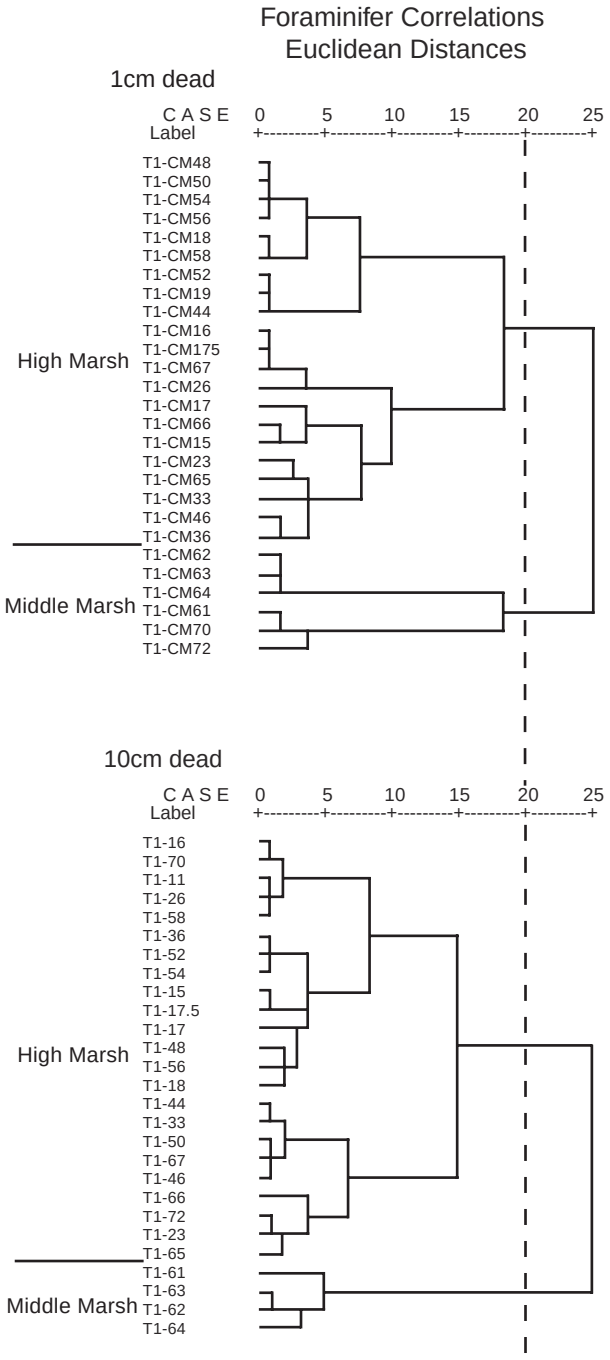

Fig. 3. Q-mode cluster dendrograms of foraminiferal samples for 0–1 and 0–10 cm marsh surface samples. Clusters of samples at Euclidean distances greater than a selected level (dashed vertical line) are considered to be assemblage zones.

where X_i is the abundance of each taxon in a sample, N_i is the total abundance of the sample, and S is equal to the species richness of the sample.

The results of the SDI analysis were utilized as a proxy value in stepwise linear regression analysis (SLR), alongside taxonomic data, as previous research has shown significant relationships between SDI and other environmental parameters (Dalby, 2002).

2.5. Stepwise linear regression

The SLR technique available in SPSS 10 was utilized to identify and quantify covariant relationships between proxy and parametric variables (Tables 2 and 3). This variety of multiple regression analysis is considered one of the more robust techniques available, because more constraints are placed on the data used and dangers of overfitting of data are reduced (Hair et al., 1998). SLR selects the variables with the best predictive correlation with the parameter being examined. The next best predictor is then added, and so on, as long as the result increases the combined explanatory power, and if the partial correlation coefficients are statistically significant (Hair et al., 1998).

For this study the variables utilized consisted of all the species of foraminifera present in statistically significant populations and the SDI, and comparing them to the elevation of sample stations AMSL. Prior to SLR analysis, the level of normality in the data was assessed by examining the skewness and kurtosis of all data (Hair et al., 1998). Skewness is the measure of how off-center the distributional curve is found to be, and is corrected by employing a natural logarithm (ln) function to the data (Dalby, 2002). Kurtosis is the amplitude of the highest part of the distributional histogram and is also corrected again by utilizing the natural logarithm (Dalby, 2002).

3. Results

3.1. Q-mode cluster analysis

Q-mode cluster analyses of the 0–1 and 0–10 cm data sets yielded similar results that we have informally subdivided into ‘high’ and ‘middle’ marsh faunal groupings (Figs. 2 and 3). Marsh foraminiferal faunas are often discussed in the terms of ‘low’, ‘middle’ and ‘high’ or ‘upper’ marsh. This usage has become the norm in papers examining the distribution of foraminifera in marshes both to informally denote position in the marsh but to establish absolute elevations (e.g. Scott and Medioli, 1978, 1980b; Patterson et al., 2000). The boundary between these subdivisions within marsh areas changes locally depending on many factors, particularly tides.

Most samples examined here clustered as part of a typical high marsh foraminiferal fauna dominated by *J. macrescens* (e.g. Patterson et al., 2000). Four samples found between 2.38 and 2.79 m AMSL in both the 0–1 and 0–10 cm data sets had higher proportions of *M. fusca* (up to 69.2% dead) and clustered into a grouping typical of middle marsh environments in the Maritimes region (e.g. Scott and Medioli, 1980b). Samples T1-70 and T1-72 in the 0–1 cm data set clustered anomalously

with the middle marsh cluster. Both of these samples are overwhelmingly dominated by *C. williamsoni* (85.5–93.3% dead) bearing little resemblance to the *J. macrescens* and *M. fusca* dominated middle marsh-type samples. The SDI values for these samples (0.160 and 0.267) are extremely low as well setting them apart from all other samples examined. SDI values of <0.5 are generally associated with impoverished environments (Patterson and Kumar, 2000). It is also interesting to note that *C. williamsoni*, so dominant in these two samples, is not even present in the 0–10 cm data set collected at the same sample stations, making the faunal makeup of these two samples even more anomalous.

3.2. Stepwise linear regression

Stepwise linear regression was performed on the data to relate them to environmental parameters. Data generated included the R, R^2 (measure of goodness of fit) and R'^2 (adjusted measure of goodness of fit) scores. The adjusted goodness of fit is particularly useful as it takes into account the number of explanatory values, a greater number of which can lead to overfitting (Jobsen, 1991). SLR R'^2 values of <0.5 are considered to be statistically unreliable (Dalby, 2002).

Six SLR analyses were carried out on living, dead, and total foraminiferal fractions for both the 0–1 and 0–10 cm data sets (Table 4). For all analysis carried out on the 0–10 cm sample data set values of between 0 and 0.244 were obtained indicating that any possible relationship between these samples was statistically insignificant. Statistically significant results were obtained for all three 0–1 cm samples data sets including the paleoecologically important dead foraminifera subset ($R^2 = 0.705$; $R'^2 = 0.609$).

The predictor variables that were found to drive the relationship for the dead foraminifera 0–1 cm data set at Little Dipper Harbour were ln (*M. fusca*), SDI, and *C. williamsoni* (Table 5). Based on the cluster analysis results these predictors are not unexpected (Figs. 2 and 3). For example, *M. fusca* distinctly characterizes the Middle Marsh Assemblage. Other research has indicated that a single, or small group of species in a marsh foraminiferal assemblage can be a primary predictor. For example, Guilbault and Patterson (2000) observed that in the marsh at Zeballos, Vancouver Island, British Columbia a strong correlation was shown by *M. fusca* (−0.94) and by the grouping of *B. pseudomacrescens*, *J. macrescens* and *T. salsa* (0.92) to elevation. Similarly, Gehrels and van de Plassche (1999) found that in the salt marshes of New England and Atlantic Canada *B. pseudomacrescens* alone could be used as a useful sea-level indicator. The presence of *C. williamsoni* and SDI as predictors (Table 5) are probably more a function of the anomalous samples at T1-70 and T1-72, where *C. williamsoni* overwhelmingly dominates, and the SDI is very low.

Table 4
Goodness of fit (R^2; R'^2) results generated from stepwise linear regression analysis of foraminiferal distributional data for both the 0–1 and 0–10 cm marsh surface samples at Little Dipper Harbour

10 cm live		10 cm dead		10 cm total	
R^2	R'^2	R^2	R'^2	R^2	R'^2
0.244	0.211	*None*	*None*	*None*	*None*
1 cm live		**1 cm dead**		**1 cm total**	
R^2	R'^2	R^2	R'^2	R^2	R'^2
0.902	0.89	0.705	0.669	0.833	0.805

Table 5
Predictor taxa as derived from stepwise linear regression analysis of foraminiferal distribution data for the 0–1 cm marsh surface samples at Little Dipper Harbour

1 cm live	1 cm dead	1 cm total
J. macrescens	ln (*M. fusca*)	*J. macrescens*
T. inflata	*C. williamsoni*	*T. inflata*
ln (*T. comprimata*)	SDI	ln (*C. williamsoni*)
		H. germanica
10 cm live	**10 cm dead**	**10 cm total**
M. fusca	None	None

4. Discussion and conclusions

It has been demonstrated in several recent foraminiferal studies carried out in salt marshes in British Columbia and Georgia that the best baseline for paleoenvironmental reconstruction in those regions is not the marsh surface (0–1 cm) but rather assemblages preserved through the top ~10 cm of the marsh surface (Goldstein and Watkins, 1999). The reason suggested has been that although some common agglutinated marsh foraminiferal species such as *M. fusca* are epifaunal most others are shallow to intermediate infaunal dwellers with cements that are highly susceptible to degradation. As a result, selective preservation and downcore enrichment of some infaunal species quickly results in significant alteration of the percent abundance of some paleoenvironmentally significant species (Jonasson and Patterson, 1992; Ozarko et al., 1997; Goldstein and Watkins, 1999; Patterson et al., 1999; de Rijk and Troelstra, 1999). In constrast, several studies carried out on the distribution of marsh foraminiferal faunas in nearby Nova Scotia indicate that 0–1 cm samples are suitable for paleoenvironmental research (Scott and Medioli, 1978, 1980b), although the utility of thicker surface samples have never been assessed. This study was carried out to determine

whether foraminifera from 0–1 cm, or the assemblages preserved in the top 10 cm of the marsh surface, are most suitable for paleoecological research in the Bay of Fundy area of New Brunswick.

The results obtained using Q-Mode analysis of the Little Dipper Harbour data were ambiguous, as dendrograms produced by both the 0–1 and 0–10 cm foraminiferal data sets were nearly identical. This result varied from the outcome of similar studies carried out in British Columbia, where Q-mode cluster analysis results generated by 0–1 and 0–10 cm data sets were generally quite different (Ozarko et al., 1997; Patterson et al., 1999).

To further test the reliability of the 0–1 and 0–10 cm foraminiferal data sets SLR tests were also carried out. These results indicate that the goodness-of-fit values obtained using 0–1 cm dead foraminifera data were statistically significant ($R^2 = 0.705$; $R'^2 = 0.609$) and therefore suitable for assessing paleoenvironmental data. The goodness of fit (R^2, R'^2) values obtained for the 0–10 cm data were statistically insignificant and not suitable for carrying out paleoenvironmental research. In contrast, the outcome of similar SLR analyses carried out on marsh foraminiferal distributional data from Nanaimo and Zeballos, Vancouver Island British Columbia produce opposite results when SLR is carried out, with the 0–1 cm data producing statistically insignificant results and the 0–10 cm data producing statistically significant results (Patterson, unpublished data, 2002).

The salt marsh ecotone is a harsh environment characterized by only a limited number of cosmopolitan foraminiferal species, throughout the temperate regions of the world. For example, *J. macrescens* almost always dominates high marsh faunas, while *M. fusca* is more characteristic of lower marsh environments. The expectation therefore would be that most salt marshes would be fundamentally similar. The profound differences observed in the preferred infaunal habitats foraminifera from Little Dipper Harbour and British Columbia and Georgia marshes indicate that this generalization cannot be accurate. The difference in the distributional characteristics of the foraminifera found in these marshes can probably be related to a number of factors including:

(1) *Tidal range*. The Bay of Fundy has the highest tides in the world, which has a significant impact on any organisms inhabiting the intertidal zone. This parameter is generally the only non-foraminiferal parameter measured by most marsh researchers.
(2) *Salinity*. The measurement of salinity in the tidal marsh has long been discussed as a significant contributor to controlling the makeup of marsh foraminiferal assemblages (e.g. Scott and Medioli, 1980b; Patterson, 1990). Unfortunately, salinity varies considerably through the tidal cycle so no attempt is generally made to measure it. For future studies it might be appropriate to take several salinity measurements of ocean water in the immediate vicinity of the salt marsh transect at both high and low tide to determine the approximate range for the location.
(3) *Mean annual temperature*. Mean annual temperature and the climate at a particular marsh locality has a significant impact upon biological productivity, which directly influences the distribution of marsh foraminiferal taxa (Patterson, 1990). At Little Dipper Harbour, New Brunswick the temperature in the marsh varies considerably between the winter lows (January; High -1.8°C, Low -12.2°C, Mean -7°C) and summer highs (July; High $+21.4^\circ$C, Low $+12^\circ$C, Mean $+15.7^\circ$C; Environment Canada, 2003). The salt marsh at Little Dipper Harbour actually freezes solid for several months in the winter season, which severely impacts productivity. At the Nanaimo, British Columbia marsh where Ozarko et al. (1997) carried out their research the climate is markedly different, with the contrast between winter temperature lows (January; High $+6.1^\circ$C, Low 1.1°C, Mean $+3.6^\circ$C) and summer highs being much less significant (July; High $+21.8^\circ$C, Low $+13.6^\circ$C, Mean $+17.7^\circ$C; Environment Canada, 2003). In this area biological activity continues throughout the entire year directly impacting marsh foraminiferal assemblage development.
(4) *Oxygenation of the marsh substrate*. The level of oxygenation is an important parameter in determining the degree of infaunal penetration into the substrate of marsh foraminifera (Walker and Goldstein, 1999). Substrate oxygenation is directly impacted by bioturbation (discussed below), which varies considerably depending on many additional parameters, including mean annual temperature. Part of the reason that level of oxygen in marsh substrates has not been directly measured in the past is that the available probes were not robust enough to be pushed through the tough marsh substrate to directly measure oxygen cm × cm. However, a new generation of oxygen probes has come to market recently, which should permit researchers to directly measure this important parameter.
(5) *Bioturbation*. Bioturbation can have a major influence on the distribution of marsh foraminiferal assemblages, particularly where burrowing fiddler crabs are common (Wolf et al., 1975). In addition to the physical movement of foraminifera up and down in the substrate as the direct result of burrowing, dissolution is greatest in areas of high

bioturbation. This is because alkalinity is impeded by increased flow of fluids through burrows, which also enhances aerobic respiration mediated carbonic acid production (Aller and Aller, 1992). For example in the Great Marshes near Barnstable, Cape Cod, Massachusetts, roughly climatically analogous to conditions at Little Dipper Harbour, fiddler crabs are only observed along creek banks (de Rijk and Troelstra, 1999). In Georgia marshes, however, fiddler crabs are much more active and burrows are found throughout the marsh right up to the high marsh area (Wolf et al., 1975). Even varying rates in the growth of roots of marsh vegetation can have an impact on levels of bioturbation and oxygenation of the marsh substrate (de Rijk and Troelstra, 1999).

(6) *Selective preservation*. Selective preservation of foraminiferal tests is an important controlling parameter on fossil assemblage formation in salt marsh environments. Although calcareous tests are most commonly thought of as being most susceptible to dissolution, selective preservation impacts agglutinated taxa as well (Goldstein and Harben, 1993; Goldstein et al., 1995). Goldstein and Watkins (1999) report that foraminiferal densities decline by as much as 80–90% from 0–10 cm down core in coastal Georgia marshes. The results of the research discussed here suggests that this taphonomically active zone may be much shallower in the cooler climate marsh at Little Dipper Harbour.

Many researchers are involved in the development or transfer function training sets utilizing marsh foraminiferal distributional data to reconstruct past sea levels. Marsh foraminiferal species should be ideal for reconstructing paleo-sea level as there are relatively few elevationally constrained cosmopolitan species. Unfortunately, the infaunal habitat and differential preservation of some species presents taphonomic difficulties that may limit their utility (Gehrels et al., 2001). The results obtained here at Little Dipper Harbour where we determined that a 0–1 cm sample horizon is preferable to samples from through the top 10 cm of marsh surface at marshes in Georgia and British Columbia provide confirmation of this finding. The results obtained here may also partially explain why researchers have had difficulty applying transfer function training sets outside of a limited area. The application of SLR analytical techniques utilizing as many parameters as possible, including salinity data, oxygen, local climate data, etc. in addition to elevational data may help overcome many of foraminiferal taphonomic and infaunal habitat difficulties, and permit the development of more widely applicable training sets.

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