MCKAY BAY DREDGE HOLE RESTORATION MONITORING

Pre-Restoration Benthic Sampling Data Report

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Data Report 1

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Introduction

Dredge holes are submerged borrow sites left when sediments are dredged to provide fill for construction projects or to create navigation channels. The Tampa Bay Estuary Program conducted a study evaluating the habitat quality, fisheries use and restoration potential of dredge holes in Tampa Bay (Tampa Bay Dredged Hole Habitat Assessment Advisory Team, 2005). Of the 11 dredge holes evaluated in that study, the McKay Bay dredge hole was ranked as the worst in terms of poor water and sediment quality, a degraded benthic community and low utilization by fish. The study made the recommendation that this dredge hole should be filled to the surrounding depth in order to eliminate hypoxic conditions, cap potentially contaminated sediments and allow for the establishment of a healthy benthic community. The McKay Bay dredge hole also had a high feasibility for filling due to its location near the Port of Tampa (Tampa Bay Dredged Hole Habitat Assessment Advisory Team, 2005). Fill material from the dredging of a new berth in the Port of Tampa and from a Port of Tampa mitigation project on the McKay Bay peninsula has been made available for the filling of a portion of the McKay Bay dredge hole (Swingle and Brice, 2011).

The Environmental Protection Commission of Hillsborough County has been contracted by the Southwest Florida Water Management District to conduct pre- and post- restoration benthic monitoring. This report presents the results of the pre-restoration sampling.

Materials and Methods

Study Design and Site Selection

This study employs a Before-After-Control-Impact (BACI) study design (Green, 1979) in order to assess the post-restoration recovery of the benthic infaunal community. The advantage of the BACI approach is that it provides both a spatial and temporal control to better detect environmental changes resulting from a disturbance, or in this case, due to the restoration of an impacted site. This is achieved through collecting samples in a control or reference area with similar physical characteristics as the impacted site to provide for a spatial control and both are sampled before and after the restoration to control for temporal changes.

A total of 30 locations (sampling sites) were sampled in August 2011(Table 1, Figure 1). Fifteen sites were within the dredge hole restoration area (impact treatment) and 15 sites were located outside of the dredge hole restoration area (control treatment). Twenty-one of the 30 sites were selected from locations previously sampled between 1999 – 2010 as part of the EPCHC's Hillsborough Independent Monitoring Program (HIMP) or other EPCHC studies that provided baseline monitoring data in McKay Bay (Grabe et al. 2000, 2001; Karlen et al., 2012). These sites were selected based on their similarity to the expected post-restoration depth of the dredge hole and the sediment composition of the fill material (Swingle and Brice 2011). All previous samples were collected during the same season (late summer). Most of these 21 sites were sampled multiple times over the course of the EPCHC monitoring program. In order to select previous data at a given site to use as a baseline comparison, a cluster analysis was done based on the environmental parameters measured (depth, % silt/clay and bottom depth measurements for temperature, salinity, pH, and dissolved oxygen) for the 2011 samples and all subsequent sample years at that site. The sample year with the highest similarity to 2011 was selected as the baseline for that individual site. This procedure was done for all 21 sites with prior sampling data using PRIMER v6. The data were log transformed and normalized and the Euclidian distance was uses as the similarity measure for the cluster analysis. These 21 sites included all 15 control sites and six of the dredge hole sites. An additional nine sites were added within the restoration area to give a total of 15 dredge hole sites to balance the sampling design. Table 1 shows the 30 sampling sites, their treatment (control or dredge hole), site number designation, coordinates, sample date and time and the year used for corresponding baseline data. The nine added dredge hole sites are designated by their higher site numbers (11MCB461 – 11MCB469).

| Treatment | Site Number | Latitude | Longitude | Sample Date | Sample Time | Baseline Year |
|--------------------|--------------------|----------|-------------|--------------------|--------------------|----------------------|
| Control | 11MCB062 | 27.94648 | -82.42709 | 15-Aug-2011 | 8:50 AM | 2008 |
| Control | 11MCB068 | 27.94765 | -82.41423 | 9-Aug-2011 | 8:20 AM | 2008 |
| Control | 11MCB076 | 27.94419 | -82.42662 | 15-Aug-2011 | 9:05 AM | 2004 |
| Control | 11MCB088 | 27.94208 | -82.43037 | 15-Aug-2011 | 8:32 AM | 2009 |
| Control | 11MCB091 | 27.94250 | -82.42334 | 15-Aug-2011 | 9:24 AM | 2003 |
| Control | 11MCB102 | 27.93892 | -82.43106 | 15-Aug-2011 | 8:14 AM | 2000 |
| Control | 11MCB103 | 27.94159 | -82.42823 | 15-Aug-2011 | 10:49 AM | 2006 |
| Control | 11MCB117 | 27.93858 | -82.42868 | 15-Aug-2011 | 11:04 AM | 2004 |
| Control | 11MCB129 | 27.93684 | -82.43283 | 15-Aug-2011 | 7:58 AM | 2008 |
| Control | 11MCB138 | 27.93599 | -82.41419 | 15-Aug-2011 | 12:52 PM | 2002 |
| Control | 11MCB149 | 27.93408 | -82.41975 | 15-Aug-2011 | 12:32 PM | 2006 |
| Control | 11MCB161 | 27.93109 | -82.42379 | 15-Aug-2011 | 11:18 AM | 2007 |
| Control | 11MCB164 | 27.93095 | -82.41904 | 15-Aug-2011 | 12:16 PM | 2009 |
| Control | 11MCB176 | 27.92899 | -82.42339 | 15-Aug-2011 | 11:46 AM | 2002 |
| Control | 11MCB178 | 27.92955 | -82.41776 | 15-Aug-2011 | 12:00 PM | 2001 |
| Dredge Hole | 11MCB094 | 27.94129 | -82.41802 | 9-Aug-2011 | 10:45 AM | 2008 |
| Dredge Hole | 11MCB095 | 27.94264 | -82.41501 | 9-Aug-2011 | 9:09 AM | 2007 |
| Dredge Hole | 11MCB106 | 27.94085 | -82.42216 | 9-Aug-2011 | 11:39 AM | 2002 |
| Dredge Hole | 11MCB107 | 27.93994 | -82.42058 | 9-Aug-2011 | 11:23 AM | 2006 |
| Dredge Hole | 11MCB108 | 27.94012 | -82.41896 | 9-Aug-2011 | 11:09 AM | 2000 |
| Dredge Hole | 11MCB119 | 27.93971 | -82.42423 | 15-Aug-2011 | 10:31 AM | 2000 |
| Dredge Hole | 11MCB461 | 27.94229 | -82.42123 | 15-Aug-2011 | 9:42 AM | NA |
| Dredge Hole | 11MCB462 | 27.94252 | -82.41735 | 9-Aug-2011 | 10:05 AM | NA |
| Dredge Hole | 11MCB463 | 27.94143 | -82.41672 | 9-Aug-2011 | 10:23 AM | NA |
| Dredge Hole | 11MCB464 | 27.94208 | -82.41564 | 9-Aug-2011 | 9:48 AM | NA |
| Dredge Hole | 11MCB465 | 27.94224 | -82.41391 | 9-Aug-2011 | 8:43 AM | NA |
| Dredge Hole | 11MCB466 | 27.93990 | -82.42201 | 9-Aug-2011 | 11:56 AM | NA |
| Dredge Hole | 11MCB467 | 27.93992 | -82.42376 | 15-Aug-2011 | 10:08 AM | NA |
| Dredge Hole | 11MCB468 | 27.93885 | -82.42354 | 9-Aug-2011 | 12:15 PM | NA |
| Dredge Hole | 11MCB469 | 27.93894 | -82.42442 | 9-Aug-2011 | 12:29 PM | NA |

Table 1. McKay Bay Pre-Restoration Sampling Locations, Times, and Corresponding Baseline Year.

Field Collection

Field and laboratory methods were adopted from the EMAP-E Louisianan Province operations manual (Macauley, 1993) and modified for the Tampa Bay monitoring program (Versar, 1993; Courtney et al. 1995). A hydrographic profile was taken at each site using a Hydrolab® Quanta multi-probe sonde. Measurements were taken from the surface (0.1 meters) and bottom for temperature, salinity, pH, and dissolved oxygen.

Sediment samples for benthic macrofaunal community analysis were taken at each site using a Young-Modified Van Veen grab sampler (or Young grab). The grab sample was taken to a sediment depth of 15 cm and covered an area of 0.04 m^2 . A 60 cc corer was used to take a subsample for Silt+Clay analysis. Samples were sieved through a 0.5 mm mesh sieve and the remaining fraction was rinsed into plastic sample jars. Samples were fixed in 10% buffered formalin for a minimum of 72 hours and then transferred into 70% isopropyl alcohol for preservation and storage. Rose Bengal was added to the formalin and isopropyl alcohol solutions to stain the organisms.

Laboratory Analysis

The silt+clay analysis followed procedures outlined in Versar, 1993. Benthic sorting and identification work was conducted by EPCHC staff. Benthic sediment samples were rough sorted under a dissecting microscope into general taxonomic categories (annelids, molluscs, crustaceans, and miscellaneous taxa). Resorting was done on 10% of the samples completed by each technician for QA/QC. The sorted animals were identified to the lowest practical taxonomic level (species level when possible) and counted. Taxonomic identifications were conducted using available identification keys and primary scientific literature. All identification and count data were recorded on laboratory bench sheets and entered into a Microsoft Access® database maintained by the EPCHC.

Data Analysis

Univariate Statistical Analysis

Parametric and non-parametric statistical analysis was done with SigmaStat ® 3.5 (SYSTAT Software, Inc. 2006a). Data were transformed for normality where needed for the parametric tests. Analysis of Variance (ANOVA) with a Holm-Sidak method pair-wise post hoc test was used to test for differences between sampling events. Where the assumptions of the ANOVA could not be met by the data transformation, a non-parametric Kruskal Wallace test was used along with a Dunn's Pairwise Multiple Comparison test.

Multivariate Statistical Analysis and Benthic Community Indices

PRIMER v6 software (PRIMER-E, Ltd. 2006; Clarke and Gorley 2006) was used for all multivariate statistical analysis and for calculating univariate biological metrics (species richness, abundance, Shannon diversity index and Pielou's evenness index). Species richness (*S*) was defined as the total number of taxa. Abundance (*N*) was expressed as the number of individuals per m² (calculated as the raw count x 25) except for colonial organisms which were counted as present/absent. The Shannon diversity index (*H'*) calculations employed the natural logarithm opposed to log base 2 (Clarke and

Warwick 2001). The zero-adjusted Bray-Curtis similarity (Clarke et al. 2006) was calculated on square root transformed abundance data and the resulting similarity matrix was used for running Cluster Analysis, Non-metric Multi-Dimensional Scaling (MDS), Similarity Percentage (SIMPER), and Analysis of Similarity (ANOSIM). The BIO-ENV procedure (Clarke and Ainsworth 1993) was used to find correlations between the environmental parameters and benthic community structure. All environmental parameters were normalized and log transformed prior to analysis. The Tampa Bay Benthic Index (TBBI) was calculated for each site following the methods established in Janicki Environmental (2005) and Malloy et al. (2007). The TBBI threshold scores for "Degraded" (< 73), "Intermediate" (between 73 to 87) and "Healthy" (> 87) benthic habitats were established by Janicki Environmental (2005) and Malloy et al. (2007) .

Spatial and Graphical Analysis

Graphs were generated using SigmaPlot® 10.0 software (Systat Software, Inc. 2006b). Maps were generated by the Environmental Protection Commission of Hillsborough County using ArcGIS 9.2 (ESRI 2006).

Figure 1. McKay Bay Dredge Hole Restoration Sampling Sites. The red line indicates the boundary of the dredge hole fill area.

Results

Physical Parameters

 The median, minimum and maximum measured values of physical parameters for each treatment (control, dredge hole) and time period (baseline, pre-restoration) are shown in Table 2.

Table 2. Median, minimum and maximum physical parameter measurements for McKay Bay by treatment and sampling period.

Overall sample depths at the control sites ranged from $0.5 - 2.0$ meters and from $1.0 - 4.2$ meters at the dredge hole sites (Table 2). Within each time period, the depths were significantly shallower at the control sites relative to the dredge hole sites. There was no significant difference in the sample depth among the control sites or the dredge hole sites between the two sampling periods (Figure 2).

 Bottom water temperatures were higher at the pre-restoration control sites relative to the baseline control and dredge hole sites, but not significantly different from the pre-restoration dredge hole sites (Figure 3). There were no significant differences in water temperature between the control and dredge hole sites within either sampling period (figure 3).

Figure 2. Mean depth by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

Figure 3. Mean bottom temperature by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

 The bottom salinities tended to be higher at the dredge hole sites within both sampling periods, but median values were lower by about 2 psu during the 2011 pre-restoration sampling period relative to the baseline samples (Table 2; Figure 4). The bottom salinities were significantly lower at the prerestoration control sites (Figure 4). Overall bottom salinities tended to be within the polyhaline range (18 – 30 psu). The baseline sites had the widest range for salinity (14.8 – 28.0 psu) while the other treatment/sampling periods generally had salinities that only varied between 3 – 5 psu between their minimum and maximum values (Table 2).

Figure 4. Mean bottom salinity by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean. Dashed line = 18 psu threshold for polyhaline salinity level.

 The bottom dissolved oxygen was significantly lower at the dredge hole sites compared to the control sites within both the baseline and pre-restoration sampling periods (Figure 5). There were no significant differences found between sampling periods for either the dredge hole or control treatments (Figure 5). Bottom dissolved oxygen readings at the control sites were variable, ranging from 0.7 to 8.0 mg/L. Median values at the baseline control sites were higher relative to the 2011 pre-restoration control sites (Table 2). The bottom dissolved oxygen conditions in the dredge hole sites were generally hypoxic $(< 2$ mg/L).

Figure 5. Mean bottom dissolved oxygen by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean. Dashed lines indicate threshold levels for hypoxic conditions (lower line = 2 mg/L) and normoxic conditions (upper line = 4 mg/L).

The bottom pH was lower at the dredge hole sites relative to the control sites during both sampling periods (Figure 6). Although there was an overall statistically significant difference in pH, individual pair-wise comparisons did not indicate significant differences between combinations of treatments and sampling periods (Figure 6).

Figure 6. Mean bottom pH by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

The percent silt+clay content was significantly higher in the dredge hole sediments within sampling periods, while there was no significant difference between sampling periods for either the control or dredge hole treatments (Figure 7). The dredge hole sediments were generally classified as muds (% Silt +clay > 25.95%) and the control sites were predominantly fine to very fine sandy sediments (Figure 7).

Principal component analysis (PCA) is a multivariate ordination method used to group samples based on the resemblance of their physical parameters. In PCA the samples are plotted along multidimensional vectors representing the physical parameters. The plotted samples are projected onto orthogonal axes in 2-dimentional space referred to as principal components (PCs). The eiganvalue represents the amount of variation among the data accounted for by the PC axis. The eigenvalues are ranked in descending order so that the $1st$ principle component axes (PC1) explains the largest percentage of the variation. The eigenvectors represent the contribution or "weight" of each parameter vector to the PC axis.

The PCA of the physical parameters is shown in Figure 8. The first principal component axis (PC1) explains 55.2% of the variability in the data (Table 3). The sites group along PC1 by treatment (control

vs. dredge hole) with the higher depth and percent silt/clay dredge hole sites towards the positive (right) direction and the higher dissolved oxygen and pH control sites on the negative (left) side of PC1 (Table 4). The second principal component axis (PC2) accounted for 18% of the variation and was weighted primarily by the bottom temperature (Tables 3 & 4). The sites group along this axis according to sampling period, with the baseline samples towards the positive (upper) direction and the prerestoration samples towards the negative (lower) end of the axis.

Figure 8. Principal Components Analysis of McKay Bay physical parameters.

| PC Axis | Eigenvalues | %Variation | Cumulative %Variation | | |
|----------------|--------------------|------------|------------------------------|--|--|
| | 3.31 | 55.2 | 55.2 | | |
| | 1.08 | 18.0 | 73.2 | | |
| ર | 0.703 | 11.7 | 84.9 | | |
| | 0.533 | 8.9 | 93.8 | | |
| | 0.261 | 4.4 | 98.2 | | |

Table 3. Principal Components Analysis Eigenvalues and percent variation explained.

Table 4. Principal Components Analysis Eigenvectors

| Variable | PC ₁ | PC ₂ | PC ₃ | PC4 | PC ₅ |
|-------------|-----------------|-----------------|-----------------|----------|-----------------|
| Depth | 0.482 | -0.113 | -0.195 | 0.155 | 0.813 |
| Temperature | -0.029 | -0.952 | -0.038 | -0.120 | -0.042 |
| Salinity | 0.376 | 0.132 | -0.746 | -0.432 | -0.265 |
| DO | -0.481 | 0.169 | -0.344 | 0.285 | 0.318 |
| pH | -0.455 | -0.178 | -0.529 | 0.262 | -0.072 |
| Silt/Clay | 0.431 | -0.052 | -0.076 | 0.790 | -0.402 |

Benthic Community

The median, minimum and maximum values for five benthic community metrics for each sampling period and treatment are presented in Table 5.

Species Richness (*S*) refers to the number of unique species or taxa present at a site. Past samples collected by EPCHC from 1999-2010 recorded a total 384 taxa in McKay Bay with a median of 28 taxa per site and ranging from 0 – 67. A total of 148 taxa were identified from the 15 baseline control sites with a median of 33 taxa per site. Species richness at the baseline dredge hole sites was significantly lower (Figure 9) with a total of 44 taxa identified and a median of 10 taxa per site (Table 5). A total of 107 taxa were identified from the 2011 pre-restoration control sites with a median of 34 taxa per site (Table 5). The pre-restoration dredge hole sites had significantly lower species richness with only 64 taxa total and median of 2 taxa per site (Table 5; Figure 9). There was no significant difference in species richness among the control treatments or dredge hole treatments between the two sampling periods (Figure 9).

Abundance (*N*) is the number of individual animals counted at a site. This index is usually standardized by sampling area and expressed as the number of organisms per square meter (m²). Past EPCHC samples from McKay Bay (1999-2010) had a median of 6200 organisms/ m^2 and ranged from 0 – 63,225/m². The abundance of benthic organisms in the current study was significantly lower at the dredge hole sites compared to the corresponding control sites within each sampling period (Figure 10). Among the control and dredge hole treatments there was no significant difference in the abundance between the two sampling periods (Figure 10). The benthic abundance varied widely ranging from 0 at two of the pre-restoration dredge hole sites to over 63,000 organisms/ $m²$ at one baseline control site.

The abundances were generally around an order of magnitude higher at the control sites relative to the dredge hole sites.

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Figure 9. Mean benthic species richness by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

Figure 10. Mean benthic abundance by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

Diversity indices are measures which account for the species richness and the proportion of the abundance represented by each species (referred to as evenness).The Shannon diversity index (*H'*) is the most commonly used index in ecological studies. Past McKay Bay samples the median *H'* was 2.33 and ranged from 0 – 3.49. In this study, *H'* showed a similar pattern as the species richness and abundance with higher values at the control sites and lower values at the dredge hole sites (Table 5; Figure 11). The baseline period the median diversity was lower at the dredge hole sites, but not statistically significant from the baseline control sites (Figure 11). The diversity at the pre-restoration dredge hole sites was significantly lower that at the pre-restoration control sites (Figure 11), but there was no significant difference between the baseline and pre-restoration control sites or dredge hole sites.

Figure 11. Mean benthic Shannon diversity by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

Evenness refers to the distribution of the abundance among the species at a site and the Pielou evenness index (*J'*) is the most common measure used to express this metric. Lower evenness values indicate the dominance of a single or a few species in a sample. The maximum value for *J'* is 1 when all species at a site have an equal abundance. A higher *J'* generally indicates a more diverse site, however sites with a low species richness and abundance can often result in high J' values also. Previous samples collected in McKay Bay (1999-2010) had a median *J'* of 0.73. The evenness in this study was higher at the dredge hole sites, due mainly to the fact that there were few taxa and low abundances. The baseline period had no significant difference in benthic evenness between the two treatments although the median value was higher at the dredge hole sites (Table 5, Figure 12). The pre-restoration period evenness index was significantly higher for the dredge hole sites. There was no significant differences between the two sampling periods for either the control or dredge hole treatments (Figure 12).

Figure 12. Mean benthic evenness by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

The Tampa Bay Benthic Index values were significantly lower for the dredge hole sites compared to the control sites within the two sampling periods but there was no significant difference between the sampling periods for either the control or dredge hole treatments (Figure 13). The control sites generally rated as "Fair" to "Good" while the dredge hole sites were rated as "Poor" to "Fair". The baseline control sites had 40% of sites in the "Good" range and 53% in the "Fair" range with only a single site rated as "Poor". Half of the baseline dredge hole sites were rated as "Poor" while the other half were rated as "Fair". The pre-restoration control sites had 47% of the sites rated as "Good", 47% rated as "Fair" and 6% (one site) rated as "Poor". The pre-restoration dredge hole had 40% of sites rated as "Fair" and 60% as "Poor" (two sites being completely depauperate).

Figure 13. Mean Tampa Bay Benthic Index scores by treatment and statistical pair-wise comparisons. Error bars indicate ± 1 s.d. about the mean.

The top five dominate taxa for each sampling period and treatment based on their relative abundance and frequency of occurrence among the sites are presented in Table 6. The amphipod *Ampelisca abdita* was dominant in both the control and dredge hole sites during the baseline period. , The dominant species during the 2011 pre-restoration sampling period was the polychaete *Monticellina* cf. *dorsobranchialis* in both the control and dredge hole sites, followed by *Ampelisca abdita*. In all cases, the top ranked dominant species accounted for 20 – 25% of the total abundance. Three of the dominant taxa for the pre-restoration control treatment were found at all 15 sites: *Monticellina* cf. *dorsobranchialis, Ampelisca abdita* and the polychaete *Paraprionospio pinnata.* Two taxa were present at 14 (93%) of the sites: the polychaete *Aricidea taylori* and isopod *Xenanthura brevitelson.*

Table 6. Top five dominant benthic taxa for each treatment and time period. Dominance calculated as the geometric mean of the relative abundance (left value) and frequency of occurrence (right value). Rankings weighted by frequency of occurrence.

The dredge hole sites generally had similar taxa present as at the control sites, but lower overall species richness and abundances. The baseline dredge hole sites were unique by the presence of acorn worms (Entropneusta), pea crabs (*Pinnixa* spp.) and the polychaete *Mellinna maculata*. The prerestoration dredge hole sites were characterized by the polychaete *Sabaco elongatus.*

The non-metric multidimensional scaling analysis (Figure 14) shows that the species similarity is relatively high among most of the control sites (and several dredge hole sites) across both sampling periods. A group of dredge hole sites, primarily from the pre-restoration period separate out from the other sites due largely to low numbers of taxa and abundances (Figure 14).

Figure 14. Non-metric multidimensional scaling (MDS) plot of benthic species similarity among McKay Bay sampling sites.

The BIO-ENV analysis found the strongest correlation between the benthic community structure and the physical parameters was with the combination of depth and the % silt/clay with a Spearman correlation coefficient of 0.618 (Table 7). Individually depth and the % silt/clay had correlations of 0.530 and 0.525 respectively with the community structure.

Table 7. BIO-ENV correlations between the benthic community structure and physical parameters.

Discussion and Conclusions

Salinity and temperature were variable over time while the other physical parameters were more stable over time. Most of the benthic community measures were also relatively stable within the control and dredge hole sites between sampling periods. Many of the same taxa were consistently found in both treatment sites and sampling periods. There was an observed shift in the dominant species between the baseline and pre-restoration periods, which may be due to the lower salinities and higher temperatures recorded during the 2011 sampling. The baseline data were drawn from a pool of samples collected over a 10 year period while the pre-restoration samples were collected only in August 2011 so the observed shift in dominance may simply be a random event.

The benthic community structure was largely influenced by depth and the sediment composition. This is consistent with an earlier analysis of the EPCHC McKay Bay benthic data which found that the spatial trends in the benthic community structure were driven by the sediment composition (% silt+clay), while temporal trends were primarily influenced by changes in salinity (Karlen et al. 2012).

The dredge hole samples were characterized by greater depths, sediments with a high silt+clay content and lower dissolved oxygen in the bottom waters relative to the surrounding areas of McKay Bay. The bottom salinities tended to be higher in the dredge hole possibly due to poor flushing and stratification of the water column. These conditions further result in an impoverished benthic community reflected in the low species richness, abundance and diversity observed at the dredge hole sites. The few organisms that did comprise the dredge hole benthic community were predominantly deposit feeders and species which can tolerate the hypoxic conditions, such as the polychaete *Sabaco elongatus* and the hemichordate Enterpneusta.

This study represents the "Before" sampling of the BACI design employed to evaluate the status of the benthic macroinvertebrate community within the project area. These results will provide the basis for comparison with the post –restoration samples which are anticipated to be collected in August 2013 – approximately 1 year after the dredge hole filling is complete. These samples will be collected at the same 30 sites and compared with the pre-restoration results using a repeated measures ANOVA design. These current results indicate that the benthic community structure is largely a factor of depth and sediment composition. Restoring the dredge hole to the depth of the surrounding area and using fill material of similar sediment type is expected to improve the benthic community in the restored area. If the dredge hole filling is successful, there should be no significant difference between the postrestoration dredge hole and control sites in either the physical parameters or the benthic community metrics and greater species similarity in the community composition among all of the sites.

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