CHARACTERIZATION OF ESTUARINE ENVIRONMENTS AND SUB-ENVIRONMENTS USING MOLLUSK ASSEMBLAGES

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INTRODUCTION

An estuary is simply defined as the region of interaction between inland freshwater sources and the salt waters of the open ocean (Hobbie 2000, p. 1). Within such a region a number of environments and sub-environments occur that are characterized by various environmental factors including salinity and substrate (Parkinson 1987). These factors create the boundaries of habitat for a multitude of estuarine organisms. Mollusca is such a class of organisms, occurring in great ubiquity throughout an estuary and in such diversity that each of the molluscan species requires a unique set of environmental parameters (Davies 1972). It is this diversity, ubiquity, and high potential for preservation that make mollusks ideal for use in characterizing many estuarine environments.

The characterization of environments becomes important when determining rate and direction of sea level oscillations. Wanless, Parkinson, & Tedesco (1994) reported a modern transgressive phase of sea level rise at a rate of 23 cm/100 years. In a transgressive phase there should be evidence of environment migration inland; low- salinity indicator species would be found preserved under the modern depositional environments of the open ocean. Molluscan indicator species may aid in identification of estuarine paleo-environments. The purpose of this study is to test the hypothesis that molluscan species serve as indicators for specific estuarine environments and sub-environments. It will also provide an index of indicator species for use in identification of modern and paleo-environments.

METHODS

Sample Site

I conducted this study primarily within the Rookery Bay National Estuarine Research Reserve, located in southwestern Florida. This area is characterized by brackish rivers opening into a chain of coastal bays that are sheltered from the ocean by numerous oyster reefs, mangrove islands, and barrier islands. I took 19 samples from three major salinity environments identified by Parkinson (1987) as open-ocean shoreface (OOS), inter-island bays (IIB), and chain of bays (CB). A fourth salinity environment, riverine (R), was unique to this study. These samples also included sub-environments characterized by sediment grain size.

Procedure

I determined possible sample sites using Parkinson's (1987) site map. I took each sample from a skiff using two modified cocktail shakers bolted together and attached to a sixty-foot rope. For each sample, I cast the shakers into the water at a radius from the boat of approximately 25 feet. I pulled the shakers along the floor of the waterway and up

to the boat. I repeated the sampling process, casting the shakers in numerous directions around the boat in order to collect 3600 mL of sediment. An additional sample was taken for analysis of grain size, percent carbonate, and percent organic matter. Each 3600 mL sample was sieved to obtain a 2-mm and a 1mm fraction. I then separated the 2-mm fraction of sieved shells into complete individuals (fully articulated, closed bivalves or complete gastropods), hinged (articulated open bivalves), and fragmented (one valve or less in bivalves and less than 85% complete gastropod) shells. I identified all shells measured anterior to posterior lengths in the bivalves with at least one complete valve and the apical to aperture lengths in all full length gastropods.

Sedimentary Analysis

Each sediment sample was analyzed for percent calcium carbonate with a treatment of 20% HCL and for percent organic material using the procedure described in Moore and Reynolds (1989).

The percent sand, clay, and silt were determined by wet sieve and pipette analysis as described in Folk (1974).

Statistical Analysis

I calculated the Shannon-Weaver diversity indice H' for each sample using the formulas found in Zar (1999). Because I could not meet the assumption of normality to perform an ANOVA, I ran a nonparametric Kruskal-Wallis test on JMP (SAS Institute) to determine if the means of the diversity indices in each salinity environment were statistically different. I also compared the means of the numbers of individuals of each mollusk species found in the four salinity environments, but I could not meet the assumption of normality. I also ran a Kruskal-Wallis test for these data to determine statistical differences.

RESULTS

I identified approximately 3500 individuals representing about 110 mollusk species from both the complete and fragmented fractions of the nineteen samples. The statistics did indicate significant differences in the diversity of the four salinity environments and also the distribution of members of a mollusk species throughout these salinity environments. Figure 1 shows that in the fragmented fraction of shells the riverine salinity environment had significantly lower diversity values than the other three environments. The complete fraction showed no significant differences in diversity among the salinity environments. Some mollusk species did show differential distribution throughout the four salinity environments. There were five such species in the complete fraction that showed significance in mean number of individuals (Figure 2). *Nucula proxima, Terebra protexta, and Parvilucina nassula* all appear in the greatest numbers in the open-ocean environment, while the majority of *Anomalocardia auberiana* and *Tellina tampaensis* individuals appear in the chain of bays and riverine habitats.

Twelve mollusk species from the fragmented fraction showed significant differences in mean number of individuals among the salinity environments. *Anomalocardia auberiana* again appears in the greatest numbers in the riverine environment as does *Mytilopsis leucophaeta* (Figure 3). The inter-island bay environment is shown to have the highest concentration of the species *Carditamera floridana* of all the other habitats (Figure 3). The other species are significantly

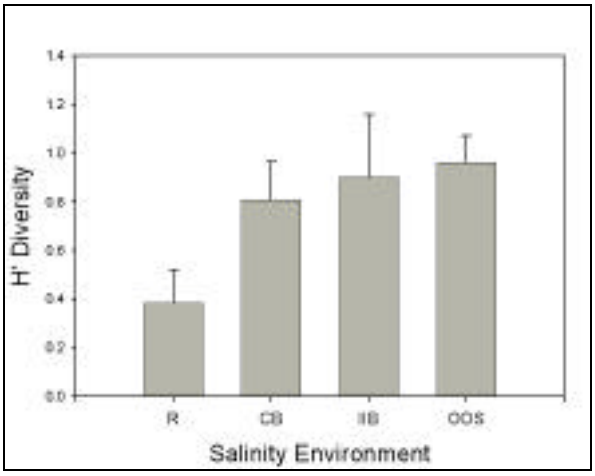

Figure 1: Shows the means of Shannon-Weiner diversity indices for fragmented samples found in each salinity environment.

greater in number in the open-ocean shore face than any other environment (Figures 3 and 4). The statistical significance among the means of these species in the salinity environments allows me to draw conclusions on what

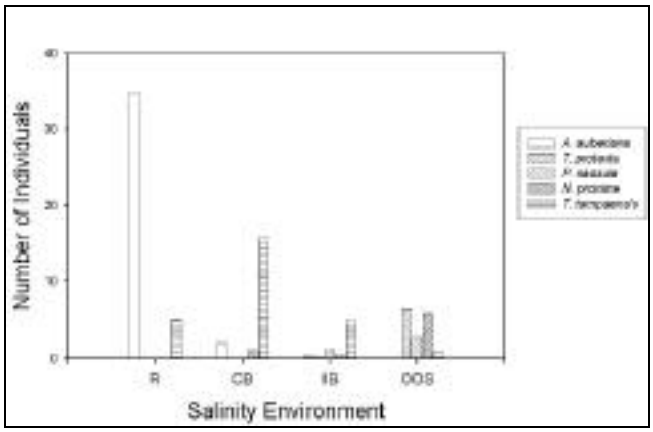

Figure 2: Distribution of mollusk species (complete individuals) over four salinity environments. The values represented are the mean number of individuals occurring in all samples of that environment. Onlyspecies that show statistical significance are presented.

mollusks will most likely be found in a particular environment. Of the thirty-five major mollusk species tested from both fragmented and complete fractions, eighteen showed no statistical significance in the mean number of individuals among the salinity environments. I did not include these in the graphical representation of data.

The sedimentary data were not included in this analysis as there were no differences in the grain sizes among the tested samples. Also, the calcium carbonate and organic material content of the sediment showed no statistical relationship to the distribution of mollusks.

DISCUSSION

In accordance with Parkinson (1987), I found that salinity is a primary factor acting on the distribution of mollusk species throughout the Rookery Bay estuary. The riverine environment can be characterized by a high relative concentration of complete and fragmented individuals of the species *A. auberiana* and fragmented individuals of *M. leucophaeta*. *T. tampaensis* (complete) and *C. floridana* (fragmented) also contribute to the mollusk assemblage of the riverine salinity environment. This environment is also characterized by a significantly lower diversity of fragmented individuals than the other environments. The low relative salinity concentration and the low-energy system that prevail in this environment are most likely the

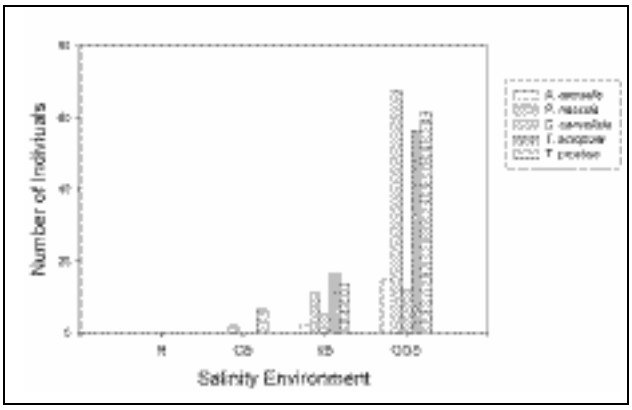

Figure 3: Shows the distribution of mollusk species (fragmented individuals) over four salinity environments. The values represented are the mean number of individuals occurring in all samples of that environment. Only species that show statistical significance are presented.

cause of this difference in diversity (Barnes 1989) and fragmentation. The chain of bays environment is characterized by a high relative concentration of complete individuals of *T. tampaensis*. Likewise, a high relative concentration of *C. floridana* can be a descriptor of the inter-island bay environment. The open-ocean environment has greater concentrations of *A. aequalis, P. nassula, C. cancellata, T. acropora, T. proxima, N. acuta, C. caribeae, T. divisus, and T. similis* than any of the other environments. This assemblage can be said to characterize the open-ocean

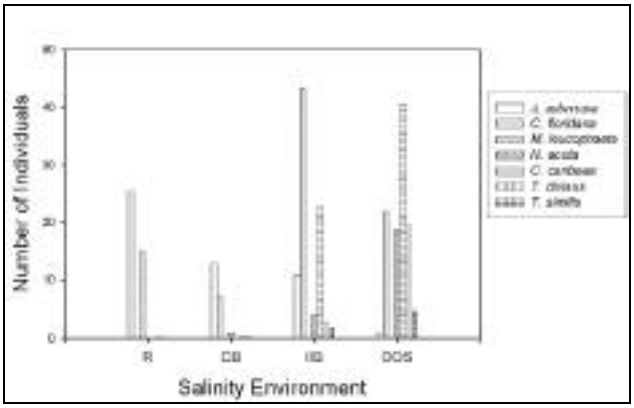

Figure 4: Shows the distribution of mollusk species (fragmented individuals) over four salinity environments. This graph is similar to graph 3 and shows the distributions of the other five statistically significant species of the fragmented fraction of shells.

salinity environment.

Davies (1972) showed that mollusk species live along a physical environmental gradient as an effect of environmental stress. This study has used one of those environmental stresses, salinity, and determined the preferred habitats of a number of mollusk species. Those mollusks that are constrained to a very narrow saline environment can be used as indicator species for that environment. The results of this study have provided a number of examples of such indicator species. The indicator species from the fragmented fraction demonstrate the highest preservation potential as many of these species maintain high population numbers in high energy environments. These indicator species as complete individuals would be preferred for use in characterizing modern and paleo-environments because they are the most likely to be preserved in large quantities.

The major limitation of this study originated in the low number of sample replications from each environment. Because of the lack of replication, the number of individuals of many species is too low to statistically analyze. An increase in the number of replicates would also allow for more generalized conclusions about particular environments than can be made from this study. Ordination, a type of multivariate analysis, is the optimal analysis for a study of this kind as it has been generally used for similar ecological studies as this. The nonparametric analysis that I performed leads to a greater degree of inference as to what assemblage is characteristic of an environment than would be preferred.

Also two of the four environments had only one mollusk species that could be used to characterize them. An effective index should include many more indicator species.

This study served as a preliminary investigation into the feasibility of environmental characterization by mollusk assemblage. I would suggest that future studies perform many more replications in many more environments and sub-environments. Also these studies should employ ordination to analyze those data that are collected. I believe that such a study would result in an effective and thorough index for the identification of paleo-environments and current environmental health.

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