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**GULF OF CALIFORNIA PLEISTOCENE AND MODERN
MOLLUSCAN COMPARISON AS A TEST FOR GLOBAL CHANGE**

**A Thesis Presented to the Faculty of
San José State University
through
Moss Landing Marine Laboratories**

**In Partial Fulfillment
of the Requirements for the Degree
Masters of Science in Marine Sciences**

**By
Carlos E. Cintra-Buenrostro**

December 2000

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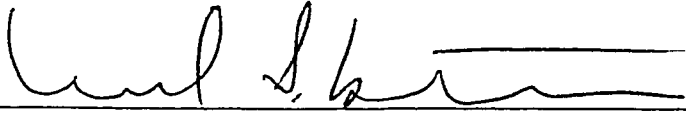
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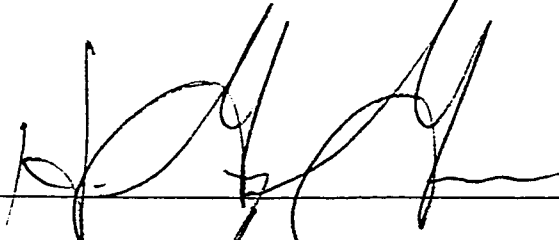
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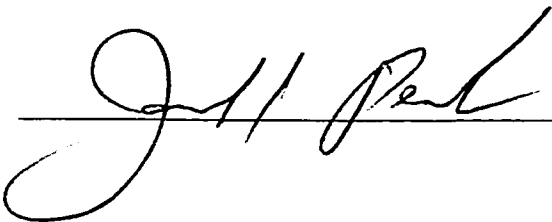


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ABSTRACT

GULF OF CALIFORNIA PLEISTOCENE AND MODERN MOLLUSCAN COMPARISON AS A TEST FOR GLOBAL CHANGE

by Carlos E. Cintra Buenrostro

Marine assemblages experienced distinct temporal changes related to climate and sea level changes during the past several hundred thousand years. To evaluate the potential effects of these changes on marine mollusc richness and similarity, modern assemblages associated with rhodolith beds in the Gulf of California were compared to their fossil counterparts that experienced higher temperature (~ 3° C) and sea level (~ 6 m), approximately 125,000 years ago. A combined total of 219 taxa were found in fossil (F) and modern (M) assemblages. In general, richness was significantly greater in F than in M, and differences between assemblages suggest F is a time-averaged deposit. Variation in similarity between F versus M was greater than that within F, which may be a strong indication of change in assemblage taxonomic composition. The results suggest the mollusc assemblage changed over time, but the amount of change is difficult to quantify due to time-averaging.

Although the fossil record cannot be used routinely to study details of population and assemblage interactions and dynamics, it can reveal patterns of association and change in assemblage composition over time scales that are beyond the reach of neontology, and to which modern patterns cannot necessarily be extrapolated.

Valentine and Jablonski (1993).

To my wonderful country, my loved and missed México

To my nieces Natasha V. and A. Michelle

For the one always present in my heart (ACL, I'm deeply sorry!)

**Buscando en el vacío me encuentre con la materia.
A través del andar he ido conociéndola,
sabiendo muy poco de ella,
preguntando y urgando entre los que dicen haberla estudiado
y todo esto me ha llevado a innumerables viajes;
en los que me tope a la ignorancia
mala consejera pero dadivosa de mañas y malos hábitos,
a la que considere amiga por momentos,
pero defraudome y causome sentir
esta realidad de no saber nada.**

**There's a dreamer
Who wishes to solve his problems,
but feels lonely even beside his girlfriend,
one of his greatest supports during those times,
and life is running
to introduce him into marine sciences
because he wants to learn sea mysteries and life,
which takes him away from his family and friends
something hard to do,
especially in a strange country,
but he is trying his best
just to be the person he always dreamed.**

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1. Introduction

The effects of global climate change on assemblages of marine organisms are, at present, difficult to predict, but good predictions are imperative since food resources from the sea are difficult to replace and the fisheries industry employs and supports directly and indirectly a large proportion of the human population (Fields et al., 1993). How might present environmental change affect modern assemblages? A logical approach to this question is to look at the geologic past (Burke et al., 1990). By using the fossil record, we can begin to test whether assemblages are constant or ephemeral through time and to relate the degree of assemblage persistence to global environmental change. This has, for example, been done with coral reefs whose fossil records are comparatively good (Pandolfi, 1996; Pandolfi and Minchin, 1995).

The Gulf of California is a region of high diversity of Pleistocene and recent benthic faunas of the Tropical Panamian Province (Valentine, 1961). Prominent formations of Pleistocene fossil bearing marine sediments (formed during the sea level high stand of oxygen isotope substage 5e, *I.S.* 5e, ~125,000 years old; Aharon, (1983) are common and well preserved along the coast. These fossil rich deposits, commonly called shell beds, contain high concentrations of invertebrate bioclastic material representing community, storm, beach berm, tidal channel or current/wave-winnowed beds (Meldahl, 1993). The recency of *I.S.* 5e is especially relevant for evaluating global climate change questions because the geologic record of the earth's most recent past has better time resolution than earlier geological periods, contains extant faunas, and is the closest to present conditions (Burke *et al.*, 1990). Moreover, subtropical and tropical ecosystems

appear to have suffered disproportionately high levels of extinction during past environmental changes (Jablonski, 1989), and may thus be particularly sensitive to climate change. The comparison of fossil and modern faunas in these regions is the primary focus of many global change studies (Wilson, 1992).

Knowledge of the recent geological history of living reefs is essential to interpret their long-term assemblage dynamics (Jackson, 1992). The contribution of rhodoliths, unattached nongeniculate coralline algae, to sediments and fossil assemblages is increasingly being assessed by geologists and used to establish paleoenvironmental conditions (Bosence, 1983; Johnson and Hayes, 1993). Rhodolith-forming algae can be the most important carbonate producers in shallow subtropical/temperate waters (Foster et al., 1997), and can record and preserve information on depth, geography, temperature and prevailing hydraulic energy (Bosence, 1983). The worldwide distribution of modern and fossil rhodolith assemblages gives them an advantage over geographically limited coral reefs as environmental indicators. A fossil rhodolith bed is thus a potential record of paleontologic and stratigraphic information that can be compared to a modern bed. The abundance of modern rhodolith beds and the occurrence of widespread, well preserved Pleistocene rhodolith assemblages in the southern Gulf of California have only recently been recognized (Steller and Foster, 1995; Foster et al., 1997) and suggests such comparative studies in this region would be particularly fruitful.

The Quaternary was a period of major environmental changes, possibly greater than at any other time in the last 60 million years (Bradley, 1985). It is now accepted that sea level has risen ~100 m between 18,000 and 6,000 years ago (during the Holocene

transgression) (Kennett, 1982; Bradley, 1985), after which time sea level has remained close to that of the present day. By 5,000 years ago, sea level was within 5 m of its present level. During *I.S. 5e* sea level was 6 m above the present level (Kennett, 1982). Mollusc data indicate that water temperatures along the western coast of North America were significantly cooler during the Last Glacial Maximum (~18,000 years), and that biogeographic regimes moved south as a result (Fields et al., 1993). In contrast Pleistocene marine assemblages in California, the Gulf of California and the central Pacific experienced warmer climatic conditions (~2 – 3° C) and higher sea level (~5 – 10 m) during *I.S. 5e* (~125,000 years ago) (Ortlieb, 1987; Valentine, 1989; Paulay, 1991). Subsequent warming caused a northward shift in species ranges and additional warming cause these ranges to shift further (Wise and Schopf, 1981; Davis, 1986; Valentine, 1989; Fields et al., 1993; Valentine and Jablonski, 1993; Di Michelle, 1994; Enquist et al., 1995). Thus, the differences between *I.S. 5e* and modern assemblages can indicate changes that may occur as a result of future global warming, as well as how did the assemblages persisted (or changed) since 125,000 years ago. Predicting assemblage response to global climatic warming, however, becomes particularly difficult as the forecasted temperature increase exceeds that of any period of the last 120,000 years. The paleoecological record reveals that non-analog assemblages and our ability to predict assemblage response to climate change diminishes as climate parameters move beyond the boundaries of existing climates. Future climates may lie outside not only the existing climate domain, but also outside our paleoclimate database and outside the climate to which existing species are evolutionarily adapted (Graham and Grimm, 1990).

Molluscs are the most conspicuous fauna inhabiting rhodolith beds in the southwestern Gulf of California (Steller, 1993; Foster et al., 1997; pers. observ.), and qualitative observations suggest that modern-Pleistocene species correspondence is high in the region. A perfect correspondence is unlikely. A critical question is: do observed differences reflect real differences in assemblage structure, or other effects (geographic, taphonomic, etc.)? If the former, predictions about global climatic change effects can be made (assuming the predicted change is within the range of past change). If not, the question is: what are these other effects, and can they be eliminated to determine real differences in assemblage structure? For example, differences between modern and Pleistocene assemblages may indicate the vagaries of fossil preservation. If a species is present in the modern fauna but absent in the Pleistocene fauna, this may reflect ecological differences (modern species could not tolerate Pleistocene conditions in that area) or preservation failure (the species was present in the assemblage but was not preserved). If differences reflect effects other than environmental change, then at least the faunal composition in each formation can be characterized, extending the time frame of observations on species and assemblage behaviors in the Gulf.

In this study, modern and Pleistocene (*I.S. 5e*) molluscan marine assemblages associated with rhodolith beds in the southwestern Gulf of California at Punta Chivato and Punta Galeras-Canal de San Lorenzo, B.C.S., México (Fig. 1) were compared. Molluscs were selected because nearly all of the marine mollusc species that presently occur along the Pacific coast of North America also occur virtually unchanged in Pleistocene deposits in the same region (Valentine, 1989; Kidwell and Bosence, 1991).

Thus, it's appropriate to use Pleistocene samples as an approach to test how future global climate change might affect molluscan assemblages associated with rhodolith beds in the southwestern Gulf of California. Also, both modern and Pleistocene molluscs are well studied in the Gulf (Keen, 1971; Brusca, 1980; Bernard et al., 1991; Meldahl, 1993; Meldahl and Cutler, 1992; Meldahl et al., 1997), are generally well preserved (Kidwell and Bosence, 1991; Kidwell and Flessa, 1995; Libbey and Johnson, 1997) and most studies that compare modern, death and fossil assemblages focus on this group.

Differences between modern and Pleistocene mollusc assemblages were documented, a determination if these differences reflect real assemblage changes versus geographic or preservation effects was performed. To determine if the Pleistocene mollusc assemblage (bivalves and gastropods) represents a once living local assemblage (e.g. rhodolith bed) that persisted over geologic time or if it is an artifact of accumulation over time, three assemblage attributes were compared: 1) number of species (richness), 2) rarefied species richness, and 3) similarity between modern and Pleistocene assemblages.

This information was used to distinguish among the following models: Model I. Pleistocene deposits are representative of a once living assemblage in a rhodolith bed (a "snapshot" assemblage), Model II. Pleistocene deposits are time averaged rhodolith beds, Model III. Pleistocene deposits are an accumulation of molluscs from different habitats, Model IV. Pleistocene deposits are the result of a combination of the previous models, and Model V. Pleistocene deposits have lower values of the above assemblage attributes than modern assemblages due to preservation losses. If Model I is accepted, then modern-Pleistocene comparisons can be used to indicate how these assemblages

changed since the Pleistocene, and thus predict how they may change as a result of future global warming and sea level rise. However, Model II is probably valid based on the high concentration of shells and rhodoliths, high species richness, dominance of disarticulated shells not in life position and evidence of strong wave and current winnowing (e.g. coarse sediment grain sizes and cross-bedding) common characteristics of other Pleistocene time-averaged deposits (Staff et al., 1986; Fürsich and Aberhan, 1990; Kidwell, 1991; Kidwell and Bosence, 1991; Kidwell and Flessa, 1995).

Time-averaged fossil deposits, those in which many generations of individuals are preserved within one stratigraphic layer, may record and mix a wide variety of environmental conditions and ecological interactions (Flessa and Kowalewski, 1994). Removing time averaging effects is critical to the interpretation of the past histories of marine ecosystems (Staff et al., 1986; Fürsich and Aberhan, 1990; Kidwell and Bosence, 1991; Kidwell and Flessa, 1995; Pandolfi and Minchin, 1995). To test the null hypothesis that the Pleistocene samples are drawn from the same population but more time-averaged than modern samples, artificial time averaging was done by combining modern samples one by one to mimic time averaging. An additional taxa richness reduction to the lowest value observed (rarefaction analyses) was also used to test time averaging.

This approach also helped to determine if Pleistocene deposits reflect their ancient source assemblage and whether the molluscan assemblages persisted through geologic time. A fidelity (percent of modern species occurring as fossil in the same site) analysis was performed, indicating how much assemblage variation occurred since the *I.S. 5e*

Pleistocene. How environmental change affected mollusc assemblages may be determined if there was not much variation.

2. Materials and Methods

2.1 Study Areas

Modern rhodolith beds have been found in two main environment types: 1) gently sloping, subtidal soft bottoms with moderate wave action (wave beds; 2 to 12 m deep), and 2) relatively level bottoms in channels with tidal currents (current beds; below 12 m) (Foster et al., 1997). Pleistocene (*I.S.* 5e) and modern mollusc assemblages were sampled in two general areas in the Gulf of California. Modern beds were sampled as near as possible to the locations of Pleistocene beds.

One area was Punta Chivato and Bahía Concepción (Fig. 1). Punta Chivato is a small headland abutting directly into the open waters of the Gulf of California, and affected by seasonal shifting winds and high wave energy from the north, east and south (Libbey, 1995; Johnson, 1996; Libbey and Johnson, 1997; Johnson and Ledesma-Vázquez, 1999). Consequently, all of its shores rise abruptly out of the water. From the shoreline the land rises abruptly to elevations between 60 to 100 m (Johnson, 1996). Abundant carbonate debris accumulates along the shoreline, indicative of high nearshore productivity in shelled invertebrates and calcareous red algae (Ortlieb, 1984). Carbonate shoreline deposits are important to this study as they are also present in the Pleistocene record, helping to establish a continuum between the past and present in the Punta Chivato area (Meldahl, 1993; Libbey and Johnson, 1997). Ortlieb (1984) interpreted a

succession of terraces at elevations of 15, 18, 25, 40, 50 and 75 m above sea level, the lowest two being Pleistocene (*I.S. 5e*). Many of the Pleistocene sections exposed in coastal arroyos at Punta Chivato are suggestive of the vertical stratification in modern current beds. The modern rhodolith bed in Punta Chivato (Fig. 1) does not correspond to any Foster et al. (1997) categories; its a “deep” (~12 m) subtidal bed apparently controlled by wind generated waves.

Modern rhodolith beds in Bahía Concepción were sampled to mimic time averaging by adding them individually to modern samples from Punta Chivato (see methods below). These beds correspond to Foster et al. (*op. cit.*) wave beds. They are shallow subtidal (<12 m) assemblages controlled by water motion and sedimentation (Steller and Foster, 1995). Mollusc assemblages among Bahía Concepción habitats are overlapping and gradational, with many species shared among habitats and high variability within habitats (Meldahl et al., 1997).

In the second area (Punta Galeras; Fig. 1), rhodolith beds occur in the San Lorenzo Channel (Schlanger and Johnson, 1969; Foster et al., 1997) an area of strong tidal currents between the islands and the coast (Roden, 1964; Marrack, 1999). These are “deep” (≥ 12 m) subtidal beds controlled by tidal currents (Foster et al., *op. cit.*). Van Andel (1964) described the nearshore sediments as calcarenite shelf facies characterized by coarse, fairly well-sorted calcarenite sand containing a variety of skeletal debris, and Schlanger and Johnson (1969) recognized distinct fossil depositional facies, some of which were characterized by the presence of abundant rhodoliths. The approximately 1 m thick Pleistocene (*I.S. 5e*; Sirkin *et al.*, 1984) deposit exposed along the shoreline at

Punta Galeras (Fig. 1) is a matrix of intact rhodoliths, molluscs and cobbles and may be representative of the modern beds in this wave exposed area (Foster et al., 1997; K. Meldahl pers comm.).

2.2 Methods

2.2.1 Sampling and identification

The mollusc assemblages in Pleistocene and modern rhodolith beds were sampled in both areas. At Punta Chivato (PC), Bahía Concepción (BC) and Canal de San Lorenzo (CSL) (Fig. 1) modern beds were sampled with SCUBA during four field trips (one in March 1997, two in June 1997 and one in March 1999). At PC and CSL ten random samples were collected at minimum 50 m from each other using a steel cylinder with a saw-like edge buried into the substratum. Material within the encircled area was collected to ~20 cm deep and sieved underwater through a 1 cm mesh screen. At BC, each sample was from one of the beds described in Steller and Foster (1995). A sample was obtained by combining 3 to 4 subsamples collected along the 3 to 12 m depth gradient in each bed. For all samples, the total volume sieved was ~200,000 cm³. Sample volumes after sieving was ~20,000 cm³.

Exposed strata of Pleistocene rhodolith deposits at PC and Punta Galeras (Fig. 1) were sampled systematically by choosing areas with high abundance of preserved rhodolith material and molluscs. The Pleistocene sediments were easily disaggregated, and thus could be bulk-sampled like the modern samples. During June 1997, ten samples were collected at each location and sieved through a 1 cm mesh screen. For all samples,

the total volume sieved was ~50,000 cm³. Sample volumes after sieving were ~10,000 cm³. The difference in sieved volume between the modern and Pleistocene samples was due to low abundance of material in the former. Standardization of units (e.g. individuals/cm³) was not appropriate given the composition of samples and variation in total sieved volumes.

Molluscs were sorted and identified to the lowest taxonomic level possible using Durham (1950), Keen (1971) and Skoglund (1991, 1992). Scallops (Pectinidae) and limpets (Archaeogastropoda) were excluded from the analyses because the key features for identification (auricles and internal shelf, respectively) were not preserved in the majority of the fossilized individuals. The abundance of each species beak or apex was recorded for each sample. All clam valves were counted and divided by two to represent bivalves (all data in Appendix 1).

2.2.2 Analyses

Species richness, rarefied richness and similarity were compared between the modern and Pleistocene data sets. The analyses (similarity, raw and rarefied richness) were performed at the taxonomic levels of all taxa (meaning all taxonomic categories identified to their lowest level) and genus, and their trends compared.

Several lines of evidence (e.g. rarefaction of replicate live samples and maximum individual longevity in an assemblage) suggest that several sampling decades in coastal subtidal settings are necessary to improve the sampling of ephemeral and otherwise sparse species to match time averaging (Kidwell and Flessa, 1995). Sampling over such

an extended period was not possible. Instead, to test for time averaging in Pleistocene rhodolith deposits, samples from the ten modern rhodolith beds in Bahía Concepción (BC) were used. Since within habitat assemblages sum within habitat perturbations in assemblage state or physical environment (Kidwell and Bosence, 1991), using samples from additional modern rhodolith beds in different habitats may compensate for the lack of time replication. Time averaging was tested by adding one by one each of the ten modern samples from BC to PC modern bed samples, to mimic shell accumulation through time. To achieve a total of 10 modern samples combined, modern samples were added in two different ways: 1) by randomly selecting a sample from each locality and 2) by adding each BC to PC samples in the numerical order in which they were collected (Appendix 1). Both approaches gave similar results and the second procedure is presented in the results section. This allowed a test for time averaging (Model II) in the Pleistocene beds. The assumption of statistical independence was violated in mimicking time averaging because individual sample values were used more than once. Therefore in this case, analyses on raw number and rarefied richness were done using only descriptive statistics (e.g. mean and standard error).

A major effect of time averaging is to increase taxonomic richness in an assemblage (Kidwell and Bosence, 1991; Flessa, 1993). Rarefaction analyses were performed to correct for differences in raw richness. Rarefaction is a statistical method for estimating the number of species expected in a random sample of individuals (Rozenzweig, 1997). A reduction of taxa number to the lowest expected number observed among a group of samples could remove the effect of taxa accumulating

through time, providing an alternative to test for time averaging (Model II). Rarefaction should remove the effects of time averaging on richness in the Pleistocene beds. If it does not, the differences between modern and Pleistocene may still be due to time averaging, but may also reflect other effects (e.g. habitat averaging or Pleistocene deposits naturally richer than modern beds). If no significant differences are detected between Pleistocene and modern samples, time averaging effects may have been removed by the analyses. Alternatively, if significant differences remain, but modern sample richness overlap more Pleistocene values than those for raw richness numbers rarefaction suggests time averaging in Pleistocene deposits. Rarefaction is independent of species names, but assemblages to be compared by rarefaction should be taxonomically similar (Krebs, 1999). Therefore, after analyzing the total molluscan assemblages in each area, the faunas were split into bivalves and gastropods, each analyzed separately, and their trends compared with analyses at the Phylum level.

A two-sample t-test, $\alpha = 0.05$ (testing each area separately, e.g. Punta Chivato modern bed versus Pleistocene bed, Punta Galeras modern bed versus Pleistocene bed, etc.) was used to determine if raw and rarefied richness were different between modern and Pleistocene beds. Any necessary data transformations are given in the results. Several desired numbers of individuals are required by the rarefaction analysis. In this study 25 categories were used (2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 400 and 500) however, only results for the first 10 categories were obtained. Because rarefaction yielded several expected numbers of species for each sample, each expected number was used in the statistical analyses (two-

sample t-tests). Just one rarefied species expected number is presented, it was selected based on confidence intervals and precision estimates (standard errors, SE). Normal distributions are very infrequent in death assemblages from bay environments (Cummins et al., 1986a) so non-normality was expected in Pleistocene deposits. Kolmogorov-Smirnov tests were used to check normality (Zar, 1996; Sokal and Rohlf, 1997). Non-normality was common (either with or without transformed data), but two sample t-tests were still used with non-transformed data because such tests are robust to violations of this assumption (Underwood, 1997).

Taxonomic composition among rhodolith bed samples (modern and Pleistocene) was compared using species presence-absence data. While coarser than relative abundance, presence-absence is likely more robust because of factors that could alter relative abundance in either the modern or the Pleistocene (e.g. selective harvesting of commercial species from the modern beds, or selective preservation in the Pleistocene beds) (Mc Donald, 1976; Fürsich and Aberhan, 1990).

Time averaging and Pleistocene-modern assemblage differences were examined using similarity. Results using Punta Chivato data from all the available indices in Kenney and Krebs (1998) were compared to determine which performs best based on estimated precision (Appendix 2). The values from each analysis were statistically tested under the null hypothesis of no differences in assemblage similarity between Pleistocene and modern samples, and within the Pleistocene samples. If similarities among Pleistocene samples were less than similarities between Pleistocene and modern samples, this would suggest high Pleistocene sample variation, implying that Pleistocene-modern

samples should not be compared. Similarity analyses, in combination with rarefaction analyses, is also used to test if time or habitat averaging effects were removed. If similarities within Pleistocene samples and between Pleistocene and modern samples are not significantly different, then averaging effects (time or habitat) may not be large (supporting Model I) and the Pleistocene deposit may be used to evaluate future global climate change effects.

Similarity analyses were performed using ANOSIM at $\alpha = 0.05$ (Primer.4 program, Plymouth Marine Laboratory, 1997) under the null hypothesis (H_0) of no difference in similarities within Pleistocene samples and between Pleistocene and modern samples. The ANOSIM coefficient R is ~ 0 if the H_0 is true (Clarke and Warwick, 1994). Sample interdependence can be a problem in similarity analyses because individual sample values are used more than once. This problem may be compensated for by randomization techniques (Sokal and Röhlf, 1997), and ANOSIM performs such a procedure compensating for interdependence (R. Clarke, Plymouth Marine Laboratories, pers. comm.).

Because habitat averaging may have an influence on Pleistocene deposits (Model III), a literature search was used to determine where the “exclusive” Pleistocene taxa normally occur. Distributional and habitat information was obtained from the taxonomic references above and other published records (Oldroyd, 1924; Olsson, 1961; Wara and Wright, 1964; Carpenter, 1967; Radwin and D’Attilio, 1976; Santos-Galindo, 1977; Houbrick, 1978; Mc. Lean, 1978; Bernard, 1983; Kaiser, 1997). To further test for Model III, analyses were also done only at the species level, excluding taxa only found in

the Pleistocene deposits. Analyses were performed assuming that even if some species common in both times occurred intertidally, all could be present in a Pleistocene rhodolith bed at the time of deposition.

3. Results

3.1 Composition of taxa

3.1.1 Lowest identified taxonomic level

A total of 30,433 shells were found, yielding 219 mollusc taxa in the modern and Pleistocene beds combined (Appendix 1 and 3), representing 101 and 118 “species”, 59 and 63 “genera”, 27 and 31 families, 8 and 4 orders of bivalves and gastropods, respectively. Twenty seven clam and 39 snail taxa could not be identified to species level (Appendix 3), either because of damage or lack of appropriate identification within Pleistocene taxa. Two bivalve and 3 gastropod generic identifications were doubtful due to erosion or encrustations. Of the 101 bivalve taxa, 2 were undetermined, and of gastropods, 6 out of 118 were undetermined (Appendix 3).

Geographically, there were 172 taxa in the Punta Chivato area (PC), increasing to 189 when Bahía Concepción (BC) was included. Punta Galeras-Canal de San Lorenzo (PG from here on) richness was 148. By class, PC had 84 bivalve (B) and 88 gastropod (G) taxa, PC + BC had 92 B and 97 G, and PG had 66 B and 82 G taxa.

Overall, 16.4 % of total taxa were found only in the modern and 35.2 % found only in the Pleistocene samples. Thus, 36 of the modern taxa were not found as fossils, and 77 of the Pleistocene taxa were not represented in modern populations. Omitting BC

samples, 24 modern taxa were not found as fossils, and 101 Pleistocene taxa were not found in modern beds. “Exclusiveness” was geographically distributed as 41 taxa for PC (14 B and 27 G), 18 for PC + BC (17 B and 1 G), and 30 for PG (9 B and 21 G).

Among the 101 total clams, 22 of the modern taxa were not found as fossils, and 16 of the Pleistocene taxa were not represented in modern population samples. If samples from BC are omitted, the figures are 18 and 34 for modern and Pleistocene taxa, respectively. Among the 118 snails, 14 of the modern taxa were not found as fossils, and 61 of the Pleistocene taxa were not represented in modern populations. Without BC, this became 6 modern and 67 Pleistocene taxa.

3.1.2 Genus level

Geographically, there were 104 total genera in PC samples (increasing to 115 when BC was included), and 100 genera in PG samples. Composition by class was PC = 52 and 52, PC + BC = 57 and 58, and PG = 44 and 56 B and G taxa, respectively.

Overall, 15.2 % of total genera were found only in the modern and 27.3 % only in the Pleistocene samples. Thus, 20 of the modern genera were not found as fossils, and 36 of the Pleistocene genera were not represented in modern populations. Excluding samples from BC there were 13 and 49 for modern and Pleistocene taxa, respectively.

“Exclusiveness” was geographically distributed as 12 genera for PC (5 B and 7 G), PC + BC had 12 (11 B and 1 G), while PG had 17 (5 B and 12 G).

On average, taxa richness versus sample size in each locality leveled off around 6 samples suggesting a very robust estimation of richness in the present study ($n = 10$ / area / time).

3.2 Numerical analyses

3.2.1 Lowest identified taxonomic level

Based on total taxa, Pleistocene samples were richer than modern ones. Segregation by class yielded a greater number of bivalve taxa in modern rhodolith beds, while gastropods were richer in the Pleistocene beds (Table I). Averaged taxonomic richness was greater in the more northern PC area (Table D). To achieve homoscedasticity, total (T) and B richness within the PC samples from both times were square root transformed for statistical analyses. Taxa richness was significantly higher in the Pleistocene for all taxonomic levels (two sample t-tests $_{0.05 (18)}$: $t = 7.6$, $P < 10^{-7}$; $t = 5.93$, $P < 10^{-6}$; $t = 7.59$, $P < 10^{-7}$ for T, B and G taxa, respectively). No transformation was necessary for PG samples, and taxa richness at all taxonomic levels was also significantly higher in the Pleistocene (two sample t-tests $_{0.05 (18)}$: $t = 7.03$, $P < 10^{-7}$; $t = 7.6$, $P < 10^{-6}$; $t = 5.63$, $P < 10^{-5}$ for T, B and G, respectively).

Expected number of individuals varied among rarefaction analyses, as explained in methods, one was selected based on its performance (confidence intervals after statistical tests). Selected expected number of individuals from rarefaction analyses were 35, 45 and 45 for T, B and G, respectively. Taxa richness of PC Pleistocene samples remained significantly higher than modern beds at all taxonomic levels (two sample t-test

$0.05_{(18)}$: $t = 3.7$, $P < 10^{-4}$; $t = 3.3$, $P = 0.002$ and $t = 6.4$, $P < 10^{-6}$ for T, B and G, respectively). Although differences were highly significant, the number of modern samples overlapping Pleistocene sample within taxa richness (raw versus rarefied, respectively) ranges between Pleistocene and modern samples increased from 0 to 4 for T, 3 to 4 for B and G did not change.

Rarefied taxa richness of Pleistocene versus modern samples from PG was not significantly different when expected number of individuals was 20 for T (two sample t-test $0.05_{(18)} = -1.1$, $P = 0.14$). Bivalve rarefied richness was significantly higher in Pleistocene samples when the expected number of individuals was 15 (two sample t-test $0.05_{(18)} = -2.9$, $P = 0.005$). Gastropod rarefied richness within PG samples was not homoscedastic and square root transformation did not make it so. The statistical test was, however, performed assuming robustness. Pleistocene sample richness was significantly higher when expected number of individuals was 45 (two sample t-test $0.05_{(18)} = 3.2$, $P = 0.002$). Although significant differences were detected at the class level, in general the number of modern samples overlapping Pleistocene samples within richness (raw versus rarefied, respectively) ranges between Pleistocene and modern samples increased from 2 to 5 for B and from 1 to 2 for G.

When modern PC samples were combined with modern BC samples to test for differences in total richness between Pleistocene and modern samples, statistical testing was not possible due to lack of independence. Descriptive statistics and trends suggest total taxa were not different after combining the first 4 samples from BC with modern PC samples. Further additions of BC samples yielded differences related to the bivalve fauna

(Fig. 2a). As more BC samples were added, the number of bivalve modern taxa exceeded the Pleistocene, while gastropod taxa richness remained relatively constant until the last four samples were added (Fig. 2a). Results for total rarefied taxa were similar (Fig. 2b). Rarefaction comparisons are presented with a fixed (35) and variable expected number of individuals based on their two sample t-test precision estimates (see above) and when considering individually the more robust expected numbers, respectively. Given the results and the test performance (graphic outcome), it is recommended to use only the fixed number in future analyses as the expected trends won't be detected with the variable expected number of individuals.

Similarity within Pleistocene samples at PC was significantly higher than similarity between Pleistocene and modern samples (ANOSIM test $R = 0.86$, $R = 0.78$, $R = 0.68$ for T, B and G, respectively with $P = 0.001$ in all cases). The same results and P values were obtained for PG (ANOSIM test $R = 0.92$, $R = 0.8$, $R = 0.92$ for T, B and G, respectively). When combined samples were used to mimic time averaging the differences remained and became slightly larger as BC samples were added to modern PC samples (Table II).

3.2.2 Genus level

Overall, Pleistocene samples were richer than modern ones (Table III). Fossil PC average taxa richness was higher than PG richness (Table III). Generic richness in PC Pleistocene samples was significantly higher (two sample t-test $_{0.05(18)}$: $t = 6.92$, $P < 10^{-7}$; $t = 5.23$, $P < 10^{-5}$; $t = 7.79$, $P < 10^{-7}$ for T, B and G taxa, respectively). To achieve

homoscedasticity, square root transformation was necessary for bivalves in PG samples. Generic richness between Pleistocene and modern samples in this region was also significantly higher in the Pleistocene at all taxonomic levels (two sample t-test $_{0.05 (18)}$: $t = 6$, $P < 10^{-6}$; $t = 4.45$, $P < 10^{-4}$; $t = 5.36$, $P < 10^{-5}$ for T, B and G, respectively).

Expected number of individuals varied among rarefaction analyses, as explained in methods, one was selected based on its performance (confidence intervals after statistical tests). Selected values were 30, 45 and 45 for T, B and G, respectively. Generic rarefied richness between Pleistocene and modern samples in PC was still significantly higher in Pleistocene samples at all taxonomic levels (two sample t-test $_{0.05 (18)}$: $t = 3.1$, $P = 0.003$; $t = 2.1$, $P = 0.02$ and $t = 5.1$, $P < 10^{-5}$ for T, B and G, respectively). Although significant differences were detected, in general the number of modern samples overlapping Pleistocene samples within richness (raw versus rarefied, respectively) ranges between Pleistocene and modern samples increased from 1 to 5 for T, 4 to 5 for B and 1 to 2 for G.

Rarefied genera richness of Pleistocene versus modern samples from PG was not significantly different when expected number of individuals was 20 for T (two sample t-test $_{0.05 (18)} = -1.4$, $P = 0.09$). Bivalve rarefied richness was significantly higher in Pleistocene samples when the expected number of individuals was 15 (two sample t-test $_{0.05 (18)} = -3.3$, $P = 0.002$). Gastropod rarefied richness within PG samples was not homoscedastic and square root transformation did not make it so. The statistical test was, however, performed assuming robustness. Pleistocene sample richness was significantly higher when expected number of individuals was 15 (two sample t-test $_{0.05 (18)} = -3.3$, $P =$

0.002). Although significant differences were detected at the class level, in general the number of modern samples overlapping Pleistocene samples within richness (raw versus rarefied, respectively) ranges between Pleistocene and modern samples increased from 4 to 6 for B and did not change for G.

In summary, all statistical analyses (all taxa and generic level) in PC showed greater molluscan richness (raw and rarefied) in the Pleistocene deposits. On the other hand, PG did not show significant differences in total richness (all taxa or generic), but analyses at the class level yielded significantly richer fauna (all taxa and generic) in the Pleistocene.

Similarity within Pleistocene samples at both areas (PC and PG) was significantly higher than similarity between Pleistocene and modern samples (ANOSIM test $R = 0.82$, $P = 0.001$ for both). When taxa were segregated into class the differences remained (ANOSIM test $R = 0.77$ and 0.58 for B and G, respectively in PC, and $R = 0.71$ and 0.77 for B and G in PG, all at the same P value = 0.001). Because this generic approach was used only to compare trends between the lowest taxonomic level identified and genus, the fauna was not analyzed using combined modern (M) PC with MBC samples.

3.3 Distribution analyses

To evaluate time and habitat averaging within Pleistocene samples, the distribution of taxa found only in these samples was evaluated. Of the 77 Pleistocene taxa not found in modern samples, 16 were bivalves (a total of 48 shells), and 61 were

gastropods (726 shells). The difference may be related to better preservation of the stronger snail shells.

Five clam taxa were damaged and could not be identified to species. Two species, *Mactra* sp. cf. *isthmica* and *Trachycardium panamense*, have not previously been recorded in the recent shell fauna within the Gulf of California. *Mactra* sp. cf. *isthmica* has not been reported in the Pleistocene, but the record must await certain species identification. Of the 10 species with information on bathymetric distribution, all occur within the sampled depth. Six of these also occur in the intertidal zone, and none have been associated with calcareous algal environments (Table IV).

Distribution analyses of Pleistocene “exclusive” taxa indicates that modern and Pleistocene environments are highly comparable. Information was found on the bathymetric distribution of 15 of the snail species; all but one (*Tegula funebris*) occurs within the sampled depth. Sixteen of the 33 species also occurred in the intertidal zone and only *Persicula imbricata* has been associated with calcareous algae rubble (Table V). Twenty eight snail taxa were not identified to species level due to damage or encrustations. Distribution analyses of the 33 remaining taxa indicated 4 species (*P. imbricata*, *Splendrillia* sp. cf. *arga*, *Tegula funebris* and *Terebra hancocki*) that have not been previously recorded for the Gulf. Again, this first record of *S. sp. cf. arga* must be considered tentative. The remaining 3 species were found only in the Pleistocene, and are the first known records in the Gulf.

These distributional data indicate the Pleistocene deposits contain taxa not now associated with rhodolith beds. The abundance of “alien” taxa was negligible (~2.4 % of

the total individuals), but their contribution to taxonomic composition was substantial (~35.2 %), and thus affected the analyses conducted on presence-absence data. To test for “alien” effects additional analyses were done only at the species level, excluding all “exclusive” Pleistocene taxa to remove possible habitat averaging effects. Overall, Pleistocene samples remained richer than modern ones but differences were not as large as in previous analyses. Segregation by class yielded similar results: bivalve taxa richness was higher in modern rhodolith beds, but now gastropods were not richer than bivalves in the Pleistocene beds (compare Table I versus VI). Average taxa richness was greater in PC than in PG (Table VI). Pleistocene samples were also significantly richer than modern in PC at all taxonomic levels (two sample t-test_{0.05 (18)}: $t = 6.5$, $P < 10^{-6}$; $t = 5.25$, $P < 10^{-5}$; $t = 7.1$, $P < 10^{-7}$ for T, B and G taxa, respectively). Punta Galeras richness showed similar results (two sample t-test_{0.05 (18)}: $t = 5.33$, $P < 10^{-5}$; $t = 5.55$, $P < 10^{-5}$; $t = 3.62$, $P < 10^{-4}$ for T, B and G, respectively).

Rarefaction analyses were done after removing “exclusive” Pleistocene species. Again, rarefied richness in PC Pleistocene samples was higher than in modern samples (two sample t-test_{0.05 (18)}: $t = 2.67$, $P = 0.008$; $t = 2.71$, $P = 0.007$ and $t = 3.63$, $P < 10^{-4}$ for T, B and G, respectively) when expected number of individuals were 25, 45 and 25 for T, B and G, respectively. The number of modern samples overlapping Pleistocene samples within richness (raw versus rarefied, respectively) ranges between Pleistocene and modern samples also increased from 1 to 6 for T, 4 to 5 for B and 1 to 3 for G.

Pleistocene Punta Galeras T rarefied taxa richness without “exclusive” Pleistocene species became significantly higher than modern (two sample t-test_{0.05 (18)} = -

2.42, $P = 0.013$), expected number of individuals was 25. Bivalve rarefied richness remained significantly higher in the Pleistocene when expected number of B was 15 (two sample t-test $_{0.05(18)} = -3.09$, $P = 0.003$). A significantly higher Pleistocene rarefied G richness (heteroscedasticity and assumed test robustness) remained within PG when the expected number of individuals was 15 (two sample t-test $_{0.05(18)} = -1.09$, $P = 0.14$). Again, there were more modern samples overlapping Pleistocene samples within the compared richness (raw versus rarefied) T increased from 1 to 4 and B from 2 to 7.

Both (PC and PG) within Pleistocene similarities were significantly higher than between Pleistocene and modern samples (PC: ANOSIM test $R = 0.75$, $R = 0.75$, $R = 0.56$ for T, B and G, respectively with $P = 0.001$ in all cases. PG: ANOSIM test $R = 0.84$, $R = 0.75$, $R = 0.78$ for T, B and G, respectively with $P = 0.001$ for T and B, and $P = 0.002$ for G). Positive values of R indicate that similarities between Pleistocene and modern samples tend to be lower than similarities within the Pleistocene samples.

4. Discussion and conclusions

Raw taxa richness was greater in the Pleistocene deposits than in any modern bed (Table I, Fig. 2a). The richness of modern beds in Bahía Concepción was closest to a Pleistocene bed (Table I), suggesting that sampling additional modern rhodolith beds in a different geographic area can compensate for the lack of time replication when testing for time averaging effects. Greenstein and Curran (1997) reported a similar pattern for coral assemblages at Devils Point.

Mollusc richness (raw and rarefied) in modern and Pleistocene rhodolith beds was significantly different. If the differences are attributed to greater richness in the Pleistocene deposits expected global climatic change would have a positive effect on molluscan faunas associated with rhodolith beds in the southwestern Gulf of California. Alternatively, differences may be due to time averaging (Model II). The fact that taxonomic richness remained higher in the Pleistocene even after pooling of modern samples (MPC + MBC) further supports Model II. The absence of significant differences for total rarefied PG richness (specific or generic) indicates some time averaging bias can be removed with rarefaction analyses. However, it also suggests that the Pleistocene rhodolith beds had a richer molluscan fauna when sea level and water temperature were higher than today, again implying that future global climate change may not reduce the richness of this particular fauna in the Gulf. Given all environmental fluctuation in between the Pleistocene and modern deposits, the important question is how the molluscan taxa persisted or changed as a result of changes in sea level and water temperature? Most of the analyses (including rarefied richness) yielded significantly higher richness in Pleistocene samples, which supports a time averaged Pleistocene deposit. Furthermore, when “exclusive” Pleistocene species were removed to avoid possible habitat averaging the differences in fauna composition between Pleistocene and modern samples remained, supporting a time averaged hypothesis based on more modern samples with overlapping Pleistocene values within richness (raw and rarefied) ranges. Therefore, mollusc Pleistocene deposits associated with rhodolith beds in the southwestern Gulf of California can be considered as within habitat time averaged

assemblages *sensu* (Johnson, 1960). While reworking of fossils cannot conclusively be eliminated, it probably represents only a minor fraction of any Pleistocene sample.

Energy levels on the coast of Punta Chivato during the winter are, and probably were in the Pleistocene, affected by waves refracted around it (Johnson and Ledesma-Vázquez, 1999). The Pleistocene beds are sedimentologic concentrations as there are no nonbioclastic matrices, and the shells have undergone some transportation, behaving as sedimentary particles (Libbey, 1995). According to Meldahl (1993) large, robust and well-cemented corals tend to resist displacement and transport better than molluscs. Thus a greater proportion are preserved as autochthonous assemblage beds. Rhodolith beds act similarly, but most rhodoliths in the sampled Pleistocene material were preserved as small fragments. Corals were present (especially among Punta Galeras) and indicate little habitat transport. For total PG rarefied richness (all taxa and generic) time averaging bias was efficiently removed, could this be an effect of corals in Pleistocene samples reducing the amount of interhabitat transportation or an artifact of combining gastropod and bivalves? Because analyses at PC showed differences at all taxonomic levels (both classes and Phylum) the second option is unlikely. Thus, it is concluded that PG is probably a within habitat time averaged deposit, while PC may have experienced important out of habitat effects either by leakage or transportation.

Based on different shell presence (e.g. *Turbo fluctuosus*) Johnson (pers. comm.) suggests that the PC molluscan fauna in Pleistocene rhodolith beds may be intertidal. However, nowadays there is hardly any “intertidal” zone in the area. The relative frequencies of the number of specimens associated with different substrata is indicative

of the habitat type (Russell, 1991) and the bulk sampled material was associated with rhodolith beds (no living rhodoliths have been found intertidally in the Gulf), in a subtidal environment, as suggested by Libbey (1995). Even if *T. fluctuosus* are numerically more representative of an intertidal environment, they were also collected alive (Appendix 1) supporting the assumption of taxa presence from two different environments (intertidal and subtidal) used in habitat averaging analyses. Furthermore, many of the Pleistocene sections exposed in coastal arroyos at Punta Chivato are suggestive of the vertical stratification in modern current rhodolith beds. Based on species composition and results, it seems that the Pleistocene deposit in PC was more like Bahía Concepción modern rhodolith beds if the deposit is merely time averaged and not a mixture of Models II and III. The ~1m thick deposit exposed along the shore at Punta Galeras is a matrix of intact rhodoliths, clams and cobbles and may be representative of the modern beds in this wave exposed area (Foster et al., 1997). Unfortunately, due to time averaging bias this could not be precisely determined.

Overall, there were 36 modern (~16.4 %) and 77 Pleistocene (~35.2 %) taxa not shared, adding to > 50 % of all the taxa. When habitat averaging was removed, there was a reduction among positive values of the ANOSIM coefficients, indicating an increase in similarity between Pleistocene and modern samples and within Pleistocene assemblages at both localities. Differences in similarity can be the result of stochastic processes of dispersal and persistence, but this seems unlikely given suggested averaging (time and habitat) effects. Differences in similarity between Pleistocene and modern samples and within Pleistocene are attributed to the low amount of taxa overlap. Overall, PC data

show ~48 % taxa overlap, leaving around 52 % different, a much greater difference than when specific samples are compared (Table VII).

Taxa not identified to species level (Tables IV and V, Appendix 3) may have had an influence on the similarity results, but the generic analyses indicate this effect is not important. Furthermore, in a comparison of biotas from different ages it is useful to incorporate data from several levels in the taxonomic hierarchy in the same similarity coefficient (Briggs and Gall, 1990). Segregation by class also yielded the same results as the Phylum similarity analyses. As expected, a few variations in particular analyses were observed (e.g. P values varied an order of magnitude but remained appropriate when testing the null hypotheses). ANOSIM coefficients varied by as much as 15 % (gastropod analyses for PG), but P values were the same in all the analyses. Thus, to save time in future, similar mollusc comparisons in the studied areas and environments there is no need to segregate taxa into class components.

Positive values of ANOSIM coefficient (R) indicate that similarities between Pleistocene and modern samples tend to be lower than within the Pleistocene, suggesting that the taxonomic composition of the assemblages changed somehow between the Pleistocene and the modern. Four factors may influence the degree of taxonomic similarity: age, environment, taphonomy and recorded diversity (Briggs and Gall, 1990). While relative age may have an insignificant influence on the comparison between geologic times, the effect of environment may be pronounced. However, this was not the case because most of the Pleistocene species were found in modern beds and distributional analyses showed that both environments are highly comparable.

Taphonomic losses can clearly reduce the diversity of organisms preserved, but as the sampled Pleistocene deposits were richer than the modern assemblages, this is not the case for molluscs from the studied southwestern Gulf of California localities. Pleistocene beds were richer than their modern counterparts, primarily because of the lack of a variety of mollusc taxa in modern rhodolith beds. Finally, the results of this study suggest greater variability in the taxonomic composition of mollusc shell assemblages between the Pleistocene and modern samples than within Pleistocene rhodolith beds, a possible strong indication of assemblage change with time.

The Pleistocene samples were much richer in taxa, especially gastropods, suggesting that the Pleistocene samples are more time-averaged than the modern samples. Alternatively, Pleistocene rhodolith beds may have been naturally richer. Most of the 77 Pleistocene taxa not found in the modern populations (Tables IV and V, Appendix 3) are still extant based on Keen (1971). While not all taxa could be identified to species and some need confirmation, the lack of similarity cannot be attributed to extinction, even if this occurred in a few taxa. Local extinction could be possible since at least 35 % of the “exclusive” Pleistocene taxa are known to be economically important food resources in the Gulf of California and have been exploited constantly for a considerable period of time. Around 60 % of the most common bivalves are still being exploited essentially without regulation, and their remains are found on beaches and close to shore. Their absence in modern samples may reflect this, but it should have no effect on Pleistocene samples. The presence of taxa in the Pleistocene but not in the modern assemblages can be explained in other ways. First, taxa may have been transported into the study area

dead (Kidwell, 1991; Kidwell and Bosence, 1991; Nebelsick, 1992; Kidwell and Flessa, 1995). This would support Model III (habitat averaging Pleistocene deposit) or Model IV (a combination of Model I: a “snapshot”, Model II: a time averaging assemblage and Model III). Secondly, the assemblage may be characterized by multiple stable points (Connell and Sousa, 1983), some taxa that are normally present and characteristic of the modern assemblage may have failed to recruit during the study (Cummins et al., 1986a), which would support Models I or II. Thirdly, opportunistic species may have failed to recruit during the study (Flessa, 1993) also supporting time averaging in Pleistocene samples. Finally, environmental changes may have been great enough so that the habitat supported two or more assemblages representing different environmental conditions (Staff et al., 1986), which would support Model III if remains from more than one habitat are preserved. On the other hand, Model II (time averaging deposit) is supported if only environmental conditions changed and affected rhodolith beds at different times, and a third possibility would support Model IV (a combination of Models I: a “snapshot” assemblage, II and III).

Transportation of material to the area is possible, as most organisms found in modern samples were small suggesting they were recent recruits. Species that died before reaching reproductive maturity might indicate settlement in a marginal habitat even if they are numerically abundant (Cummins et al., 1986a; Staff et al., 1986). This may be exemplified by *Laevicardium* spp. in modern PC samples, where many small shells were found, but no living adults, even when at least one of the two species

(*Laevicardium elatum* (Sowerby 1840)) in the area is quite abundant in onshore accumulations of empty shells.

Transportation in modern habitats has been suggested to occur in this area via water motion induced by local winds (Steller and Foster, 1995; Foster et al., 1997) and currents and hurricanes (Schlanger and Johnson, 1969). Beaches become a reservoir for shells transported from a variety of environments giving a high diversity assemblage, but hydrodynamic sorting can segregate taxa by shell morphology giving a low diversity or monospecific assemblage (Meldahl and Cutler, 1992). Moreover, Russell (1991) indicated that subtidal sandy environments offer little topographic relief and the remains of dead organisms, especially small ones, are easily swept away. This may happen in recent rhodolith beds because most of the surrounding areas (especially in PC) are sandy habitats, and rhodolith beds may act as traps for shell remains. If this is correct and transportation plays an important role within modern rhodolith beds then species richness should be different than reported here.

The degree of shell transport in the marine environment (either past or recent) depends upon shell hydrodynamic properties such as shape, size and density and the type and strength of the transporting agent (Cummins et al., 1986b; Kidwell, 1986). Transported individuals may all be small (Cummins et al., 1986a). However, many recent time-averaged assemblages show little evidence of significant between habitat transport (Kidwell, 1991; Kidwell and Bosence, 1991; Kidwell and Flessa, 1995). Moreover, regardless of size, adults are better preserved than juveniles because the delicate architecture and high surface area to volume ratio makes small individuals

especially prone to post-mortem destruction by physical or chemical means (Flessa, 1993). This may explain why smaller individuals occurred abundantly in modern beds. Because no comparison was done between living versus recent death assemblages to test for interhabitat transportation, the argument applies to mollusc shells (alive or not) in modern rhodolith beds. Furthermore, transported shells can be recognized as such because they are chaotically distributed, broken and abraded in shallow water deposits (Cadée, 1991). This was not observed in modern bed samples where the bulk sample consisted of unarticulated small shells, confirming Kidwell and Bosence's (1991) hypothesis.

After removal of exclusively Pleistocene species (possible habitat averaging in Pleistocene deposits) differences between Pleistocene and modern samples in taxonomic composition and similarity remained. None of the eleven clam species found only in the Pleistocene are known to associate with rhodolith beds or other calcareous algal environments (Table IV), and only 1 gastropod (*Persicula imbricata*) of the 16 on which reliable data were available is associated with such a habitat (Table V). Could this be an indication of small habitat transportation or mixing in the Pleistocene deposits? As previously mentioned, between habitat transportation was unlikely in modern beds. However, Pleistocene deposits had taxa unrelated to rhodolith beds, suggesting transportation may be important. Many hydraulic concentrations in supratidal and intertidal environments carry away shells < 2 mm, but in level bottom subtidal habitats transportation is generally minor even above storm and far-weather wave bases (Kidwell, 1991). Although exotic shells were an important component of the Pleistocene deposits

(over 30% based on presence-absence data) is hard to attribute their presence to out of habitat transportation. Thus, Model III is disregarded.

Another possible reason for the reduction of taxa in modern samples is the common practice of shell collecting. Because shell collection effects are higher in relative abundance than in presence-absence data, and given the small number of divers in rhodolith beds within the Gulf of California, collection effects are highly unlikely.

Why do 77 taxa occur only in Pleistocene deposits? The difference in class composition may be related to preservation effects due to the stronger shells of snails. Cummins et al. (1986a) found that on the average, gastropods had more adults than bivalves. Gastropod survivorship may be generally higher or taphonomic loss may be greater for adult bivalves. Consequently, gastropods may preserve better, but where do the “exclusive” Pleistocene taxa occur? Even if *Chama* sp., *Lithophaga* sp., *Saccella* spp., *Semele* spp. 2, the undetermined bivalve Sp. 1 and 28 snail taxa (Table V) were preserved, shells were deteriorated such that it was not possible to determine species, and their presence in modern rhodolith beds could not be corroborated. Undetermined taxa should reduce richness either in modern or Pleistocene samples, such that differences in taxonomic composition between Pleistocene and modern samples will not be as large. Their presence in the data analyses did not have a significant effect; results were the same when they were removed (see analyses, especially test for Model III: habitat averaging, or at generic level).

Among exclusive clams: *Mactra* sp. cf. *isthmica*, *Protothaca columbiensis* and *Trachycardium panamense* have distributional margins south of the study areas,

suggesting warmer temperatures during the Pleistocene in the Gulf of California. Even if *T. panamense* is not a rare species in the modern Gulf, it is noteworthy that there were no records on it in the reviewed literature. The presence of “extralimital” species in Pleistocene deposits is commonly thought to indicate that the marine thermal regime was at times warmer, cooler or at least quite different than it is today (Valentine, 1989; Fields et al., 1993; Di Michele, 1994; Enquist et al., 1995). Distribution analyses of the 33 snail taxa identified to species found only 4 taxa (*Persicula imbricata*, *Splendrillia* sp. cf. *arga*, *Tegula funebris* and *Terebra hancocki*) that were not currently distributed within the study areas. Records for *T. funebris*, a north Pacific species, are hard to explain as the other 3 snail taxa also have actual distribution ranges on southern localities also suggesting warmer temperatures in the Gulf during the Pleistocene. Not only is the geographic distribution of *T. funebris* unrelated, the species is exclusively intertidal. Thus, the presence of *T. funebris* in the Pleistocene in a southern location and in presumably deeper water may indicate migration to cooler water (Hall, 1960; Maluf, 1988; Fields et al., 1993), although, transportation by hermit crabs may also be a possibility (Fürsich and Aberhan, 1990; Kidwell and Bosence, 1991; Russell, 1991; Flessa and Kowalewski, 1994). However, 3 cool periods occurred during the Pliocene (Johnson and Simian, 1996), and Punta Chivato Pleistocene assemblages are surrounded by Pliocene deposits (Durham, 1950; Ortlieb, 1984, 1987). Thus, *T. funebris* may be representative of the Pliocene fauna, as were some echinoids found in Pleistocene samples. A very low rate of uplift may allow amalgamation of widely aged deposits (Johnson and Libbey, 1997). This is unlikely at Punta Chivato as Ortlieb’s (1984, 1987)

studies and ages were supported by Libbey and Johnson (1997), Johnson and Ledesma-Vázquez (1999) and Meldahl (pers. comm. 1999). Moreover, high uplift rates have been suggested in the Punta Chivato area (Johnson and Simian, 1996; Johnson et al., 1997; Johnson and Ledesma-Vázquez, 1999).

Alternatively, there may have been leakage from stratigraphically older deposits (Kidwell and Bosence, 1991). Faunal condensation, when bioclasts not only from successive generations (time averaged), but from successive assemblages and successive chronozones become telescoped into a single stratigraphic interval (Kidwell, 1993) may have played a role in what appear to be out of habitat “exclusive” Pleistocene taxa. Both ideas may be relevant in other areas they are unlikely for Punta Galeras, or Punta Chivato. The amount of leaked Pliocene shells is insignificant. Pliocene shells are easily distinguished from Late Pleistocene shells by their significantly poorer preservation, particularly dissolution due to subaerial exposure (Meldahl pers. comm.). Given results and the abundance of *T. funebris*, Meldahl hypothesis seems feasible.

Environmental change during the period of accumulation may have influenced the deposit. During the Pleistocene, species may have shifted independently up and down the shelf as sea level rose and fall, and northward or southward as temperature warmed and cooled; the living biota at any time was merely a “snapshot” of this process. The shifts probably did not involve entire assemblages as such, but rather responses of individual taxa (Wise and Schopf, 1981; Davis, 1986; Fields et al., 1993; Valentine and Jablonski, 1993). Libbey (1995) found that Pleistocene species did not change from arroyo to arroyo across Playa La Palmita, at Punta Chivato, indicating all samples

represent the same widespread assemblage. Thus, conditions such as substrate and wave energy were probably consistent across the site, and the environment at this site in the Pleistocene remained stable enough through the substage 5e transgression and regression that the same species could continue to exist until the water finally drained away (Libbey, 1995). Whenever environmental conditions remain similar (or return to a similar geographic configuration, e.g. in glacial-interglacial climatic cycles) the range boundaries and the regional pattern of abundance of an individual species should be relatively unchanged (Enquist et al., 1995).

In conclusion, there is no evidence of wholesale replacement or reorganization of mollusc faunas associated with rhodolith beds in the southwestern Gulf of California between Pleistocene and modern samples. A similar pattern has been suggested for marine faunas through the Pleistocene even though there were considerable changes in habitable area (Wise and Schopf, 1981). Mollusc assemblages in Pleistocene PC and PG rhodolith deposits in the southwestern Gulf of California are within habitat time averaged assemblages. Overall, analyses at the genus level yielded similar results and precision estimates as those obtained at the lowest identified taxonomic level achieved. General trends also remained, but, as expected, there were a few variations related to the assumptions for particular test at specific levels. Thus, time will be saved in future, similar research in the area with analyses and identifications at the genus level, supporting Campbell and Valentine (1977), Wise and Schopf (1981), Erwin (1990), and Williams and Gaston (1994) suggestions. Results also suggest that although some change in taxonomic composition occurred over time, the amount of variation is difficult

to quantify due to time averaging effects. After removal of these effects as best as possible, it is suggested that, in spite of pronounced changes in sea level and temperature that occurred globally during Late Pleistocene and Holocene time, the nearshore molluscan fauna of the southwestern Gulf of California rhodolith beds persisted with only minor changes in taxonomic composition.

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Fig. 1. Study areas in the southwestern Gulf of California. PC = Punta Chivato, BC = Bahía Concepción, CSL = Canal de San Lorenzo, PG = Punta Galeras.

Fig. 2. Effects of sample combination on taxonomic richness. **A)** Average raw total richness between Pleistocene and modern samples for PC and PC + BC combined. Standard errors did not exceed ± 5 and are not shown. **B)** Average rarefied total richness between Pleistocene and modern samples for PC and PC + BC combined data. $r \#$ = expected number of individuals (fixed at 35 and variable; see methods). Standard errors did not exceed ± 2 and are not shown. FPC = Fossil Punta Chivato, MPC = Modern Punta Chivato and MBC = Modern Bahía Concepción. Numbers preceding MBC indicate how many of these samples were added to MPC. $n = 10$.

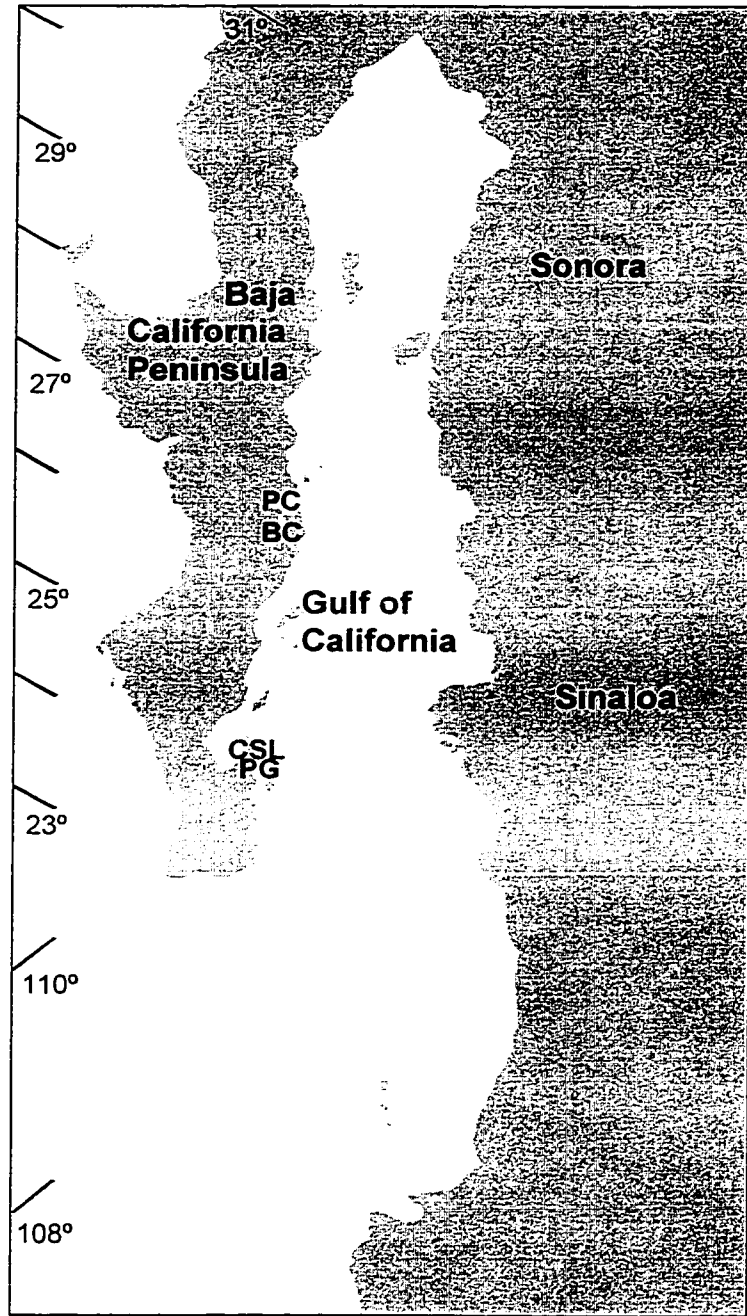


Fig. 1.

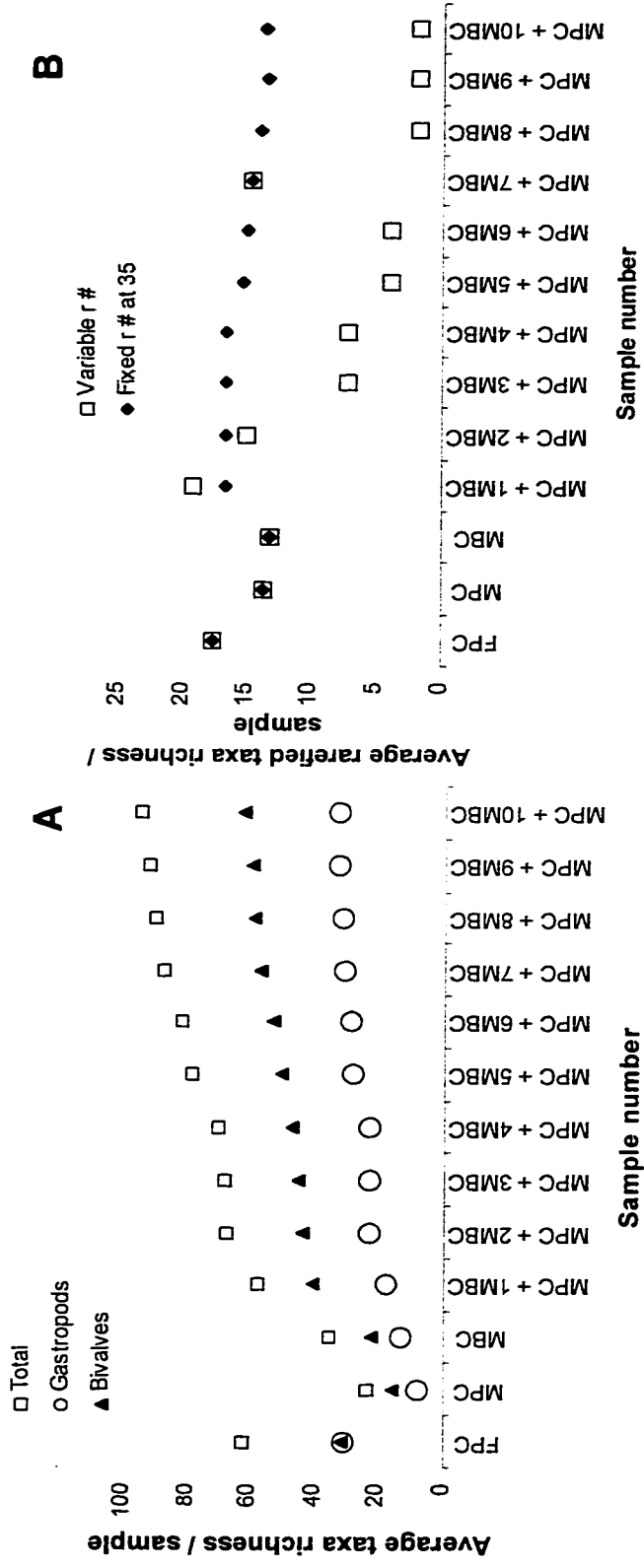


Fig. 2.

Table I. Total and averaged (n = 10) taxa richness by locality and time. SE = Standard error, B = Bivalves, G = Gastropods, T = Total (both classes), PC = Punta Chivato, BC = Bahía Concepción, and PG = Punta Galeras. Samples volume from BC was greater than in other modern areas (see text), and only modern beds were sampled.

Area / Time	T Total	B Total	G Total	T Mean (SE)	B Mean (SE)	G Mean (SE)
PC Pleistocene	155	73	82	62.4 (4.9)	31.6 (2.5)	30.8 (2.7)
PC Modern	76	46	30	23.4 (2.4)	15.4 (1.2)	8 (1.4)
BC Modern	89	59	30	35.4 (2.8)	22.2 (1.7)	13.2 (1.6)
PG Pleistocene	123	50	73	54.1 (3.4)	26.3 (1.1)	27.8 (2.9)
PG Modern	74	41	33	22.7 (2.9)	13.2 (1.8)	9.5 (1.5)

Table II. ANOSIM coefficients for Bray-Curtis similarity within Pleistocene deposit and between Pleistocene and modern samples for PC and PC + BC combined. MPC = Modern Punta Chivato and MBC = Modern Bahía Concepción. Numbers preceding MBC indicate the number of samples from this area added to MPC. $n = 10$. P values were all 0.001 except for MPC + 6 MBC, which was 0.002.

Area	R
MPC + 1 MBC	0.92
MPC + 2 MBC	0.92
MPC + 3 MBC	0.92
MPC + 4 MBC	0.94
MPC + 5 MBC	0.92
MPC + 6 MBC	0.94
MPC + 7 MBC	0.96
MPC + 8 MBC	0.95
MPC + 9 MBC	0.96
MPC + 10 MBC	0.95

Table III. Total and averaged (n = 10) genera richness by locality and time. SE = Standard error, B = Bivalves, G = Gastropods, T = Total (both classes), PC = Punta Chivato, BC = Bahía Concepción, and PG = Punta Galeras. Samples volume from BC was greater than in other modern areas (see text), and only modern beds were sampled.

Area / Time	T Total	B Total	G Total	T Mean (SE)	B Mean (SE)	G Mean (SE)
PC Pleistocene	97	47	50	47.2 (3.2)	24.3 (1.8)	22.9 (1.6)
PC Modern	58	34	24	20.8 (2.1)	13.3 (1.1)	7.5 (1.2)
BC Modern	63	40	23	30.8 (2.4)	19.4 (1.5)	11.4 (1.3)
PG Pleistocene	82	32	50	43.3 (2.5)	20.8 (0.7)	22.5 (2.1)
PG Modern	62	33	29	21.7 (2.6)	12.5 (1.6)	9.2 (1.3)

Table IV. Geographic distribution and habitat of bivalves found only in Pleistocene samples. Depth in m. B = Bahía, I = Isla or Islas, G = Gulf, Ca = California, Int = Intertidal and # = abundance (1 –10 = “rare” to “common”). See text for references.

Taxa	Geographic	Habitat	Depth	#
<i>Amerycina cultrata</i>	Ca and Guaymas to I Partida, BCS		5 – 91	0.5
<i>Chama</i> sp.				0.5
<i>Ctena clarionensis</i>	B San Carlos to I Clarión, Revillagigedo		35	0.5
<i>Cumingia</i> <i>lamellosa</i>	Ca to Chile, including I Galápagos	Int on sand, clay, rock crevices and sponges	0 – 25	2
<i>Donax culter</i>	Ca to Panamá	Int on sandy beaches or bays	0 – 25	8
<i>Fugleria illota</i>	Puerto Peñasco to Perú, including I Galápagos	Int on rocky shores	0 – 70	2.5
<i>Leporimetis</i> <i>cognata</i>	Sonora to Perú, including I Galápagos	Int	0 – 100	5
<i>Lithophaga</i> sp.				1

Table IV. Continued.

Taxa	Geographic	Habitat	Depth	#
<i>Maetra</i> sp. cf.	El Salvador and	Int	0 – 15	1.5
<i>isthmica</i>	Nicaragua to Panamá			
<i>Protothaca</i>	Topolobampo to Perú	Intertidal		1.5
<i>columbiensis</i>				
<i>Saccella</i> spp.				1
<i>Semele</i> spp. 2				2.5
Sp. 1				0.5
<i>Trachycardium</i>	Panamá	Int on mud	0 – 15	7.5
<i>panamense</i>				
<i>Trachycardium</i>	Baja Ca to Perú	Int and shallow muddy	0 – 25	12
<i>senticosum</i>		bottoms		
<i>Trachycardium</i> sp. cf.	G of Ca to Chile,		5 – 15	1.5
<i>procerum</i>	including I Galápagos			

Table V. Geographic distribution and habitat of gastropods found only in Pleistocene samples. Depth in m. B = Bahía, I = Isla or Islas, Pto = Puerto, G = Gulf, Ca = California, Int = Intertidal, S = Southern and # = abundance (1 –10 = “rare” to “common”). See text for references.

Taxa	Geographic	Habitat	Depth	#
<i>Astraea unguis</i>	Guaymas to Ecuador	Rocky areas at low tide, offshore		1
<i>Attiliosa nodulosa</i>	Pto Peñasco to Panamá		18 – 80	1
<i>Caducifer biliratus</i>	G of Ca to I Galápagos		7 – 146	3
<i>Calliostoma bonita</i>	B San Carlos to Acapulco		37 – 100	30
<i>Calliostoma</i> sp.				1
<i>Cancellaria</i> <i>cassidiformis</i>	San Diego to Perú, including G of Ca	Int at extreme low tides	0 – 37	2
<i>Cancellaria</i> sp. 1				6
<i>Cancellaria</i> sp. 2				4
<i>Cancellaria</i> sp. 3				1
<i>Cerithium</i> ? sp.				2

Table V. Continued.

Taxa	Geographic	Habitat	Depth	#
<i>Chicoreus</i> sp.				1
<i>Columbella</i>	I Cedros to			13
<i>aureomexicana</i>	Topolobampo			
<i>Columbella fuscata</i>	B San Carlos to Perú, including I Galápagos	Int under stones		97
<i>Columbella</i> sp.				5
<i>Columbella</i>	G of Ca to Perú	Under rocks between tides		1
<i>strombiformis</i>				
<i>Conus californicus</i>	Sparingly into the Panamic Province	Rocky and sandy bottoms	0 – 30	1
<i>Conus diadema</i>	B San Carlos to I Galápagos	Int on rocky ledges		35
<i>Crassispira</i> sp. 1				1
<i>Crassispira</i> sp. 2				3
<i>Crassispira</i> spp.				7
<i>Dermomurex bakeri</i>	G of Ca to Manzanillo			1
<i>Fusinus</i> sp.				5

Table V. Continued.

Taxa	Geographic	Habitat	Depth	#
<i>Hexaplex princeps</i>	Guaymas to Perú, including I Galápagos	Int on rocks and offshore in shallow waters		1
<i>Kurtziella plumbea</i>	Central Alaska to Mazatlán and in G of Ca		10 – 50	1
<i>Leukozonia ? sp.</i>				1
<i>Liocerithium juthithae</i>	B Magdalena to Mazatlán	Under rocks between tides		10
<i>Mancinella speciosa</i>	B Magdalena to Perú, including I Galápagos	Rocks between tides		11
<i>Mancinella triangularis</i>	G of Ca to Perú, including I Galápagos	Int on rocks		1
<i>Mancinella tuberculata</i>	G of Ca to Mazatlán, Costa Rica and I Galápagos as ?	Rocks between tides		1

Table V. Continued.

Taxa	Geographic	Habitat	Depth	#
<i>Mitra</i> sp.				4
<i>Nassarius iodes</i>	G of Ca to Mazatlán			82
<i>Natica</i> sp. 1				4
<i>Natica</i> sp. 2				1
<i>Oliva davisae</i>	G of Ca			31
<i>Persicula imbricata</i>	Cabo San Lucas to Ecuador, including I Galápagos	Rubble	16 – 60	1
<i>Pilsbryspira</i> sp. 1				2
<i>Pilsbryspira</i> sp. 2				1
<i>Polinices</i> sp.				4
<i>Pyramidella</i> sp.				4
<i>Rhinoclavis</i> <i>gemmata</i>	B Magdalena to Ecuador, including I Galápagos	Subtidally on sandy bottoms	3 – 130	150
<i>Rhinocoryne</i> sp. cf. <i>humboldti</i>	Sonora to Chile	Estuaries and offshore	0 – 27	8
<i>Solenosteira</i> sp. 1				6

Table V. Continued.

Taxa	Geographic	Habitat	Depth	#
<i>Solenosteira</i> sp. 3				5
<i>Solenosteira</i> sp. 4				1
<i>Splendrillia</i> sp. cf. <i>arga</i>	Huatulco		15	4
<i>Strombina</i> sp. cf. <i>solidula</i>	G of Ca	Int	0 – 73	137
<i>Subcancilla sulcata</i>	Guaymas to Ecuador, I Galápagos as ?	Int	0 – 112	4
<i>Tegula funebris</i>	Vancouver Island to central Baja Ca	Int, abundant in rocky areas	0 – 2	2
<i>Tegula rugosa</i>	G of Ca	Rocks in upper int		2
<i>Terebra hancocki</i>	I Mariás to Ecuador	Int and offshore	0 – 90	1
<i>Terebra intertincta</i>	Baja Ca to Ecuador	Int	0 - 37 m	2
<i>Terebra</i> spp.				1
<i>Trivia solandri</i>	S Ca to Perú, including G of Ca and I Galápagos	Int, under rocks and in beach drift		5

Table V. Continued.

Taxa	Geographic	Habitat	Depth	#
<i>Turritella lentiginosa</i>	G of Ca			1
<i>Turritella</i> sp. 2				2
UNK 1				1
UNK 2				1
UNK 4				1
UNK 5				6
<i>Vermetus indentatus</i>	Pto Peñasco to I Marías			1
<i>Vermicularia pellucida</i>	S Ca to Ecuador,	Among gravel and		4
<i>eburnea</i>	including I Galápagos	small stones		

Table VI. Total and averaged ($n = 10$) taxa richness by locality and time with Pleistocene “exclusive” species removed. SE = Standard error, B = Bivalves, G = Gastropods, T = Total (both classes), PC = Punta Chivato, and PG = Punta Galeras.

Area / Time	T Total	B Total	G Total	T Mean (SE)	B Mean (SE)	G Mean (SE)
PC Pleistocene	96	59	37	49.7 (3.3)	28.1 (2.1)	21.6 (1.4)
PC Modern	76	46	30	23.3 (2.4)	15.4 (1.2)	8 (1.4)
PG Pleistocene	78	42	36	41.4 (2.1)	24 (0.9)	17.4 (1.6)
PG Modern	74	41	33	22.7 (2.9)	13.2 (1.8)	9.5 (1.5)

Table VII. Molluscan taxa from Punta Chivato. $n = 10$. F = fossil, M = Modern and t = times. Each row represents richness from a combination of one sample per time, e.g. fossil versus living (FPC1 versus MPC).

Total richness	Taxa present in both t	Exclusive F taxa	Exclusive M taxa
66	8	56	2
57	21	19	17
64	18	36	10
72	16	54	2
52	11	29	12
76	14	57	5
65	16	43	6
99	15	78	6
72	13	52	7
75	25	43	7

Appendix 1. Continued.

	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Globivenus isocardia</i>	0	0	0	0	0	0	0	0	0	0
<i>Glycymeris</i> spp. 1	7	1	1	3	6	10	33	53	33	31
<i>Glycymeris</i> spp. 2	15	1	7	2	24	2	16	28	20	15
<i>Laevicardium</i> spp.	19	7	7	14	32	6	22	11	4	32
<i>Leporimetis cognata</i>	0	0	0	1	1	0	0	2	2	1
<i>Linga cancellaris</i>	0	0	0	0	0	0	0	0	0	0
<i>Lithophaga aristata</i>	0	0	0	0	0	0	0	0	0	0
<i>Lithophaga</i> sp.	2	0	0	0	0	0	0	0	0	0
<i>Lucina centrifuga</i>	0	0	0	0	0	0	0	0	0	0
<i>Lucina fenestrata</i>	0	0	0	1	0	1	0	0	0	0
<i>Lucina lingualis</i>	0	0	2	2	1	1	17	33	3	3
<i>Lucina</i> spp.	1	0	1	1	0	6	6	53	9	8
<i>Mactra</i> sp. cf. <i>isthmica</i>	0	0	0	0	0	0	0	3	0	0
<i>Megapitaria</i> spp.	75	12	34	40	37	34	15	45	69	40
<i>Modiolus capax</i>	0	0	3	0	0	0	0	0	0	0
<i>Modiolus</i> sp. cf. <i>americanus</i>	0	0	0	0	0	0	0	0	0	0
<i>Ostrea</i> spp.	1	4	10	1	0	1	0	3	22	0
<i>Papyridea aspersa</i>	0	0	0	1	0	0	0	0	2	0
<i>Parvilucina approximata</i>	1	0	0	2	0	0	0	3	0	0
<i>Pinctada mazatlanica</i>	0	0	0	0	0	0	0	0	0	0
<i>Pinna rugosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Pitar helenae</i>	0	0	0	0	0	0	0	0	0	0
<i>Pitar</i> spp.	8	4	8	7	8	7	121	89	23	42
<i>Pitar</i> sp. cf. <i>berryi</i>	0	0	0	0	0	1	0	0	0	0

Appendix 1. Continued.

	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Plicatula</i> sp. cf. <i>inezana</i>	0	2	0	1	0	0	0	0	0	0
<i>Protothaca columbiensis</i>	0	0	0	0	0	0	0	0	0	0
<i>Protothaca grata</i>	2	1	0	0	0	4	0	2	0	0
<i>Psammotreta</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Pseudochama clarionensis</i>	8	0	4	0	0	0	4	0	0	0
<i>Pteria sterna</i>	0	0	0	0	0	0	0	0	0	0
<i>Rupellaria denticulata</i>	0	0	0	1	0	0	0	1	0	0
<i>Saccella acrita</i>	2	0	0	9	2	1	1	2	0	0
<i>Saccella</i> spp.	0	0	2	0	0	0	0	0	0	0
<i>Semele</i> sp. 1	1	0	0	1	0	0	0	0	2	0
<i>Semele</i> spp. 1	0	0	1	0	0	0	0	0	4	0
<i>Semele</i> spp. 2	2	0	0	1	0	0	3	1	0	5
Sp. 1	0	0	1	0	0	0	0	0	0	0
Sp. 2	0	0	0	0	0	0	0	0	0	0
<i>Sphenia</i> spp.	0	0	0	1	1	0	0	0	1	0
<i>Spondylus</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Strophocardia megastrophia</i>	0	0	0	0	0	1	2	4	2	5
<i>Tagelus</i> spp.	5	0	1	3	10	3	1	4	3	33
<i>Tellina</i> ? sp.	0	0	0	0	0	0	0	0	0	0
<i>Tellina coani</i>	0	0	0	0	0	0	0	3	0	1
<i>Tellina cumingii</i>	0	0	0	0	0	1	3	5	3	3
<i>Tellina ochracea</i>	6	2	0	0	0	0	0	0	1	8
<i>Tellina pacifica</i>	0	0	0	0	0	0	0	0	0	0
<i>Tellina</i> spp.	1	1	0	1	0	7	1	250	1	1

Appendix 1. Continued.

GASTROPODS	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Acanthina</i> ? sp.	0	0	0	2	0	0	0	0	0	0
<i>Anachis</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Architectonica nobilis</i>	0	0	0	0	0	1	0	0	0	0
<i>Asperiscala</i> sp. cf. <i>elenense</i>	0	0	0	0	0	0	0	0	0	0
<i>Astraea unguis</i>	0	0	0	0	0	0	0	0	1	0
<i>Attiliosa nodulosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Caducifer biliratus</i>	0	0	0	1	0	1	0	0	0	0
<i>Calliostoma bonita</i>	5	2	2	1	0	3	3	6	0	3
<i>Calliostoma</i> sp.	1	0	0	0	0	0	0	0	0	0
<i>Cancellaria cassidiformis</i>	0	1	0	0	0	0	1	0	0	0
<i>Cancellaria</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>Cancellaria</i> sp. 2	0	0	0	0	0	1	0	1	0	0
<i>Cancellaria</i> sp. 3	0	0	0	0	0	1	0	0	0	0
<i>Cantharus pallidus</i>	8	1	2	0	1	4	2	5	5	3
<i>Cassis</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cerithidea californica mazatlanica</i>	2	0	0	0	0	0	0	1	0	0
<i>Cerithium</i> ? sp.	0	0	0	0	0	0	1	0	0	1
<i>Cerithium</i> sp. cf. <i>menkei</i>	0	0	0	0	0	0	0	1	0	0
<i>Cerithium stercusmuscarum</i>	24	1	1	0	0	0	1	0	1	0
<i>Cerithium uncinatum</i>	0	0	0	0	0	0	0	0	0	0
<i>Chicoreus erythrostomus</i>	0	0	0	0	0	0	0	0	0	0
<i>Chicoreus</i> sp.	0	0	1	0	0	0	0	0	0	0
<i>Columbella aureomexicana</i>	1	0	0	9	0	0	0	1	0	0
<i>Columbella fuscata</i>	2	0	0	2	0	4	1	5	3	1

Appendix 1. Continued.

	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Columbella haemastoma</i>	0	0	0	0	0	0	0	0	0	0
<i>Columbella</i> sp.	2	0	1	0	0	0	0	0	0	0
<i>Columbella strombiformis</i>	0	0	0	0	0	0	0	0	1	0
<i>Conus archon</i>	0	0	0	0	0	0	0	0	0	0
<i>Conus brunneus</i>	0	0	0	0	0	4	0	2	0	0
<i>Conus californicus</i>	0	0	0	1	0	0	0	0	0	0
<i>Conus diadema</i>	3	0	2	2	1	1	0	2	0	0
<i>Conus poormani</i>	11	1	4	3	1	15	10	24	7	9
<i>Conus regularis</i>	2	2	1	6	5	31	7	57	10	34
<i>Costoanachis</i> sp. cf. <i>ritteri</i>	0	0	0	0	0	0	0	0	0	0
<i>Costoanachis varicosa</i>	1	0	0	1	1	2	0	8	0	1
<i>Crassispira</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>Crassispira</i> sp. 2	0	0	0	0	0	0	0	0	1	0
<i>Crassispira</i> spp.	0	0	0	0	0	0	0	1	0	0
<i>Cymatium</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cypraea albuginosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Cypraea annettae</i>	1	0	0	0	0	0	0	3	0	2
<i>Dermomurex bakeri</i>	0	0	0	0	0	0	0	0	0	0
<i>Enaeta cumingii</i>	0	0	3	2	0	0	1	0	0	2
<i>Enaeta</i> sp. cf. <i>barnesii</i>	0	0	0	0	0	0	0	0	0	0
<i>Engina fusiformis</i>	0	0	0	0	0	1	0	0	0	0
<i>Eupleura muriciformis</i>	0	0	0	1	0	0	0	0	0	1
<i>Fusinus ambustus</i>	1	0	0	2	1	0	3	1	1	0
<i>Fusinus</i> sp.	0	0	0	0	0	0	4	0	0	0

Appendix 1. Continued.

	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Haminoea angelensis</i>	31	2	0	10	0	1	3	3	0	1
<i>Hexaplex princeps</i>	0	0	0	0	0	0	0	0	1	0
<i>Kurtziella plumbea</i>	0	0	0	1	0	0	0	0	0	0
<i>Leukozonia</i> ? sp.	0	0	0	0	0	0	0	1	0	0
<i>Liocerithium judithae</i>	0	0	0	0	0	0	0	0	0	0
<i>Macrarena</i> spp.	9	5	2	15	2	10	25	20	13	17
<i>Mancinella speciosa</i>	2	0	0	0	2	2	0	0	0	1
<i>Mancinella triangularis</i>	0	0	0	0	0	0	0	0	0	0
<i>Mancinella tuberculata</i>	0	0	0	0	0	0	0	0	0	0
<i>Mitra</i> sp.	0	0	0	0	0	0	0	1	0	0
<i>Mitrella</i> sp. cf. <i>dorma</i>	0	0	0	0	0	0	0	0	0	0
<i>Modulus cerodes</i>	0	0	0	0	0	0	0	0	0	0
<i>Murexiella</i> spp.	0	0	0	0	0	0	0	1	0	0
<i>Muricopsis armatus</i>	0	0	0	0	0	0	0	0	0	0
<i>Nassarius iodes</i>	0	0	1	3	0	5	15	50	2	6
<i>Nassarius luteostomus</i>	20	3	9	13	6	7	9	36	5	29
<i>Nassarius nodicinctus</i>	6	1	0	5	5	1	3	8	11	13
<i>Nassarius</i> sp. 1	0	0	0	0	0	0	0	1	0	0
<i>Nassarius</i> sp. 2	6	0	0	3	0	2	6	6	3	9
<i>Natica grayi</i>	0	0	0	0	0	0	0	0	0	0
<i>Natica</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>Natica</i> sp. 2	0	0	0	0	0	0	0	0	0	0
<i>Nerita funiculata</i>	0	0	0	0	0	0	0	0	0	0
<i>Neverita reclusiana</i>	5	1	3	4	3	6	4	19	6	9

Appendix 1. Continued.

	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Oliva davisae</i>	0	0	1	3	4	12	0	7	4	0
<i>Oliva</i> spp.	60	9	17	36	33	113	78	195	26	50
<i>Olivella dama</i>	70	16	17	35	25	79	267	467	128	160
<i>Persicula imbricata</i>	0	0	0	0	0	0	0	0	0	0
<i>Pilsbryspira</i> sp. 1	0	0	0	0	0	0	0	0	0	1
<i>Pilsbryspira</i> sp. 2	0	0	0	0	0	0	0	1	0	0
<i>Polinices</i> sp.	0	0	0	0	0	0	0	4	0	0
<i>Polinices</i> spp.	22	5	1	14	6	35	41	69	31	42
<i>Pyramidella</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Rhinoclavis gemmata</i>	0	0	0	0	0	1	2	4	1	4
<i>Rhinocoryne</i> sp. cf. <i>humboldti</i>	0	0	0	0	0	0	0	2	0	0
<i>Solenosteira</i> sp. 1	0	0	0	0	0	3	0	0	0	0
<i>Solenosteira</i> sp. 2	0	0	0	0	0	0	0	1	0	0
<i>Solenosteira</i> sp. 3	0	0	0	0	0	1	0	0	0	0
<i>Solenosteira</i> sp. 4	0	0	0	0	0	0	0	1	0	0
<i>Splendrillia</i> sp. cf. <i>arga</i>	0	0	0	0	0	0	0	0	0	0
<i>Strombina maculosa</i>	0	0	1	0	0	0	0	2	2	2
<i>Strombina</i> sp. cf. <i>solidula</i>	0	0	0	0	0	0	0	0	0	0
<i>Strombus</i> spp.	16	5	18	23	6	42	10	13	7	16
<i>Subcancilla sulcata</i>	0	0	0	0	1	0	2	0	0	0
<i>Tegula funebris</i>	0	0	0	0	0	0	0	0	2	0
<i>Tegula rugosa</i>	1	0	0	0	0	0	0	1	0	0
<i>Tegula</i> spp.	2	3	0	7	1	17	13	43	20	22
<i>Tegula</i> sp. cf. <i>felipensis</i>	0	0	0	0	0	5	9	5	0	1

Appendix 1. Continued.

	FPC1	FPC2	FPC3	FPC4	FPC5	FPC6	FPC7	FPC8	FPC9	FPC10
<i>Terebra hancocki</i>	0	0	0	0	0	0	0	0	0	1
<i>Terebra intertincta</i>	1	0	0	0	0	0	0	0	0	0
<i>Terebra ornata</i>	0	0	0	0	0	0	0	0	0	0
<i>Terebra</i> spp.	0	0	0	0	0	0	0	1	0	0
<i>Terebra variegata</i>	5	1	5	1	1	5	7	12	4	5
<i>Trachypollia lugubris</i>	1	1	0	2	0	0	2	0	2	0
<i>Trigonostoma</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Trivia solandri</i>	0	0	0	0	0	1	0	0	0	0
<i>Turbo fluctuosus</i>	16	1	0	34	2	50	10	39	21	8
<i>Turbo squamiger</i>	5	4	4	20	2	18	1	5	0	2
<i>Turritella lentiginosa</i>	0	0	0	0	0	0	0	0	1	0
<i>Turritella nodulosa</i>	0	0	0	6	0	0	4	3	0	2
<i>Turritella</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>Turritella</i> sp. 2	0	0	1	0	0	0	0	1	0	0
UNK 1	0	0	0	0	0	0	0	0	0	0
UNK 2	0	1	0	0	0	0	0	0	0	0
UNK 3	0	0	0	0	0	1	0	5	0	4
UNK 4	0	0	0	0	0	0	0	0	0	0
UNK 5	0	0	0	0	0	0	0	0	0	0
UNK 6	0	0	0	0	0	0	0	0	0	0
<i>Vermetus indentatus</i>	1	0	0	0	0	0	0	0	0	0
<i>Vermicularia pellucida eburnea</i>	2	0	0	0	0	0	0	1	0	0

Appendix 1. Continued.

BIVALVES	MPC1	MPC2	MPC3	MPC4	MPC5	MPC6	MPC7	MPC8	MPC9	MPC10
<i>Amerycina cultrata</i>	0	0	0	0	0	0	0	0	0	0
<i>Anadara formosa</i>	0	0	0	0	0	0	0	0	0	0
<i>A. multicosata</i>	5	11 (4)	0	2	3	6 (2)	2	1	2 (1)	4
<i>A. spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Arca mutabilis</i>	0	0	0	0	0	0	0	0	0	0
<i>A. pacifica</i>	0	0	0	0	1	0	0	1	1	0
<i>A. sp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Arcopsis solida</i>	0	1	0	0	0	0	0	0	0	0
<i>Barbatia alternata</i>	0	0	0	0	0	0	0	0	0	0
<i>B. reeveana</i>	0	0	0	0	0	0	0	0	0	0
<i>Basterotia hertleini</i>	0	1	0	0	0	0	0	5 (1)	0	0
<i>Bornia sp. cf. papyracea</i>	0	0	1	0	1	0	0	1	0	0
<i>Brachidontes semilaevis</i>	0	0	0	0	0	0	0	0	0	0
<i>Carditamera affinis</i>	0	0	0	0	0	0	0	0	0	0
<i>Cardites crassicosata</i>	0	0	0	0	0	0	0	0	0	1
<i>Chama buddiana</i>	0	0	0	0	0	0	0	0	0	0
<i>C. frondosa</i>	0	0	0	0	0	0	0	0	0	0
<i>C. mexicana</i>	0	0	0	0	0	0	0	0	0	1
<i>C. sp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Chione compta</i>	0	0	0	0	0	0	0	2 (1)	0	0
<i>C. kelleitii</i>	0	0	1	0	0	0	0	0	0	0
<i>C. mariae</i>	0	0	0	0	0	0	0	0	0	0
<i>C. spp.</i>	2 (1)	11	1	7	11	6	4	17 (1)	2	6
<i>C. subimbricata</i>	0	0	1	1	0	0	0	2	0	0

Appendix 1. Continued.

	MPC1	MPC2	MPC3	MPC4	MPC5	MPC6	MPC7	MPC8	MPC9	MPC10
<i>Chionopsis gnidia</i>	0	1	0	0	0	0	0	0	0	0
<i>C. purpurisata</i>	0	0	0	0	0	0	0	0	0	0
<i>Codakia distinguenda</i>	0	0	0	0	0	0	0	0	2	0
<i>Corbula esmeralda</i>	0	0	0	0	0	0	0	0	0	1
<i>C. spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>C. sp. cf. ira</i>	0	0	0	0	0	0	0	0	0	0
<i>C. sp. cf. ovulata</i>	0	0	0	0	1	0	1	0	0	0
<i>Cryptomia californica</i>	0	0	0	0	0	0	0	0	0	0
<i>Ctena clarionensis</i>	0	0	0	0	0	0	0	0	0	0
<i>C. mexicana</i>	0	2	0	0	0	3	0	0	3	1
<i>Cumingia lamellosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Cyathodonta ? spp.</i>	0	1	0	0	0	0	0	0	0	0
<i>Diplodonta inezensis</i>	0	0	0	0	0	0	0	0	0	0
<i>Divalinga perparvula</i>	0	0	0	0	0	0	0	0	0	0
<i>Donax culter</i>	0	0	0	0	0	0	0	0	0	0
<i>Dosinia ponderosa</i>	0	1	1	0	0	0	0	0	0	0
<i>Felaniella cornea</i>	0	0	0	0	0	0	0	0	0	0
<i>Fugleria illota</i>	0	0	0	0	0	0	0	0	0	0
<i>Gari sp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Globivenus isocardia</i>	0	0	0	0	1	0	0	0	0	0
<i>Glycymeris spp. 1</i>	1	13	6	3	0	1	2	0	0	9
<i>G. spp. 2</i>	1	9 (2)	2	4	4	2	2	1	1	6
<i>Laevicardium spp.</i>	6	82 (2)	308	13	18 (2)	65	24	2	8 (1)	28
<i>Leporimetis cognata</i>	0	0	0	0	0	0	0	0	0	0

Appendix 1. Continued.

GASTROPODS	MPC1	MPC2	MPC3	MPC4	MPC5	MPC6	MPC7	MPC8	MPC9	MPC10
<i>Acanthina</i> ? sp.	0	0	0	0	0	0	0	0	0	0
<i>Anachis</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Architectonica nobilis</i>	0	1	0	0	0	0	0	0	3 (1)	0
<i>Asperiscula</i> sp. cf. <i>elenense</i>	0	0	0	0	0	0	0	0	0	0
<i>Astraea unguis</i>	0	0	0	0	0	0	0	0	0	0
<i>Attiliosa nodulosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Caducifer biliratus</i>	0	0	0	0	0	0	0	0	0	0
<i>Calliostoma bonita</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cancellaria cassidiformis</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 2	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 3	0	0	0	0	0	0	0	0	0	0
<i>Cantharus pallidus</i>	0	0	0	0	0	0	0	0	0	0
<i>Cassis</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cerithidea californica mazatlanica</i>	0	1	0	0	0	0	0	0	0	0
<i>Cerithium</i> ? sp.	0	0	0	0	0	0	0	0	0	0
<i>Cerithium</i> sp. cf. <i>menkei</i>	0	0	0	0	0	0	0	0	0	0
<i>C. stercusmuscarum</i>	0	0	0	0	0	0	0	0	0	0
<i>C. uncinatum</i>	0	0	0	0	0	0	1	0	0	0
<i>Chicoreus erythrostomus</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Columbella aureomexicana</i>	0	0	0	0	0	0	0	0	0	0
<i>C. fuscata</i>	0	0	0	0	0	0	0	0	0	0
<i>C. haemastoma</i>	0	1	0	0	1	1	0	2	1	0

Appendix 1. Continued.

BIVALVES	FPG1	FPG2	FPG3	FPG4	FPG5	FPG6	FPG7	FPG8	FPG9	FPG10
<i>Amerycina cultrata</i>	0	0	0	0	1	0	0	0	0	0
<i>Anadara formosa</i>	0	0	0	0	0	0	0	0	0	0
<i>A. multicosata</i>	0	5	8	12	3	11	8	23	18	30
<i>A. spp.</i>	0	2	0	0	0	0	0	0	0	0
<i>Arca mutabilis</i>	0	2	0	0	0	0	0	0	0	0
<i>A. pacifica</i>	0	0	0	0	0	0	0	0	0	0
<i>A. sp.</i>	0	0	0	0	0	0	0	0	1	0
<i>Arcopsis solida</i>	1	1	0	1	3	0	1	2	6	0
<i>Barbatia alternata</i>	1	0	0	0	0	0	0	0	0	0
<i>B. reeveana</i>	1	0	0	0	1	1	0	1	0	0
<i>Basterotia hertleini</i>	0	0	0	0	0	0	0	0	0	0
<i>Bornia sp. cf. papyracea</i>	0	0	0	0	0	0	0	0	0	0
<i>Brachidontes semilaevis</i>	0	0	0	0	0	0	0	0	0	0
<i>Carditamera affinis</i>	2	2	1	6	2	4	0	2	8	0
<i>Cardites crassicosata</i>	0	0	2	1	0	0	0	2	0	2
<i>Chama buddiana</i>	0	0	0	0	3	2	2	0	1	1
<i>C. frondosa</i>	0	0	0	0	0	0	0	0	0	0
<i>C. mexicana</i>	1	0	0	0	1	0	3	0	0	0
<i>C. sp.</i>	1	0	0	0	0	0	0	0	0	0
<i>Chione compta</i>	0	0	0	0	0	0	0	0	0	0
<i>C. kelletii</i>	0	0	0	0	0	0	0	0	0	0
<i>C. mariae</i>	0	0	0	0	0	0	0	0	0	0
<i>C. spp.</i>	249	91	115	205	52	121	199	249	256	181
<i>C. subimbricata</i>	4	2	1	7	6	7	3	2	1	11

Appendix 1. Continued.

	FPG1	FPG2	FPG3	FPG4	FPG5	FPG6	FPG7	FPG8	FPG9	FPG10
<i>Chionopsis gnidia</i>	0	0	0	0	0	0	0	0	0	0
<i>C. purpurisata</i>	0	0	0	0	0	0	0	0	0	0
<i>Codakia distinguenda</i>	21	5	7	5	7	12	19	23	8	4
<i>Corbula esmeralda</i>	0	0	0	0	0	0	0	0	0	0
<i>C. spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>C. sp. cf. ira</i>	0	0	0	0	0	0	0	0	0	0
<i>C. sp. cf. ovulata</i>	0	0	0	0	0	0	0	0	0	0
<i>Cryptomia californica</i>	0	0	0	0	0	0	0	0	0	0
<i>Crena clarionensis</i>	0	0	0	0	0	0	0	0	0	0
<i>C. mexicana</i>	1	0	0	1	0	1	1	1	3	2
<i>Cumingia lamellosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Cyathodonta ? spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Diplodonta inezensis</i>	0	0	0	0	0	0	0	0	0	0
<i>Divalinga perparvula</i>	44	25	14	10	10	30	16	48	50	37
<i>Donax culter</i>	0	1	0	1	0	1	0	3	2	2
<i>Dosinia ponderosa</i>	7	2	2	5	0	1	1	3	2	1
<i>Felaniella cornea</i>	0	0	0	0	0	0	0	0	0	0
<i>Fugleria illota</i>	0	0	0	0	0	0	1	0	0	0
<i>Gari sp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Globivenus isocardia</i>	0	0	0	0	0	0	0	0	1	1
<i>Glycymeris spp. 1</i>	3	1	1	1	9	0	0	0	0	6
<i>G. spp. 2</i>	3	2	2	9	1	3	5	8	6	14
<i>Laevicardium spp.</i>	24	3	5	18	11	14	8	65	48	23
<i>Leporimetis cognata</i>	0	0	0	0	0	2	0	1	0	0

Appendix 1. Continued.

	FPG1	FPG2	FPG3	FPG4	FPG5	FPG6	FPG7	FPG8	FPG9	FPG10
<i>Pteria sterna</i>	0	0	0	0	0	0	0	0	0	0
<i>Rupellaria denticulata</i>	0	0	0	0	0	0	0	0	0	0
<i>Saccella acrita</i>	0	0	0	0	0	0	0	0	0	0
<i>S. spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Semele sp. 1</i>	0	0	0	0	0	0	0	0	0	0
<i>Semele spp. 1</i>	0	0	0	0	0	0	0	0	0	0
<i>S. spp. 2</i>	0	0	0	0	0	0	0	0	0	0
<i>Sp. 1</i>	0	0	0	0	0	0	0	0	0	0
<i>Sp. 2</i>	0	0	0	0	0	0	0	0	0	0
<i>Sphenia spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Spondylus sp.</i>	1	0	0	0	0	0	0	0	0	0
<i>Strophocardia megastropa</i>	2	4	3	25	1	4	6	14	6	15
<i>Tagelus spp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Tellina ? sp.</i>	0	0	0	0	0	0	0	0	0	0
<i>Tellina coani</i>	0	0	0	0	0	0	0	0	0	0
<i>T. cumingii</i>	1	1	0	0	3	1	0	0	1	0
<i>T. ochracea</i>	0	0	0	0	0	0	0	1	0	0
<i>T. pacifica</i>	0	0	0	0	0	0	0	0	0	0
<i>Tellina spp.</i>	0	0	0	1	1	0	0	1	1	0
<i>T. sp. 1</i>	1	0	0	0	0	0	0	0	0	0
<i>Tivela spp.</i>	8	5	5	26	2	0	5	12	10	17
<i>Trachycardium biangulata</i>	45	36	14	56	18	34	25	71	70	60
<i>T. consors</i>	1	2	3	8	1	1	0	8	3	5
<i>T. panamense</i>	0	0	0	3	0	0	0	1	0	3

Appendix 1. Continued.

GASTROPODS	FPG1	FPG2	FPG3	FPG4	FPG5	FPG6	FPG7	FPG8	FPG9	FPG10
<i>Acanthina</i> ? sp.	0	0	0	0	0	0	0	0	3	0
<i>Anachis</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Architectonica nobilis</i>	1	0	0	0	0	0	0	0	1	0
<i>Asperiscala</i> sp. cf. <i>elenense</i>	0	0	0	0	0	0	0	0	0	0
<i>Astraea unguis</i>	0	0	0	0	0	0	0	0	0	0
<i>Attiliosa nodulosa</i>	0	0	0	0	0	0	0	0	1	0
<i>Caducifer biliratus</i>	0	0	0	0	0	1	0	0	0	0
<i>Calliostoma bonita</i>	1	1	1	1	0	0	0	0	1	0
<i>C.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cancellaria cassidiformis</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 1	0	1	1	2	0	0	0	0	2	0
<i>C.</i> sp. 2	0	0	0	0	0	0	1	0	1	0
<i>C.</i> sp. 3	0	0	0	0	0	0	0	0	0	0
<i>Cantharus pallidus</i>	32	4	18	7	3	6	6	5	39	6
<i>Cassis</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cerithidea californica mazatlanica</i>	0	0	0	0	0	0	0	0	0	0
<i>Cerithium</i> ? sp.	0	0	0	0	0	0	0	0	0	0
<i>Cerithium</i> sp. cf. <i>menkei</i>	0	0	0	0	0	0	0	0	1	0
<i>C. stercusmuscarum</i>	0	0	0	0	0	0	0	0	0	0
<i>C. uncinatum</i>	0	0	0	0	0	0	0	0	0	0
<i>Chicoreus erythrostomus</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Columbella aureomexicana</i>	0	0	1	0	0	0	0	0	0	0
<i>C. fuscata</i>	12	5	16	19	3	6	3	0	10	5
<i>C. haemastoma</i>	0	1	0	0	0	1	0	0	0	0

Appendix 1. Continued.

GASTROPODS	MPG1	MPG2	MPG3	MPG4	MPG5	MPG6	MPG7	MPG8	MPG9	MPG10
<i>Acanthina</i> ? sp.	0	0	0	0	1	0	0	0	0	0
<i>Anachis</i> sp.	0	0	0	0	0	1	1	0	0	0
<i>Architectonica nobilis</i>	0	0	0	0	0	0	0	0	0	0
<i>Asperiscala</i> sp. cf. <i>elenense</i>	0	0	0	0	0	0	0	0	0	0
<i>Astraea unguis</i>	0	0	0	0	0	0	0	0	0	0
<i>Attiliosa nodulosa</i>	0	0	0	0	0	0	0	0	0	0
<i>Caducifer biliratus</i>	0	0	0	0	0	0	0	0	0	0
<i>Calliostoma bonita</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cancellaria cassidiformis</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 2	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 3	0	0	0	0	0	0	0	0	0	0
<i>Cantharus pallidus</i>	0	0	0	1	0	0	0	0	0	0
<i>Cassis</i> sp.	0	0	0	0	0	0	0	1	0	0
<i>Cerithidea californica mazatlanica</i>	0	0	0	0	0	0	0	0	0	0
<i>Cerithium</i> ? sp.	0	0	0	0	0	0	0	0	0	0
<i>Cerithium</i> sp. cf. <i>menkei</i>	0	0	0	0	0	0	0	0	0	0
<i>C. stercusmuscarum</i>	0	0	0	0	0	0	0	0	0	0
<i>C. uncinatum</i>	2	0	0	0	0	1	0	0	0	0
<i>Chicoreus erythrostomus</i>	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Columbella aureomexicana</i>	0	0	0	0	0	0	0	0	0	0
<i>C. fuscata</i>	0	0	0	0	0	0	0	0	0	0
<i>C. haemastoma</i>	4 (1)	0	2	2	0	1	5	0	0	2

Appendix 1. Continued.

	MPG1	MPG2	MPG3	MPG4	MPG5	MPG6	MPG7	MPG8	MPG9	MPG10
<i>Columbella</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>C. strombiformis</i>	0	0	0	0	0	0	0	0	0	0
<i>Conus archon</i>	0	0	0	0	0	0	0	0	0	0
<i>C. brunneus</i>	0	0	0	0	0	0	16	0	0	0
<i>C. californicus</i>	0	0	0	0	0	0	0	0	0	0
<i>C. diadema</i>	0	0	0	0	0	0	0	0	0	0
<i>C. poormani</i>	0	0	0	0	0	0	0	0	0	0
<i>C. regularis</i>	0	0	0	0	0	0	2	0	0	0
<i>Costoanachis</i> sp. cf. <i>ritteri</i>	2	0	0	1	0	0	0	0	0	0
<i>C. varicosa</i>	0	0	0	2	0	0	0	0	0	0
<i>Crassispira</i> sp. 1	0	0	0	0	0	0	0	0	0	0
<i>C.</i> sp. 2	0	0	0	0	0	0	0	0	0	0
<i>C.</i> spp.	0	0	0	0	0	0	0	0	0	0
<i>Cymatium</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Cypraea albuginosa</i>	0	0	0	0	0	0	0	0	0	1
<i>C. annettae</i>	1	0	0	0	1	0	0	0	0	0
<i>Dermomurex bakeri</i>	0	0	0	0	0	0	0	0	0	0
<i>Enaeta cumingii</i>	0	0	0	0	0	0	0	1	0	0
<i>E.</i> sp. cf. <i>barnesii</i>	0	0	0	0	0	0	0	0	0	0
<i>Engina fusiformis</i>	0	0	0	1	0	2	1	0	0	0
<i>Eupleura muriciformis</i>	0	0	0	0	0	0	0	1	0	0
<i>Fusinus ambustus</i>	0	0	0	0	0	0	0	0	0	0
<i>F.</i> sp.	0	0	0	0	0	0	0	0	0	0
<i>Haminoea angelensis</i>	0	0	0	0	0	0	1	0	0	0

Appendix 1. Continued.

	MBC1	MBC2	MBC3	MBC4	MBC5	MBC6	MBC7	MBC8
<i>Linga cancellaris</i>	2 (1)	2 (1)	0	0	0	0	0	1
<i>Lithophaga aristata</i>	2 (1)	2 (1)	0	0	0	0	0	2
<i>L. sp.</i>	0	0	0	0	0	0	0	0
<i>Lucina centrifuga</i>	0	0	0	0	0	0	0	0
<i>L. fenestrata</i>	11	5	2	2	7 (3)	0	0	3
<i>L. lingualis</i>	2	0	0	0	0	0	0	0
<i>Lucina spp.</i>	0	0	0	0	0	0	0	0
<i>Macra sp. cf. isthmica</i>	0	0	0	0	0	0	0	0
<i>Megapitaria spp.</i>	4	14 (2)	4	8	8	3	13 (1)	7
<i>Modiolus capax</i>	0	0	0	0	0	0	0	0
<i>M. sp. cf. americanus</i>	0	0	0	0	0	0	0	0
<i>Ostrea spp.</i>	1	0	5 (1)	3 (1)	3	0	1	0
<i>Papyridea aspersa</i>	1	0	0	0	0	0	0	0
<i>Parvilucina approximata</i>	0	0	0	0	1	0	0	0
<i>Pinctada mazatlanica</i>	0	0	0	0	0	0	1	0
<i>Pinna rugosa</i>	0	0	0	0	0	0	1	0
<i>Pitar helenae</i>	0	0	0	2	0	1	2	0
<i>Pitar spp.</i>	4	3 (1)	0	1	1	1	0	1
<i>P. sp. cf. berryi</i>	0	0	0	0	0	1	0	0
<i>Plicatula sp. cf. inezana</i>	1	4 (1)	0	2	1	0	1	2
<i>Protothaca columbiensis</i>	0	0	0	0	0	0	0	0
<i>P. grata</i>	0	0	0	0	0	0	0	0
<i>Psammotreta sp.</i>	0	0	0	0	0	0	0	0
<i>Pseudochama clarionensis</i>	2	0	0	0	0	0	0	0

Appendix 1. Continued.

	MBC1	MBC2	MBC3	MBC4	MBC5	MBC6	MBC7	MBC8
<i>Trachycardium senticosum</i>	0	0	0	0	0	0	0	0
<i>T. spp.</i>	0	0	0	0	1	0	0	1
<i>T. sp. cf. procerum</i>	0	0	0	0	0	0	0	0
<i>Tranzenella puella</i>	0	0	0	0	0	0	0	0
<i>Trigonocardia granifera</i>	8	0	0	0	0	0	0	0

Appendix 1. Continued.

	MBC1	MBC2	MBC3	MBC4	MBC5	MBC6	MBC7	MBC8
<i>Columbella</i> sp.	0	0	0	0	0	0	0	0
<i>C. strombiformis</i>	0	0	0	0	0	0	0	0
<i>Conus archon</i>	0	0	0	0	0	0	0	0
<i>C. brunneus</i>	0	0	0	0	0	0	0	0
<i>C. californicus</i>	0	0	0	0	0	0	0	0
<i>C. diadema</i>	0	0	0	0	0	0	0	0
<i>C. poormani</i>	0	1	0	0	0	0	2	0
<i>C. regularis</i>	0	0	0	0	1	1	0	0
<i>Costoanachis</i> sp. cf. <i>ritteri</i>	0	0	0	0	0	0	0	0
<i>C. varicosa</i>	1	0	0	0	5	0	1	3
<i>Crassispira</i> sp. 1	0	0	0	0	0	0	0	0
<i>C.</i> sp. 2	0	0	0	0	0	0	0	0
<i>C.</i> spp.	0	0	0	0	0	0	0	0
<i>Cymatium</i> sp.	0	0	0	0	0	0	0	0
<i>Cypraea albuginosa</i>	0	0	0	0	0	0	0	0
<i>C. annettae</i>	0	1	0	0	0	0	0	0
<i>Dermomurex bakeri</i>	0	0	0	0	0	0	0	0
<i>Enaeta cumingii</i>	6(1)	1	0	3	4(2)	4	3(3)	6(1)
<i>E.</i> sp. cf. <i>barnesii</i>	0	1	0	0	0	0	1	0
<i>Engina fusiformis</i>	0	0	0	0	0	0	0	0
<i>Eupleura muriciformis</i>	0	0	0	0	0	0	0	0
<i>Fusinus ambustus</i>	0	0	0	0	1	0	0	0
<i>F.</i> sp.	0	0	0	0	0	0	0	0
<i>Haminoea angelensis</i>	0	0	0	0	1	0	3(1)	1

Appendix 1. Continued.

BIVALVES	MBC9	MBC10
<i>Amyrcina cultrata</i>	0	0
<i>Anadara formosa</i>	0	0
<i>A. multicosolata</i>	8 (2)	10 (1)
<i>A. spp.</i>	0	0
<i>Arca mutabilis</i>	0	0
<i>A. pacifica</i>	7 (1)	56
<i>A. sp.</i>	0	2
<i>Arcopsis solida</i>	4	4
<i>Barbatia alternata</i>	0	3
<i>B. reeveana</i>	0	1
<i>Basterotia herleini</i>	0	0
<i>Bornia sp. cf. papyracea</i>	0	0
<i>Brachidontes semilaevis</i>	0	0
<i>Carditamera affinis</i>	1	4 (1)
<i>Cardites crassicosolata</i>	0	0
<i>Chama buddiana</i>	0	0
<i>C. frondosa</i>	7 (3)	7
<i>C. mexicana</i>	0	0
<i>C. sp.</i>	0	0
<i>Chione compta</i>	0	0
<i>C. kellestii</i>	0	1
<i>C. mariae</i>	0	0
<i>C. spp.</i>	424 (51)	67
<i>C. subimbricata</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Chionopsis gnidia</i>	0	0
<i>C. purpurisata</i>	0	0
<i>Codakia distinguenda</i>	1	2
<i>Corbula esmeralda</i>	0	0
<i>C. spp.</i>	0	0
<i>C. sp. cf. ira</i>	0	0
<i>C. sp. cf. ovulata</i>	0	0
<i>Cryptomia californica</i>	0	0
<i>Ctena clarionensis</i>	0	0
<i>C. mexicana</i>	44 (4)	23 (2)
<i>Cumingia lamellosa</i>	0	0
<i>Cyathodonta ? spp.</i>	0	0
<i>Diplodonta inezensis</i>	1	0
<i>Divalinga perparvula</i>	0	0
<i>Donax culter</i>	0	0
<i>Dosinia ponderosa</i>	0	0
<i>Felaniella cornea</i>	0	0
<i>Fugleria illota</i>	0	0
<i>Gari sp.</i>	0	0
<i>Globivenus isocardia</i>	0	0
<i>Glycymeris spp. 1</i>	2	5
<i>G. spp. 2</i>	3	10
<i>Laevicardium spp.</i>	4	4
<i>Leporimetis cognata</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Linga cancellaris</i>	0	0
<i>Lithophaga aristata</i>	0	0
<i>L. sp.</i>	0	0
<i>Lucina centrifuga</i>	0	0
<i>L. fenestrata</i>	0	2
<i>L. lingualis</i>	0	0
<i>Lucina spp.</i>	0	0
<i>Macra sp. cf. isthmica</i>	0	0
<i>Megapitaria spp.</i>	4	0
<i>Modiolus capax</i>	0	1
<i>M. sp. cf. americanus</i>	0	0
<i>Ostrea spp.</i>	1	0
<i>Papyridea aspersa</i>	0	0
<i>Parvilucina approximata</i>	0	0
<i>Pinctada mazatlanica</i>	0	0
<i>Pinna rugosa</i>	2	0
<i>Pitar helena</i>	0	0
<i>Pitar spp.</i>	1	1
<i>P. sp. cf. berryi</i>	0	0
<i>Plicatula sp. cf. inezana</i>	0	0
<i>Protohaca columbiensis</i>	0	0
<i>P. grata</i>	0	0
<i>Psammotreta sp.</i>	0	0
<i>Pseudochama clarionensis</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Pteria sterna</i>	0	0
<i>Rupellaria denticulata</i>	0	0
<i>Saccella acrita</i>	0	0
<i>S. spp.</i>	0	0
<i>Semele</i> sp. 1	0	0
<i>Semele</i> spp. 1	0	0
<i>S. spp.</i> 2	0	1
Sp. 1	0	0
Sp. 2	0	0
<i>Sphenia</i> spp.	0	3
<i>Spondylus</i> sp.	0	0
<i>Strophocardia megastrophia</i>	0	0
<i>Tagelus</i> spp.	4	0
<i>Tellina</i> ? sp.	0	0
<i>Tellina coani</i>	0	0
<i>T. cumingii</i>	0	0
<i>T. ochracea</i>	0	0
<i>T. pacifica</i>	0	0
<i>Tellina</i> spp.	0	1
<i>T. sp.</i> 1	0	0
<i>Tivela</i> spp.	0	0
<i>Trachycardium biangulata</i>	11	9
<i>T. consors</i>	0	0
<i>T. panamense</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Trachycardium senticosum</i>	0	0
<i>T. spp.</i>	0	0
<i>T. sp. cf. procerum</i>	0	0
<i>Transenella puella</i>	2 (1)	0
<i>Trigonocardia granifera</i>	0	0

Appendix 1. Continued.

GASTROPODS	MBC9	MBC10
<i>Acanthina</i> ? sp.	0	0
<i>Anachis</i> sp.	0	0
<i>Architectonica nobilis</i>	12 (2)	1
<i>Asperiscala</i> sp. cf. <i>elenense</i>	0	0
<i>Astraea unguis</i>	0	0
<i>Attilosa nodulosa</i>	0	0
<i>Caducifer biliratus</i>	0	0
<i>Calliostoma bonita</i>	0	0
<i>C.</i> sp.	0	0
<i>Cancellaria cassidiformis</i>	0	0
<i>C.</i> sp. 1	0	0
<i>C.</i> sp. 2	0	0
<i>C.</i> sp. 3	0	0
<i>Cantharus pallidus</i>	0	0
<i>Cassis</i> sp.	0	0
<i>Cerithidea californica mazatlanica</i>	0	0
<i>Cerithium</i> ? sp.	0	0
<i>Cerithium</i> sp. cf. <i>menkei</i>	0	0
<i>C. stercusmuscarum</i>	0	0
<i>C. uncinatum</i>	0	0
<i>Chicoreus erythrostomus</i>	0	0
<i>C.</i> sp.	0	0
<i>Columbella aureomexicana</i>	0	0
<i>C. fuscata</i>	0	0
<i>C. haemastoma</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Columbella</i> sp.	0	0
<i>C. strombiformis</i>	0	0
<i>Conus archon</i>	1	0
<i>C. brunneus</i>	0	0
<i>C. californicus</i>	0	0
<i>C. diadema</i>	0	0
<i>C. poormani</i>	0	0
<i>C. regularis</i>	1	0
<i>Costoanachis</i> sp. cf. <i>ritteri</i>	0	0
<i>C. varicosa</i>	2	0
<i>Crassispira</i> sp. 1	0	0
<i>C.</i> sp. 2	0	0
<i>C.</i> spp.	0	0
<i>Cymatium</i> sp.	0	0
<i>Cypraea albuginosa</i>	0	0
<i>C. annettae</i>	0	0
<i>Dermomurex bakeri</i>	0	0
<i>Enaeta cunningii</i>	2 (1)	1 (1)
<i>E.</i> sp. cf. <i>barnesii</i>	0	0
<i>Engina fusiformis</i>	0	0
<i>Eupleura muriciformis</i>	0	0
<i>Fusinus ambustus</i>	0	0
<i>F.</i> sp.	0	0
<i>Haminoea angelensis</i>	1	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Hexaplex princeps</i>	0	0
<i>Kurtziella plumbea</i>	0	0
<i>Leukozenia</i> ? sp.	0	0
<i>Liocerithium judithae</i>	0	0
<i>Macrarenne</i> spp.	37 (12)	33 (5)
<i>Mancinella speciosa</i>	0	0
<i>M. triangularis</i>	0	0
<i>M. tuberculata</i>	0	0
<i>Mitra</i> sp.	0	0
<i>Mitrella</i> sp. cf. <i>dorma</i>	0	0
<i>Modulus cerodes</i>	1	1
<i>Murexiella</i> spp.	0	0
<i>Muricopsis armatus</i>	2	0
<i>Nassarius iodes</i>	0	0
<i>N. luteostomus</i>	4 (1)	19 (8)
<i>N. nodicinctus</i>	1	1
<i>N. sp. 1</i>	0	0
<i>N. sp. 2</i>	2	0
<i>Natica grayi</i>	0	0
<i>N. sp. 1</i>	0	0
<i>N. sp. 2</i>	0	0
<i>Nerita funiculata</i>	1	0
<i>Neverita reclusiana</i>	0	0
<i>Oliva davisae</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Oliva</i> spp.	0	0
<i>Olivella dama</i>	0	4 (4)
<i>Persicula imbricata</i>	0	0
<i>Pilsbryspira</i> sp. 1	0	0
<i>P.</i> sp. 2	0	0
<i>Polinices</i> sp.	0	0
<i>P.</i> spp.	0	0
<i>Pyramidella</i> sp.	0	0
<i>Rhinoclavis gemmata</i>	0	0
<i>Rhinocoryne</i> sp. cf. <i>humboldtii</i>	0	0
<i>Solenosteira</i> sp. 1	0	0
<i>S.</i> sp. 2	0	0
<i>S.</i> sp. 3	0	0
<i>S.</i> sp. 4	0	0
<i>Splendrillia</i> sp. cf. <i>arga</i>	0	0
<i>Strombina maculosa</i>	1	2 (1)
<i>S.</i> sp. cf. <i>solidula</i>	0	0
<i>Strombus</i> spp.	0	0
<i>Subcancilla sulcata</i>	0	0
<i>Tegula funebris</i>	0	0
<i>T. rugosa</i>	0	0
<i>T.</i> spp.	12 (2)	4 (2)
<i>T.</i> sp. cf. <i>felipensis</i>	0	0
<i>Terebra hancocki</i>	0	0

Appendix 1. Continued.

	MBC9	MBC10
<i>Terebra intertincta</i>	0	0
<i>T. ornata</i>	0	0
<i>T. spp.</i>	0	0
<i>T. variegata</i>	0	0
<i>Trachypollia lugubris</i>	0	0
<i>Trigonostoma</i> sp.	0	0
<i>Trivia solandri</i>	0	0
<i>Turbo fluctuosus</i>	10 (3)	1
<i>T. squamiger</i>	0	0
<i>Turritella lentiginosa</i>	0	0
<i>T. nodulosa</i>	0	0
<i>Turritella</i> sp. 1	0	0
<i>T. sp. 2</i>	0	0
UNK 1	0	0
UNK 2	0	0
UNK 3	0	0
UNK 4	0	0
UNK 5	0	0
UNK 6	0	0
<i>Vermetus indentatus</i>	0	0
<i>Vermicularia pellicida eburnea</i>	0	0

Appendix 2. Selection of most appropriate similarity index.

Molluscs from Punta Chivato Pleistocene and recent rhodolith assemblages were used to compare the performance of the four binary similarity indices (Jaccard, Sorensen, Baroni-Urbani and Buser, and Simple matching coefficients) provided in Kenney and Krebs (1998). Most of the indices vary between 0 and 1, but some discrepancies have been reported as a result of sample size variation (Wolda, 1981; Krebs 1999). Therefore, standardization was done if an index exceed range values. Similarity coefficients were standardized to a 0 - 1 range using proportions. The null hypothesis of no difference in similarity between Pleistocene and modern samples and within Pleistocene was tested. Selection of the “best” similarity coefficient was done based on the relative performance (precision and α level of the statistical test) of the four indices. Similarity variation among all possible balanced sample sizes for each index was compared using graphic and statistical techniques. Index performance variation was compared graphically using average similarity values and their standard errors (SE). The statistical analyses for similarity between Pleistocene and modern samples and within Pleistocene were performed with only the 20 estimated coefficients (from each index) that were independent from each other.

Similarity values were non-normally distributed and transformation did not make them normal. Nevertheless, parametric statistical tests (two sample t-tests) were still done as these tests were assumed to be robust to non-normality (Sokal and Röhlf, 1997; Underwood, 1997). Although parametric tests are also robust to heteroscedasticity (Zar,

1996), non-parametric tests (Wilcoxon ranks tests) were used when both parametric assumptions were violated. Power analysis ($\alpha = 0.05$) was estimated as $t_{\beta(1),v} \leq \delta / \sqrt{(2s^2_p / n) - t_{\alpha,v}}$ (Cohen, 1988; Zar 1996). Although Jaccard coefficient had the smallest SE among the compared indices (Table I), it was not used because it was the only index that violated both parametric criteria. The Sorensen coefficient had the best performance relative to the other indices, but because the software used (Primer IV) did not include this coefficient, Bray Curtis, the inverse of Sorensen's was used (Clifford and Stephenson, 1975).

Appendix 2, Table I. Comparison of similarity coefficients. $n = 10$ per time. For statistical analyses, only results from two sample t-tests are shown. F = within Pleistocene and B = between Pleistocene and modern samples.

Index	Mean (SE)	$t_{0.05(18)}$ (P)
F Jaccard	0.52 (0.05)	
B Jaccard	0.23 (0.02)	
F Sorensen	0.67 (0.03)	6.17
B Sorensen	0.37 (0.03)	(< 10^{-6})
F Simple matching	0.61 (0.04)	4.41
B Simple matching	0.37 (0.03)	(< 10^{-4})
F Baroni-Urbani and Buser	0.64 (0.04)	5.14
B Baroni-Urbani and Buser	0.37 (0.03)	(< 10^{-5})

Appendix 2, Literature cited

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Appendix 3. Molluscan taxa found associated with rhodolith beds in the Gulf of California. **F** = Fossil (Pleistocene), **M** = Modern. Locations: **PC** = Punta Chivato, **BC** = Bahía Concepción, **PG** = Punta Galeras. ? = Uncertain identification at the taxa level indicated.

Phylum Mollusca

Class Bivalvia Linnaeus, 1758

Order Nuculoidea (Gray, 1824 as superfamily)

Family Nuculanidae H. & A. Adams, 1858

Genus *Saccella* Woodring, 1925

Species *Saccella acrita* (Dall, 1908) **FPC, MBC**

Saccella spp. **FPC**

Order Arcoida Stoliczka, 1871

Family Arcidae Lamarck, 1809

Genus *Arca* Linnaeus, 1758

Species *Arca mutabilis* (Sowerby, 1833) **FPC, MBC, FPG**

Arca pacifica (Sowerby, 1833) **FPC, MPC, MBC**

Arca sp. **FPC, MBC, FPG, MPG**

Genus *Barbatia* Gray, 1842

Species *Barbatia alternata* (Sowerby, 1833) **FPC, MBC, FPG**

Barbatia reeveana (Orbigny, 1846) **FPC, MBC, FPG, MPG**

Genus *Fugleria* Reinhart, 1937

Species *Fugleria illota* (Sowerby, 1833) **FPC, FPG**

Genus *Anadara* Gray, 1847

Species *Anadara formosa* (Sowerby, 1833) **MPG**

Anadara multicostata (Sowerby, 1833) **In all samples**

Anadara spp. **FPC, MBC, FPG, MPG**

Genus *Arcopsis* von Koenen, 1885

Species *Arcopsis solida* Sowerby, 1833 **In all samples**

Family Glycymerididae Newton, 1922

Genus *Glycymeris* Da Costa, 1778

Species *Glycymeris* spp. 1 **In all samples**

Glycymeris spp. 2 **In all samples**

Order Mytiloida Férussac, 1822

Family Mytilidae Rafinesque, 1815

Genus *Brachidontes* Swainson, 1840

Species *Brachidontes semilaevis* (Menke, 1849) **FPC, MPG**

Genus *Lithophaga* Röding, 1798

Species *Lithophaga aristata* (Dillwyn, 1817) **MPC, MBC**

Lithophaga sp. **FPC**

Genus *Modiolus* Lamarck, 1799

Species *Modiolus* sp. cf. *americanus* (Leach, 1815) **MPC**

Modiolus capax (Conrad, 1937) **FPC, MPC, MBC**

Order Pterioida Newell, 1965

Family Pinnidae Leach, 1819

Genus *Pinna* Linnaeus, 1758

Species *Pinna rugosa* Sowerby, 1835 **MBC, MPG**

Family Pteriidae Broderip, 1839

Genus *Pteria* Scopoli, 1777

Species *Pteria sterna* (Gould, 1851) **MPG**

Genus *Pinctada* Röding, 1798

Species *Pinctada mazatlanica* (Hanley, 1856) **MBC**

Order Ostreoida Férussac, 1822

Family Ostreidae Rafinesque, 1815

Genus *Ostrea* Linnaeus, 1758

Species *Ostrea* spp. **In all samples**

Family Plicatulidae Watson, 1930

Genus *Plicatula* Lamarck, 1801

Species *Plicatula* sp. cf. *inezana* Durham, 1950 **In all samples**

Family Spondylidae Gray, 1826

Genus *Spondylus* Linnaeus, 1758

Species *Spondylus* sp. **FPG**

Order Veneroida H. & A. Adams, 1856

Family Carditidae Fleming, 1828

Genus *Cardites* Link, 1807

Species *Cardites crassicostata* (Sowerby, 1825) **FPC, MPC, FPG**

Genus *Strophocardia* Olsson, 1961

Species *Strophocardia megastrophia* (Gray, 1825) **FPC, MPC, FPG, MPG**

Genus *Carditamera* Conrad, 1838

Species *Carditamera affinis* Sowerby, 1833 **FPC, MBC, FPG**

Family Lucinidae Fleming, 1828

Genus *Lucina* Bruguière, 1797

Species *Lucina lingualis* Carpenter, 1864 **In all samples**

Lucina centrifuga (Dall, 1901) **MPC**

Lucina fenestrata Hinds, 1845 **In all samples**

Lucina spp. **FPC, MPC, FPG**

Genus *Parvilucina* Dall, 1901

Species *Parvilucina approximata* (Dall, 1901) **FPC, MBC**

Genus *Linga* de Gregorio, 1884

Species *Linga cancellaris* (Philippi, 1846) **MBC, FPG**

Genus *Codakia* Mörch, 1860

Species *Codakia distinguenda* (Tryon, 1872) **In all samples**

Genus *Ctena* Mörch, 1860

Species *Ctena clarionensis* Hertlein & Strong, 1946 **FPC**

Ctena mexicana (Dall, 1901) **In all samples**

Genus *Divalinga* Chavan, 1951

Species *Divalinga perparvula* (Dall, 1901) **FPC, FPG, MPG**

Family Ungulinidae H. & A. Adams, 1857

Genus *Diplodonta* Bronn, 1831

Species *Diplodonta inezensis* (Hertlein & Strong, 1947) **FPC, MBC**

Genus *Felaniella* Dall, 1899

Species *Felaniella cornea* (Reeve, 1850) **FPC, MBC**

Family Erycinidae Deshayes, 1850

Genus *Amerycina* Chavan, 1959

Species *Amerycina cultrata* Keen, 1971 **FPG**

Family Kellidae Clark, 1851

Genus *Bornia* Philippi, 1836

Species *Bornia* sp. cf. *papyracea* (Deshayes, 1856) **MPC, MPG**

Family Sportellidae Dall, 1899

Genus *Basterotia* Hornes, 1859

Species *Basterotia hertleini* Durham, 1950 **FPC, MPC**

Family Chamidae Blainville, 1825

Genus *Chama* Linnaeus, 1758

Species *Chama buddiana* C.B. Adams, 1852 **FPC, MBC, FPG**

Chama frondosa Broderip, 1835 **MBC**

Chama mexicana Carpenter, 1857 **FPC, MPC, MBC, FPG**

Chama sp. **FPG**

Genus *Pseudochama* Odhner, 1917

Species *Pseudochama clarionensis* Willett, 1938 **FPC, MBC**

Family Cardiidae Lamarck, 1809

Genus *Trachycardium* Mörch, 1853

Species *Trachycardium consors* (Sowerby, 1833) **FPC, MBC, FPG, MPG**

Trachycardium senticosum (Sowerby, 1833) **FPC, FPG**

Trachycardium panamense (Sowerby, 1833) **FPC, FPG**

Trachycardium sp. cf. *procerum* (Sowerby, 1833) **FPC**

Trachycardium biangulata (Broderip & Sowerby, 1829) **In all samples**

Trachycardium spp. **FPC, MBC, FPG**

Genus *Papyridea* Swainson, 1840

Species *Papyridea aspersa* (Sowerby, 1833) **FPC, MPC, MBC, FPG**

Genus *Trigoniocardia* Stewart, 1930

Species *Trigoniocardia granifera* (Broderip & Sowerby, 1829) **MBC**

Genus *Laevicardium* Swainson, 1840

Species *Laevicardium* spp. **In all samples**

Family Veneridae Rafinesque, 1815

Genus *Globivenus* Coen, 1934

Species *Globivenus isocardia* (Verrill, 1870) **MPC, FPG, MPG**

Genus *Tivela* Link, 1807

Tivela spp. **FPC, MPC, FPG, MPG**

Genus *Transenella* Dall, 1884

Species *Transenella puella* (Carpenter, 1864) **MPC, MBC, MPG**

Genus *Pitar* Römer, 1857

Species *Pitar* sp. cf. *berryi* Keen, 1971 **FPC, MPC, MBC, FPG**

Pitar helenae Olsson, 1961 **MBC**

Pitar spp. **In all samples**

Genus *Megapitaria* Grant & Gale, 1931

Species *Megapitaria* spp. **In all samples**

Genus *Dosinia* Gray, 1835

Species *Dosinia ponderosa* (Schumacher, 1817) **FPC, MPC, MBC, FPG**

Genus *Chione* Megerle, 1811

Species *Chione compta* (Broderip, 1835) **MPC**

Chione subimbricata (Sowerby, 1835) **FPC, MPC, FPG**

Chione kelletii (Hinds, 1845) **MPC, MBC**

Chione mariae (Orbigny, 1846) **FPC, MBC**

Chione spp. **In all samples**

Genus *Chionopsis* Olsson, 1932

Species *Chionopsis gnidia* (Broderip & Sowerby, 1829) **MPC, MBC, MPG**

Chionopsis purpurissata (Dall, 1902) **MBC, MPG**

Genus *Protothaca* Dall, 1902

Species *Protothaca columbiensis* (Sowerby, 1835) **FPG**

Protothaca grata (Say, 1831) **FPC, MPC, FPG**

Family Petricolidae Deshayes, 1831

Genus *Rupellaria* Fleury de Bellevue, 1802

Species *Rupellaria denticulata* (Sowerby, 1834) **FPC, MBC**

Family Mactridae Lamarck, 1809

Genus *Maetra* Linnaeus, 1767

Species *Maetra* sp. cf. *isthmica* Pilsbry & Lowe, 1932 **FPC**

Family Tellinidae Blainville, 1814

Genus *Tellina* Linnaeus, 1758

Species *Tellina coani* Keen, 1971 **FPC, MBC**

Tellina pacifica Dall, 1900 **MPC, MPG**

Tellina ochracea Carpenter, 1864 **FPC, MBC, FPG**

Tellina cumingii Hanley, 1844 **In all samples**

Tellina sp. 1 **FPC, MPC, FPG**

Tellina spp. **FPC, MBC, FPG MPG**

Tellina ? sp. **MPG**

Genus *Leporimetis* Iredale, 1930

Species *Leporimetis cognata* (Pilsbry & Vanatta, 1902) **FPC, FPG**

Genus *Psammotreta* Dall, 1900

Species *Psammotreta* sp. **MPG**

Family Donacidae Fleming, 1828

Genus *Donax* Linnaeus, 1758

Species *Donax culter* Hanley, 1845 **FPC, FPG**

Family Psammobiidae Fleming, 1828

Genus *Gari* Schumacher, 1817

Species *Gari* sp. **MBC, MPG**

Genus *Tagelus* Gray, 1847

Species *Tagelus* spp. **FPC, MPC, MBC**

Family Semelidae Stoliczka, 1870

Genus *Semele* Schumacher, 1817

Species *Semele* sp. **FPC, MBC**

Semele spp. 1 **FPC, MPC, MBC, MPG**

Semele spp. 2 **FPC**

Genus *Cumingia* Sowerby, 1833

Species *Cumingia lamellosa* Sowerby, 1833 **FPC**

Order Myoida Stoliczka, 1870

Family Myidae Lamarck, 1809

Genus *Cryptomia* Conrad, 1848

Species *Cryptomia californica* (Conrad, 1837) **FPC, MBC**

Genus *Sphenia* Turton, 1822

Species *Sphenia* sp. **FPC, MBC**

Family Corbulidae Lamarck, 1818

Genus *Corbula* Bruguière, 1797

Species *Corbula* sp. cf. *ovulata* Sowerby, 1833 **FPC, MPG**

Corbula esmeralda Olsson, 1961 **FPC, MPC, MBC**

Corbula sp. cf. *ira* Dall, 1908 **FPC, MPC**

Corbula spp. **MPG**

Order Pholadomyoidea Newell, 1965

Family Thraciidae Stoliczka, 1870 [1830]

Genus *Cyathodonta* Conrad, 1849

Species *Cyathodonta* ? spp. **FPC, MPC, MPG**

Undetermined taxa

Sp. 1 **FPC**

Sp. 2 **MPC**

Class Gastropoda Cuvier, 1797

Order Patellogastropoda Lindberg, 1986

Family Turbinidae Rafinesque, 1815

Genus *Macrarene* Hertlein & Strong, 1951Species *Macrarene* spp. **In all samples**Genus *Turbo* Linnaeus, 1758Species *Turbo fluctuosus* Wood, 1828 **In all samples***Turbo squamiger* Reeve, 1843 **FPC, MPC, FPG**Genus *Astraea* Röding, 1798Species *Astraea unguis* (Wood, 1828) **FPC**

Family Trochidae Rafinesque, 1815

Genus *Tegula* Lesson, 1835Species *Tegula rugosa* (A. Adams, 1853) **FPC***Tegula* sp. cf. *felipensis* Mc Lean, 1970 **FPC, MPC, MBC***Tegula funebris* (A. Adams, 1855) **FPC***Tegula* spp. **FPC, MPC, MBC, FPG**Genus *Calliostoma* Swainson, 1840Species *Calliostoma bonita* Strong, Hanna & Hertlein, 1933 **FPC, FPG***Calliostoma* sp. **FPC**

Family Neritidae Rafinesque, 1815

Genus *Nerita* Linnaeus, 1758Species *Nerita funiculata* Menke, 1851 **MBC, FPG**

Order Neotaenioglossa Haller, 1882

Family Vermetidae Rafinesque, 1815

Genus *Vermetus* Daudin, 1800

Species *Vermetus indentatus* (Carpenter, 1857) **FPC**

Family Turritellidae Löven, 1847

Genus *Turritella* Lamarck, 1799

Species *Turritella lentiginosa* Reeve, 1849 **FPC**

Turritella nodulosa King & Broderip, 1832 **FPC, FPG, MPG**

Turritella sp. 1 **MPC, FPG**

Turritella sp. 2 **FPC**

Genus *Vermicularia* Lamarck, 1799

Species *Vermicularia pellucida eburnea* (Reeve, 1842) **FPC, FPG**

Family Modulidae Fischer, 1884

Genus *Modulus* Potiez & Michaud, 1838

Species *Modulus cerodes* (A. Adams, 1851) **MBC**

Family Cerithiidae Fleming, 1822

Genus *Cerithium* Bruguière, 1789

Species *Cerithium* sp. cf. *menkei* Carpenter, 1857 **FPC, MBC, FPG**

Cerithium stercusmuscarum Valenciennes, 1833 **FPC**

Cerithium uncinatum (Gmelin, 1791) **MPC, MPG**

Cerithium ? sp. **FPC**

Genus *Liocerithium* Tryon, 1887

Species *Liocerithium judithae* Keen, 1971 **FPG**

Genus *Rhinoclavis* Swainson, 1840

Species *Rhinoclavis gemmata* (Hinds, 1844) **FPC, FPG**

Family Potamididae Houbrick, 1991

Genus *Cerithidea* Swainson, 1840

Species *Cerithidea californica mazatlanica* Carpenter, 1857 **FPC, MPC**

Family Batillariidae Raised from subfamily (Houbrick, 1988, 1991)

Genus *Rhinocoryne* von Martens, 1900

Species *Rhinocoryne* sp. cf. *humboldti* (Valenciennes, 1832) **FPC, FPG**

Family Strombidae Rafinesque, 1815

Genus *Strombus* Linnaeus, 1758

Species *Strombus* spp. **In all samples**

Family Naticidae Forbes, 1838

Genus *Natica* Scopoli, 1777

Species *Natica grayi* Philippi, 1852 **FPG, MPG**

Natica sp. 1 **FPG**

Natica sp. 2 **FPG**

Genus *Polinices* Montfort, 1810

Species *Polinices* sp. **FPC**

Polinices spp. **In all samples**

Genus *Neverita* Risso, 1826

Species *Neverita reclusiana* (Deshayes, 1839) **FPC, MPC, FPG**

Family Triviidae Troschel, 1863

Genus *Trivia* Broderip, 1837

Species *Trivia solandri* (Sowerby, 1832) **FPC, FPG**

Family Cypraeidae Rafinesque, 1815

Genus *Cypraea* Linnaeus, 1758

Species *Cypraea albuginosa* Gray, 1825 **MPG**

Cypraea annettae Dall, 1909 **In all samples**

Family Cassidae Latreille, 1825

Genus *Cassis* Scopoli, 1777

Species *Cassis* sp. **MPG**

Family Ranellidae Gray, 1854

Genus *Cymatium* Röding, 1798

Species *Cymatium* sp. **MPC**

Family Epitoniidae Berry, 1910

Genus *Asperiscula* De Boury, 1909

Species *Asperiscula* sp. cf. *elenense* (Sowerby, 1844) **MBC**

Family Muricidae Rafinesque, 1815

Genus *Chicoreus* Montfort, 1810

Species *Chicoreus erythrostomus* (Swainson, 1831) **MBC**

Chicoreus sp. **FPC**

Genus *Hexaplex* Perry, 1810

Species *Hexaplex princeps* (Broderip, 1833) **FPC**

Genus *Dermomurex* Monterosato, 1890

Species *Dermomurex bakeri* (Hertlein & Strong, 1951) **FPG**

Genus *Attiliosa* Emerson, 1968

Species *Attiliosa nodulosa* (A. Adams, 1855) **FPG**

Genus *Murexiella* Clench & Pérez Farfante, 1945

Species *Murexiella* spp. **FPC, MPG**

Genus *Muricopsis* Bucquoy, Dautzenberg & Dollfus, 1892

Species *Muricopsis armatus* (A. Adams, 1854) **MBC**

Genus *Eupleura* H. & A. Adams, 1853

Species *Eupleura muriciformis* (Broderip, 1833) **FPC, MPC, MPG**

Genus *Mancinella* Link, 1807

Species *Mancinella speciosa* (Valenciennes, 1832) **FPC, FPG**

Mancinella triangularis (Blainville, 1832) **FPG**

Mancinella tuberculata (Sowerby, 1835) **FPG**

Genus *Acanthina* Fischer de Waldheim, 1809

Species *Acanthina* ? sp. **FPC, FPG, MPG**

Genus *Trachypollia* Woodring, 1928

Species *Trachypollia lugubris* (C.B. Adams, 1852) **FPC, MPC, FPG, MPG**

Family Buccinidae Rafinesque, 1815

Genus *Caducifer* Dall, 1904

Species *Caducifer biliratus* (Reeve, 1846) **FPC, FPG**

Genus *Cantharus* Röding, 1798

Species *Cantharus pallidus* (Broderip & Sowerby, 1829) **FPC, FPG, MPG**

Genus *Solenosteira* Dall, 1890

Species *Solenosteira* sp. 1 **FPC, FPG**

Solenosteira sp. 2 **FPC, MPG**

Solenosteira sp. 3 **FPC, FPG**

Solenosteira sp. 4 **FPC**

Genus *Engina* Gray, 1839

Species *Engina fusiformis* Stearns, 1894 **FPC, MPC, MPG**

Genus *Nassarius* Dumèril, 1806

Species *Nassarius iodes* (Dall, 1917) **FPC**

Nassarius luteostomus (Broderip & Sowerby, 1829) **FPC, MBC, FPG**

Nassarius nodicinctus (A. Adams, 1852) **In all samples**

Nassarius sp. 1 **FPC, MBC, FPG**

Nassarius sp. 2 **In all samples**

Genus *Leukozonia* Gray, 1847

Species *Leukozonia* ? sp. **FPC**

Genus *Fusinus* Rafinesque, 1815

Species *Fusinus ambustus* (Gould, 1853) **FPC, MBC, FPG**

Fusinus sp. **FPC, FPG**

Family Columbellidae Swainson, 1840

Genus *Columbella* Lamarck, 1799

Species *Columbella aureomexicana* (Howard, 1963) **FPC, FPG**

Columbella fuscata Sowerby, 1832 **FPC, FPG**

Columbella haemastoma Sowerby, 1832 **MPC, FPG, MPG**

Columbella strombiformis Lamarck, 1822 **FPC**

Columbella sp. **FPC, FPG**

Genus *Anachis* H. & A. Adams, 1853

Species *Anachis* sp. **MPG**

Genus *Costoanachis* Sacco, 1890

Species *Costoanachis* sp. cf. *ritteri* (Hertlein & Strong, 1951) **FPG, MPG**

Costoanachis varicosa (Gaskoin, 1852) **In all samples**

Genus *Mitrella* Risso, 1826

Species *Mitrella* sp. cf. *dorma* Baker, Hanna & Strong, 1938 **MPC, MPG**

Genus *Strombina* Mörch, 1852

Species *Strombina* sp. cf. *solidula* (Reeve, 1859) **FPG**

Strombina maculosa (Sowerby, 1832) **In all samples**

Family Volutidae Rafinesque, 1815

Genus *Enaeta* H. & A. Adams, 1853

Species *Enaeta* sp. cf. *barnesii* (Gray, 1825) **MBC**

Enaeta cumingii (Broderip, 1832) **FPC, MBC, FPG, MPG**

Family Olividae Latreille, 1825

Genus *Oliva* Bruguière, 1789

Species *Oliva davisae* Durham, 1950 **FPC**

Oliva spp. **FPC, MPC, FPG, MPG**

Family Olivellidae Troschel, 1869

Genus *Olivella* Swainson, 1840

Species *Olivella dama* (Wood, 1828) **In all samples**

Family Marginellidae Fleming, 1828

Genus *Persicula* Schumacher, 1817

Species *Persicula imbricata* (Hinds, 1844) **FPG**

Family Mitridae Swainson, 1831

Genus *Mitra* Lamarck, 1798

Species *Mitra* sp. **FPC, FPG**

Genus *Subcancilla* Olsson & Harbison, 1953

Species *Subcancilla sulcata* (Swainson in Sowerby, 1825) **FPC, FPG**

Family Cancellariidae Forbes & Hanley, 1851

Genus *Cancellaria* Lamarck, 1799

Species *Cancellaria cassidiformis* Sowerby, 1832 **FPC**

Cancellaria sp. 1 **FPG**

Cancellaria sp. 2 **FPC, FPG**

Cancellaria sp. 3 **FPC**

Genus *Trigonostoma* Blainville, 1827

Species *Trigonostoma* sp. **MBC**

Family Conidae Fleming, 1822

Genus *Conus* Linnaeus, 1758

Species *Conus brunneus* Wood, 1828 **FPC, MPC, FPG, MPG**

Conus diadema Sowerby, 1834 **FPC, FPG**

Conus californicus Reeve, 1844 **FPC**

Conus poormani Berry, 1968 **FPC, MPC, MBC, FPG**

Conus regularis Sowerby, 1833 **In all samples**

Conus archon Broderip, 1833 **MBC**

Family Terebridae Mörch, 1852

Genus *Terebra* Bruguière, 1789

Species *Terebra hancocki* Bratcher & Burch, 1970 **FPC**

Terebra intertincta Hinds, 1844 **FPC, FPG**

Terebra ornata Gray, 1834 **MPC, FPG, MPG**

Terebra variegata Gray, 1834 **FPC, MPC, FPG**

Terebra spp. **FPC**

Family Turridae Swainson, 1840

Genus *Splendrillia* Hedley, 1922

Species *Splendrillia* sp. cf. *arga* Mc Lean & Poorman, 1971 **FPG**

Genus *Crassispira* Swainson, 1840

Species *Crassispira* sp. 1 **FPG**

Crassispira sp. 2 **FPC, FPG**

Crassispira spp. **FPC, FPG**

Genus *Pilsbryspira* Bartsch, 1950

Species *Pilsbryspira* sp. 1 **FPC, FPG**

Pilsbryspira sp. 2 **FPC**

Genus *Kurtziella* Dall, 1918

Species *Kurtziella plumbea* (Hinds, 1843) **FPC**

Order Heterostropha Fischer, 1885

Family Architectonicidae Gray, 1850

Genus *Architectonica* Röding, 1798

Species *Architectonica nobilis* Röding, 1798 **FPC, MPC, MBC, FPG**

Family Pyramidellidae Gray, 1840

Genus *Pyramidella* Lamarck, 1799

Species *Pyramidella* sp. **FPG**

Order Cephalaspidea Fischer, 1883

Family Bullidae Lamarck, 1801

Genus *Haminoea* Turton & Kingston in Carrington, 1830

Species *Haminoea angelensis* Baker & Hanna, 1927 **FPC, MBC, FPG, MPG**

UNK = Unknown (for the author) taxa

UNK 1 **FPG**

UNK 2 **FPC**

UNK 3 **FPC, FPG, MPG**

UNK 4 **FPG**

UNK 5 **FPG**

UNK 6 **MBC**