

**Title**

Effects of dams on downstream molluscan predator-prey interactions in the Colorado River estuary

**Authors**

Jansen A. Smith (jas933@cornell.edu)<sup>1</sup>

John C. Handley (handley@priweb.org)<sup>2</sup>

Gregory P. Dietl (gpd3@cornell.edu)<sup>1,2</sup>

**Affiliations**

1. Department of Earth and Atmospheric Sciences, Cornell University, Ithaca, NY 14853;

2. Paleontological Research Institution, Ithaca, NY, 14850

**Corresponding Author**

Jansen Smith, [jas933@cornell.edu](mailto:jas933@cornell.edu); telephone: 608-498-2331; fax: 607-273-6620

**Electronic supplementary material S4. Assessment of alternative explanations for north-south changes to predator preferences in the Colorado River estuary**

Several factors might explain the reduction in *Neverita reclusiana* preference for *Mulinia modesta*, and increased preference for alternative prey species, from north to south in the Colorado River estuary (CRE). Two can be readily dismissed (i.e., transportation bias and *M. modesta* relative abundance); however, four others require more extensive analysis.

Transportation bias [1,2] could be an important explanatory factor if: (i) there was north-south variability in formation of the shell assemblages such that certain species were more likely to be omitted or included, or (ii) drilled and undrilled shells were transported differently. Neither is likely, however, given that the same process of chenier formation occurs at each of the three sites. When cheniers form—often on scales of years or decades (e.g., the modern chenier in the CRE has been forming for approximately 90 years [3])—tidal and wave action push large clasts (e.g., sand size particles and larger) towards the shoreline [4]. Subsequently, longshore currents and resuspension of fine-grain sediments (e.g., silts, clays) lead to the removal of these small clasts [4]. Additionally, although there are between-species differences in shell morphology that

may make the shells of some species more hydrodynamically stable than others and influence shell transport on short time scales (e.g., at and below the annual scale), the process of chenier formation moves large clasts toward the shoreline and, given that the processes act over extended periods of time (i.e., decades to centuries), between-species differences do not impact the outcome. Likewise, whereas drill holes may influence the overall hydrodynamic behavior of a shell [2], the shell itself is still sufficiently large (e.g., > 5 mm sieve size in the present study) that it will remain in the chenier.

Differences in *M. modesta* relative abundance can similarly be dismissed. The reduction in preference for *M. modesta* corresponds to the reduction in *M. modesta* relative abundance in the CRE. Thus, it might be tempting to assume a causal relationship between the two variables. Such an argument is readily dismissed, however, as relative abundance is accounted for in the calculation of alpha. That is, alpha values are normalized such that they can be interpreted as the likelihood a predator would consume a given prey species in the event all prey species were present in equal abundances [5]. *Mulinia modesta* relative abundance did decrease north to south [6], but those changes have been accounted for in the analysis.

The remaining four alternative explanations require subsequent data collection or analysis in order to be dismissed. Therefore, each is given its own section below: taphonomic bias, body-size bias, durophagous predation, and multiple drilling predators. None of these alternatives provide feasible explanations for the north-south increase in predation intensity in the CRE.

#### **S4.1 Assessing common species to evaluate potential for taphonomic bias**

In this analysis, we considered only species found at all three of the localities (n=10), thereby constraining the effects of taphonomic bias, which may be an important explanatory

factor if there was an interaction between species richness and preservation potential.

Additionally, by using a consistent number of prey species the null alpha value was equivalent at all localities, facilitating a direct comparison of preferences between localities. To do so, we fitted two models, one where Manly's alpha was allowed to vary by locality and a second where the alpha was held constant across localities. The performance of these models was then compared using Deviance Information Criterion (DIC; [7]).

The models were derived from the multinomial distribution on predation counts  $r = (r_1, \dots, r_m)$ , where  $m$  is the number of taxa, for the likelihood of Manly's alpha:

$$f(r; \alpha, n) = \frac{r!}{r_1! \cdots r_m!} \prod_{i=1}^m \left( \frac{\alpha_i n_i}{\sum_{j=1}^m \alpha_j n_j} \right)^{r_i}$$

where  $r = r_1 + \dots + r_m$ ,  $n_i$  are the taxon counts, and  $\alpha = (\alpha_1, \dots, \alpha_m)$  where each  $\alpha_i \geq 0$  and  $\alpha_1 + \dots + \alpha_m = 1$ . The Bayesian model we used for Manly's alpha assumes a Dirichlet prior for  $\alpha$ :  $\alpha \sim \text{Dir}(q\mathbf{w})$ . Parameter  $q = (q_1, \dots, q_m)$  has a  $\text{Dir}(1/m, \dots, 1/m)$  prior and parameter  $w$ , which captures the variance of  $\alpha$  as a  $\text{Gamma}(0.001, 0.001)$  prior [8]. Using this distribution, the common alpha model was derived as:

$$g(\alpha; r_{IM}, r_{LI}, r_{CDA}, n_{IM}, n_{LI}, n_{CDA}) \propto f(r_{IM}; \alpha, n_{IM}) f(r_{LI}; \alpha, n_{LI}) f(r_{CDA}; \alpha, n_{CDA}) \text{Dir}(\alpha; q\mathbf{w})$$

and the different alpha model as:

$$h(\alpha_{IM}, \alpha_{LI}, \alpha_{CDA}; r_{IM}, r_{LI}, r_{CDA}, n_{IM}, n_{LI}, n_{CDA}) \\ \propto f(r_{IM}; \alpha_{IM}, n_{IM}) f(r_{LI}; \alpha_{LI}, n_{LI}) f(r_{CDA}; \alpha_{CDA}, n_{CDA}) \text{Dir}(\alpha_{IM}; q\mathbf{w}) \text{Dir}(\alpha_{LI}; q\mathbf{w}) \text{Dir}(\alpha_{CDA}; q\mathbf{w})$$

DIC was 141.3 for the common alpha model and 98.2 for the different alpha model. The smaller DIC value indicates more support for the different alpha model and, given that the DIC difference is greater than 10, there is strong support to conclude preferences were different among localities. Examination of the calculated alpha values for all three localities when the species were held constant confirms this conclusion (S4 table 1). Furthermore, the results of this analysis confirm that *M. modesta* was not the only species preferred by *N. reclusiana*.

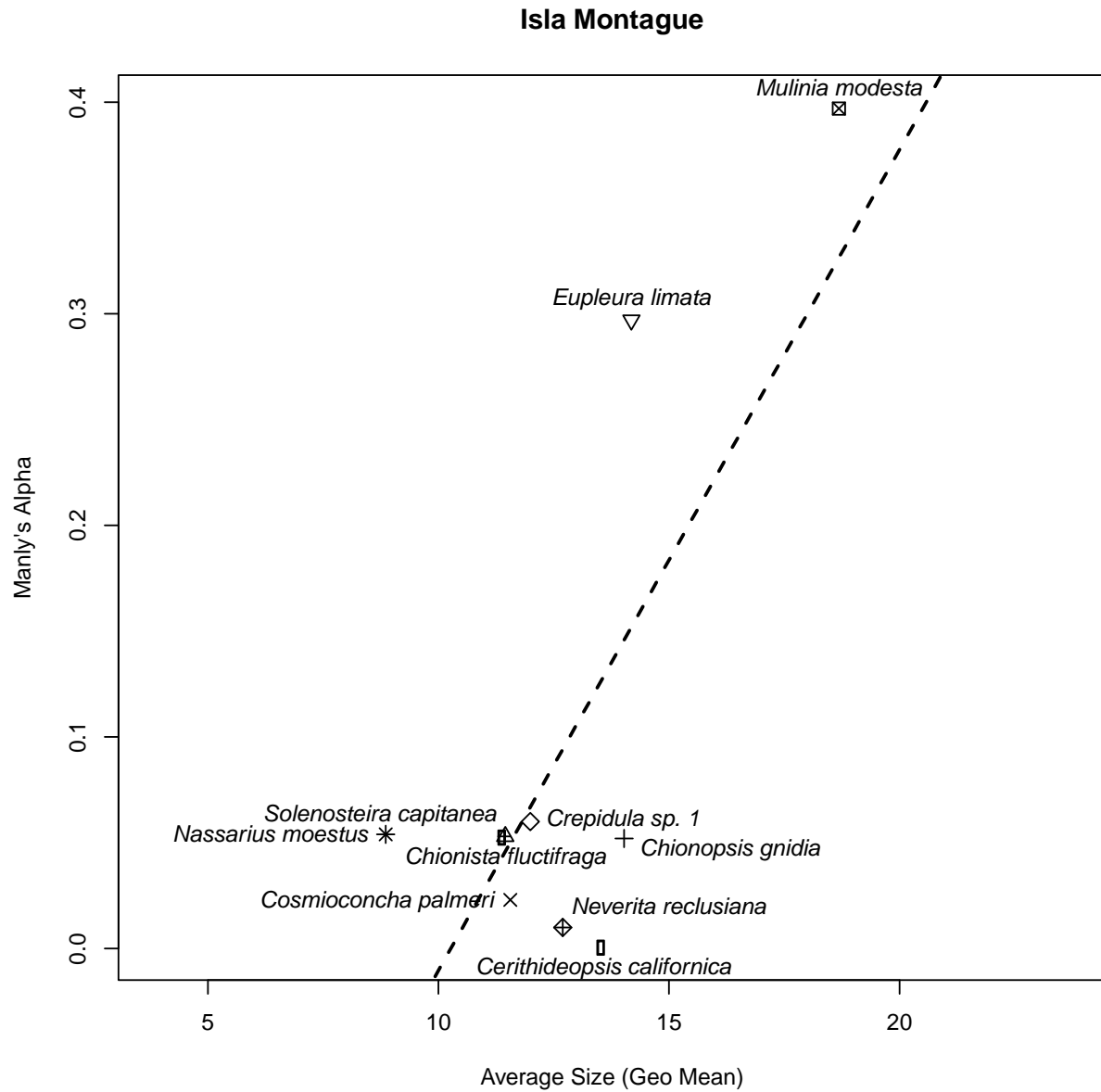
**S4 table 1.** Predator preference at all three localities when only species that occurred at all three localities are included in analysis.

Locality	Taxon	Neutral	Manly's alpha	95% Credibility Interval		Probability alpha > neutral	Probability alpha < neutral	Probability <i>Mulinia</i> alpha is greater	# drilled valves	# Individuals
Isla Montague	<i>Mulinia modesta</i>	0.1	0.314	0.162	0.482	0.999	0.001	-	36	194
	<i>Eupleura limata</i>	0.1	0.235	0.107	0.392	0.984	0.016	0.861	17	121
	<i>Solenosteira capitanea</i>	0.1	0.088	0	0.346	0.356	0.644	0.926	0	1
	<i>Crepidula</i> sp. 1	0.1	0.082	0.001	0.361	0.29	0.71	0.932	0	1
	<i>Chionopsis gnidia</i>	0.1	0.075	0	0.372	0.279	0.721	0.895	0	1
	<i>Cosmioconcha palmeri</i>	0.1	0.068	0	0.266	0.248	0.752	0.972	0	6
	<i>Chionista fluctifraga</i>	0.1	0.06	0.007	0.162	0.161	0.839	0.999	1	41
	<i>Neverita reclusiana</i>	0.1	0.031	0	0.149	0.072	0.928	0.999	0	17
	<i>Nassarius moestus</i>	0.1	0.045	0.015	0.093	0.017	0.983	1	7	281
<i>Cerithideopsis californica</i>	0.1	0.003	0	0.014	0	1	1	0	297	
Las Isletas	<i>Chionopsis gnidia</i>	0.1	0.337	0.271	0.409	1	0	0	66	103
	<i>Eupleura limata</i>	0.1	0.151	0.108	0.202	0.991	0.009	0.168	33	118
	<i>Mulinia modesta</i>	0.1	0.12	0.088	0.157	0.867	0.133	-	55	245
	<i>Cosmioconcha palmeri</i>	0.1	0.128	0.069	0.202	0.762	0.238	0.47	9	37
	<i>Chionista fluctifraga</i>	0.1	0.091	0.049	0.148	0.315	0.685	0.846	14	85
	<i>Cerithideopsis californica</i>	0.1	0.037	0.002	0.136	0.053	0.947	0.96	0	11
	<i>Neverita reclusiana</i>	0.1	0.053	0.027	0.089	0.005	0.995	0.998	12	129
	<i>Solenosteira capitanea</i>	0.1	0.016	0.001	0.058	0.003	0.997	0.998	0	26
	<i>Crepidula</i> sp. 1	0.1	0.024	0.004	0.062	0.002	0.998	1	1	36
<i>Nassarius moestus</i>	0.1	0.042	0.027	0.061	0	1	1	24	311	
Campo don Abel	<i>Chionopsis gnidia</i>	0.1	0.21	0.135	0.298	1	0	0	27	49
	<i>Nassarius moestus</i>	0.1	0.12	0.077	0.174	0.808	0.192	0.003	73	241
	<i>Chionista fluctifraga</i>	0.1	0.114	0.038	0.212	0.583	0.417	0.179	4	14
	<i>Cosmioconcha palmeri</i>	0.1	0.115	0.039	0.262	0.514	0.486	0.32	2	6
	<i>Eupleura limata</i>	0.1	0.103	0.01	0.269	0.469	0.531	0.349	1	4
	<i>Solenosteira capitanea</i>	0.1	0.088	0.007	0.254	0.35	0.65	0.512	0	1
	<i>Neverita reclusiana</i>	0.1	0.072	0.014	0.151	0.227	0.773	0.55	2	12
	<i>Crepidula</i> sp. 1	0.1	0.067	0.007	0.178	0.199	0.801	0.626	0	2
	<i>Cerithideopsis californica</i>	0.1	0.037	0	0.145	0.084	0.916	0.828	0	9
<i>Mulinia modesta</i>	0.1	0.074	0.047	0.11	0.062	0.938	-	47	251	

## S4.2 Testing for the effect of prey size on *Neverita reclusiana* preference

Naticid predator-prey interactions are often size-dependent, which, if not controlled for, may bias the interpretation of preference hierarchies [9–11]. In the present study, however, prey size was not a good predictor of predator preference. All specimens were measured and the average sizes of the prey species were plotted against Manly's alpha (independently for each locality). Gastropod height was measured from the tip of the apex to the base of the aperture/siphonal canal and width was measured perpendicular to height, across the aperture. Bivalve height was measured from the umbo to the edge of the shell—perpendicular to growth lines—and width was measured across the widest intersecting line. Geometric means—the square root of the sum of the squared length and width measurements—were used for analysis to account for variability in shape between species. After plotting, the effect of prey size on predator preference was evaluated with a linear regression for those species that were drilled at least once. At Isla Montague, there was initially a significant fit (Adjusted  $R^2=0.506$ , F-statistic=10.21, p-value=0.0127; S4 figure 1); however, closer inspection of the data using Cook's Distance—a diagnostic tool to assess the influence of data on a linear fit—showed *M. modesta* was a leverage point in the analysis (S4 table 2). When *M. modesta* is removed from the analysis, the linear regression no longer provides a significant fit (Adjusted  $R^2= -0.0477$ , F-statistic=0.636, p-value=0.451). The linear regression for Las Isletas showed no effect of size (Adjusted  $R^2=0.506$ , F-statistic=10.21, p-value=0.0127; S4 figure 2). Likewise, there was no effect for Campo don Abel (Adjusted  $R^2= -0.11$ , F-statistic=1.11, p-value=0.749; S4 figure 3).

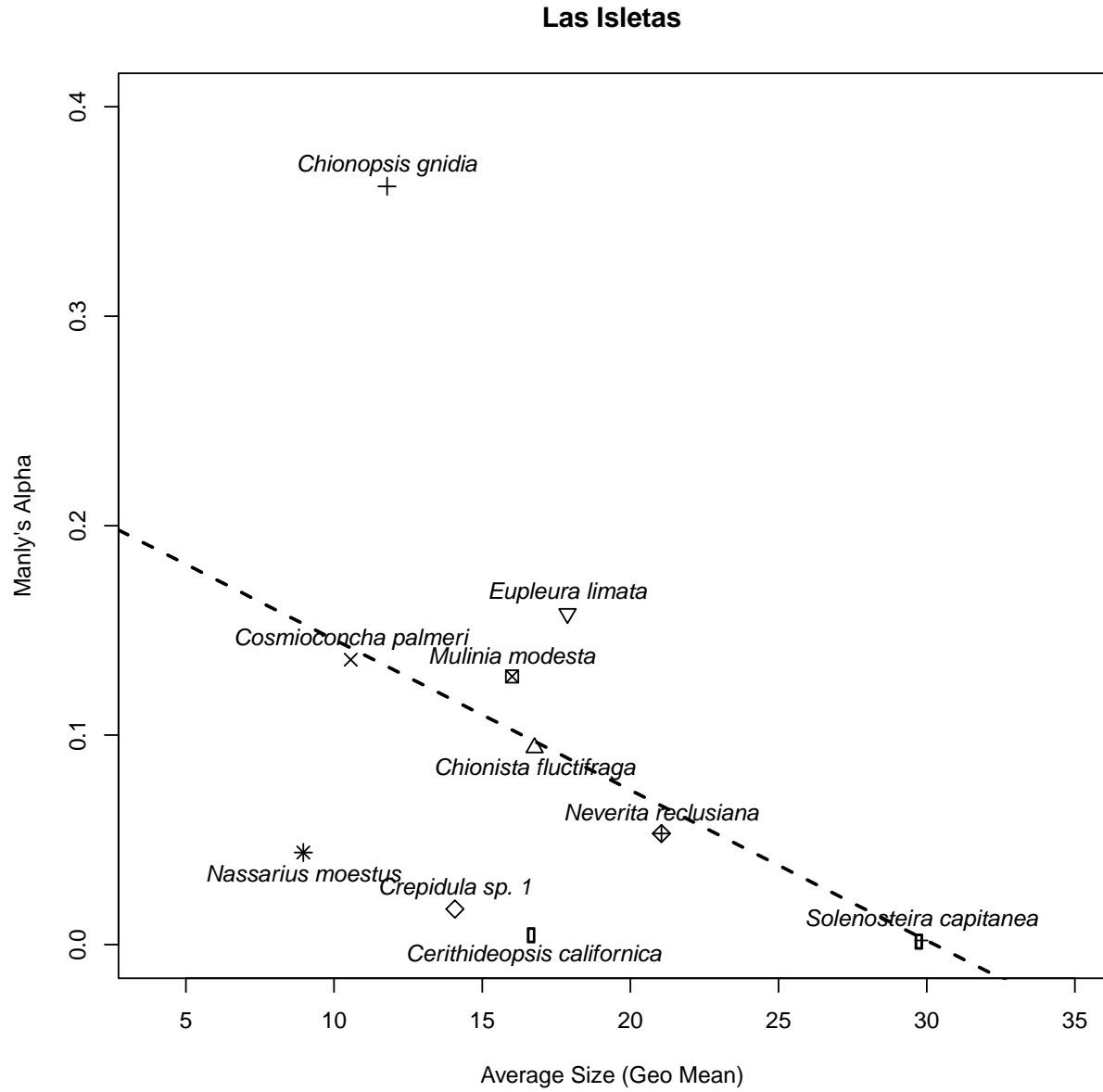
**S4 figure 1.** Manly's alpha as a function of average prey size at Isla Montague. Geo Mean = Geometric mean (millimeters).



**S4 table 2.** Cook's Distances for each species from Isla Montague. Values greater than 1 indicate significant influence and are bolded.

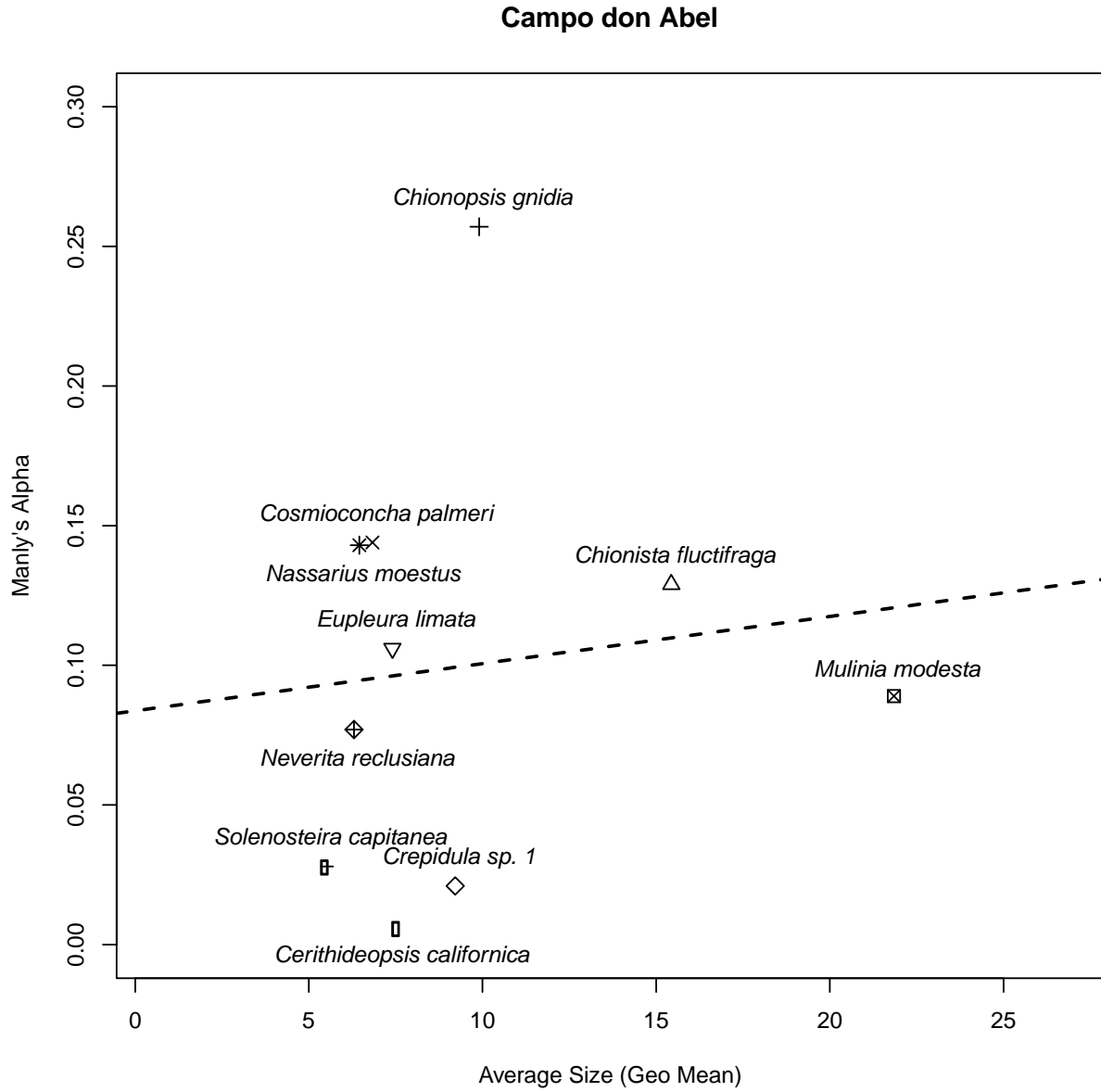
<b>Species</b>	<b>Cook's Distance</b>
<i>Cerithideopsis californica</i>	0.1256
<i>Chionista fluctifraga</i>	0.0005
<i>Chionopsis gnidia</i>	0.0797
<i>Cosmioconcha palmeri</i>	0.0069
<i>Crepidula</i> sp. 1	0.0004
<i>Eupleura limata</i>	0.2037
<i>Mulinia modesta</i>	<b>1.6917</b>
<i>Nassarius moestus</i>	0.6039
<i>Neverita reclusiana</i>	0.0496
<i>Solenosteira capitanea</i>	0.0006

**S4 figure 2.** Manly's alpha as a function of average prey size at Las Isletas. Geo Mean = Geometric mean (millimeters).





**S4 figure 3.** Manly's alpha as a function of average prey size at Campo don Abel. Geo Mean = Geometric mean (millimeters).



## R Code for Body Size Analyses:

```
# relate Manly's alpha values and body size measurements for
taxa common to all three sites
# sizes must be per site

RawData = read.csv(file = "Raw.csv", header = T,
stringsAsFactors = FALSE)
# Filter by sample:
  # Isla Montague samples: (1) IM_2_B1; (2) IM_3_B2; (3)
IM_4_B1
  # Las Isletas samples: (1) LI_A1_SB1; (2) LI_A1_SB3; (3)
LI_A1_SB5
  # Campo don Abel samples: (1) CDA_1_B1; (2) CDA_1_B2; (3)
CDA_1_B3;
  # (4) CDA_1_B4; (5) CDA_1_B5

pos = ((RawData$Locality == "Campo don Abel" &
RawData$Sample.Number %in% c("B1", "B2", "B3", "B4", "B5"))
|
(RawData$Locality == "Las Isletas" & RawData$Sample.Number %in%
c("SB1", "SB3", "SB5")))
|
(RawData$Locality == "Isla Montague" & RawData$Sample.Number
%in% c("B1", "B2")))

sum(pos)
# 5162

RawData = RawData[pos,]
dim(RawData)

CDA_Common_Counts
LI_Common_Counts
IM_Common_Counts

Las_Isletas_Common.bayes =
ManlyBayes(LI_Common_Counts, "LI_Common", comparison_taxon =
"Mulinia modesta")
Campo_don_Abel_Common.bayes =
ManlyBayes(CDA_Common_Counts, "CDA_Common", comparison_taxon =
"Mulinia modesta")
Isla_Montague_Common.bayes =
ManlyBayes(IM_Common_Counts, "IM_Common", comparison_taxon =
"Mulinia modesta")
```

```

Genus =
c("Cerithideopsis", "Chionista", "Chionopsis", "Cosmioconcha", "Crepidula", "Eupleura", "Mulinia", "Nassarius", "Neverita", "Solenosteira")
Species =
c("californica", "fluctifraga", "gnidia", "palmeri", "flat", "limata", "modesta", "moestus", "reclusiana", "capitanea")

# for each of these, need to extract the individuals of each
taxon and get size statistics
Las_Isletas_Common_Sizes = RawData[(RawData$Species %in%
c(as.character(LI_Common_Counts$Taxon))) & (RawData$Locality ==
"Las Isletas"), c("Geo.Mean", "Species")]
plot(Geo.Mean~factor(Species), Las_Isletas_Common_Sizes)
LI.fit = lm(Geo.Mean~factor(Species)+(-
1), Las_Isletas_Common_Sizes)
yoffset = c(-0.01, 0.01, 0.01, 0.01, 0.01, 0.01, -0.01, -
0.01, 0.01)
png("LI.png", width = 800, height = 800)
Taxa = as.character(Las_Isletas_Common.bayes$Taxon)
Taxa[5] = "Crepidula sp. 1"
plot(coef(LI.fit), Las_Isletas_Common.bayes$Bayes, xlab =
"Average Size (Geo Mean)", ylab = "Manly's Alpha", main = "Las
Isletas", xlim = c(min(coef(LI.fit))-5), max(coef(LI.fit))+5),
ylim = c(0, 0.4), pch = 1:10, cex = 1.2)
text(coef(LI.fit), Las_Isletas_Common.bayes$Bayes+yoffset, Taxa,
cex = 1, font = 3)
#summary(lm(Las_Isletas_Common.bayes$Bayes ~ coef(LI.fit) ))
abline(lm(Las_Isletas_Common.bayes$Bayes ~ coef(LI.fit) ), lwd =
2, lty = 2)
dev.off()

Campo_don_Abel_Common_Sizes = RawData[(RawData$Species %in%
c(as.character(CDA_Common_Counts$Taxon))) & (RawData$Locality ==
"Campo don Abel"), c("Geo.Mean", "Species")]
plot(Geo.Mean~factor(Species), Campo_don_Abel_Common_Sizes)
CDA.fit = lm(Geo.Mean~factor(Species)+(-
1), Campo_don_Abel_Common_Sizes)
png("CDA.png", width = 800, height = 800)
Taxa = as.character(Campo_don_Abel_Common.bayes$Taxon)
Taxa[5] = "Crepidula sp. 1"
plot(coef(CDA.fit), Campo_don_Abel_Common.bayes$Bayes, xlab =
"Average Size (Geo Mean)", ylab = "Manly's Alpha", main = "Campo
don Abel", xlim = c(min(coef(CDA.fit))-5), max(coef(CDA.fit))+5),
ylim = c(0, 0.3), pch = 1:10, cex = 1.2, col = "black")
yoffset = c(-0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, -0.01, -
0.01, 0.01)

```

```

text(coef(CDA.fit)+0.1,Campo_don_Abel_Common.bayes$Bayes +
yoffset, Taxa, cex = 1, font = 3) #, srt = 30, adj = -0.1)
#,srt=30)
#summary(lm(Campo_don_Abel_Common.bayes$Bayes ~ coef(CDA.fit) ))
abline(lm(Campo_don_Abel_Common.bayes$Bayes ~ coef(CDA.fit) ),
lwd = 2, lty = 2)
dev.off()

```

```

Isla_Montague_Common_Sizes = RawData[(RawData$Species %in%
c(as.character(IM_Common_Counts$Taxon)) & (RawData$Locality ==
"Isla Montague")),c("Geo.Mean", "Species")]
plot(Geo.Mean~factor(Species),Isla_Montague_Common_Sizes)
IM.fit = lm(Geo.Mean~factor(Species)+(-
1),Isla_Montague_Common_Sizes)
png("IM.png", width = 800, height = 800)
Taxa = as.character(Isla_Montague_Common.bayes$Taxon)
Taxa[5] = "Crepidula sp. 1"
plot(coef(IM.fit),Isla_Montague_Common.bayes$Bayes, xlab =
"Average Size (Geo Mean)", ylab = "Manly's Alpha", main = "Isla
Montague", xlim = c(min(coef(IM.fit))-5), max(coef(IM.fit))+5),
pch = 1:10, cex = 1.2, col = 1)
yoffset = c(-0.01,-0.01,0.01,0.01,0.01,0.01,0.01,-
0.01,0.01,0.01)
xoffset = c(0,0.9,1,0,0,0,0,0,1,-1.7)
text(coef(IM.fit)+xoffset,Isla_Montague_Common.bayes$Bayes +
yoffset, Isla_Montague_Common.bayes$Taxon, cex = 1, srt = 0,col
= 1, font = 3)
#legend("topleft", legend = Isla_Montague_Common.bayes$Taxon,
bty = "n", pch = 1:10, cex =0.8)
#summary(lm(Isla_Montague_Common.bayes$Bayes ~ coef(IM.fit) ))
abline(lm(Isla_Montague_Common.bayes$Bayes ~ coef(IM.fit) ), lwd
= 2, lty = 2)
dev.off()
cooks.distance(lm(Isla_Montague_Common.bayes$Bayes ~
coef(IM.fit) ))
data.frame(Isla_Montague_Common.bayes$Taxon,cooks.distance(lm(Is
la_Montague_Common.bayes$Bayes ~ coef(IM.fit) )))
summary(lm(Campo_don_Abel_Common.bayes$Bayes[-7] ~
coef(CDA.fit)[-7] ))

```

### S4.3 Assessment of shell fragmentation to evaluate potential bias from durophagous predation

Between-species differences along the north-south gradient in the intensity of shell-crushing (i.e., durophagous) predation by crabs could influence the interpretation of our naticid predation data. Shell-crushing predation removes an undrilled individual from the set of individuals used to estimate drilling frequency. Thus, a high incidence of crushing predation can artificially inflate observed drilling frequencies. If the behavior of shell-crushing predators changed from north to south, such that certain species were consumed more or less at a given site, the results of our study may be subject to misinterpretation. To address this potential bias, we assessed the proportion of broken versus complete individuals in commonly occurring bivalve species (after [12]). Shell fragmentation can occur post-mortem [13], meaning our analysis likely overestimates the frequency of shell-crushing predation.

**S4 table 3.** Results of fragmentation analysis for commonly occurring bivalves in the Colorado River estuary. IM = Isla Montague; LI = Las Isletas; CDA = Campo don Abel; values in parentheses are counts of all individuals (broken + complete); \* indicates a significant p-value.

<b>Species</b>	<b>IM</b>	<b>LI</b>	<b>CDA</b>	<b>p-value</b>
<i>Chionista fluctifraga</i>	0.41 (70)	0.44 (153)	0.59 (34)	0.2341
<i>Chionopsis gnidia</i>	0.00 (1)	0.23 (134)	0.22 (63)	0.9999
<i>Mulinia modesta</i>	0.59 (472)	0.63 (664)	0.51 (516)	0.0003*
<i>Tellina hiberna</i>	-	0.02 (48)	0.06 (52)	0.6185
<i>Lamelliconcha concinnus</i>	-	0.00 (9)	0.10 (10)	0.9999

Analysis with the fisher.test function in R found non-significant between-site differences in shell fragmentation for four of five species. Based on these results, it is unlikely that shell-crushing predation had a significant impact on observed drilling predation intensity. The lone

significant result was for a reduction in breakage at the southernmost site, Campo don Abel, in *M. modesta*. This result suggests that, holding all other variables constant, drilling frequency on *M. modesta* at the southernmost site was underestimated compared to those from the two more northern sites. For *M. modesta* in the south, 265 of 516 (51%) individuals were broken. Applying a breakage of 61%, which is an average of the northern two sites, the number of complete individuals drops from 251 to 201. Recalculating drilling frequency based on 201 individuals and 45 drill holes yields a frequency of 22%, or an increase of 4% from the observed drilling frequency. Recalling that mean drilling frequency at Campo don Abel was 23%—or 24% if the 50 undrilled *M. modesta* are removed from the calculation—*M. modesta* was still drilled less frequently than predicted under neutral conditions. Thus, despite the significant result for *M. modesta*, the difference in fragmentation cannot explain the north-south trend in predation intensity. Furthermore, the only evidence required to support the hypothesis that *N. reclusiana* was able to switch prey is that other prey species were also preferred and such evidence holds regardless of the slight difference due to *M. modesta* fragmentation.

### **R Code:**

```
#C.fluctifraga
C.flu <- fisher.test(matrix(c(29, 68, 20, 41, 85, 14), nrow=2,
ncol=3, byrow=TRUE))
#C.gnidia
C.gni <- fisher.test(matrix(c(0, 31, 14, 1, 103, 49), nrow=2,
ncol=3, byrow=TRUE))
#M.modesta
M.mod <- fisher.test(matrix(c(278, 419, 265, 194, 245, 251),
nrow=2, ncol=3, byrow=TRUE))
#T. hiberna
T.hib <- fisher.test(matrix(c(1, 3, 47, 49), nrow=2, ncol=2,
byrow=TRUE))
#L. concinnus
L.con <- fisher.test(matrix(c(0, 1, 9, 9), nrow=2, ncol=2,
byrow=TRUE))
```

#### **S4.4 Assessment of potential bias in predator preference due to the presence of multiple predators**

In the event that multiple drilling predators were responsible for the drill holes observed in this study, the data may reflect an average of predator preferences rather than the sole preference of *N. reclusiana*. As discussed in the introduction and methods of the main text, our samples were taken from the active cheniers in the CRE. These cheniers are composed of shells that, for the most part (>75%), originated during the pre-dam era [13]. During the pre-dam era, only one naticid was present in the CRE; however, the range of a second naticid species, *Notocochlis chemnitzii*, has extended into the CRE in the post-dam era [10]. Therefore, the fraction of shells in the active cheniers that originated in the post-dam era may have been subject to predation by two naticid species. Although naticids might be expected to have similar prey preferences, small differences may alter overall preferences. For example, *N. chemnitzii* are more capable predators of thick-shelled bivalve prey due to their utilization of edge drilling, wherein the prey shell is drilled through the thin margin of the shell rather than the thicker umbonal region. In this study, however, no prey individuals with drill holes were excluded on the basis of edge drilling, which suggests that the contribution of *N. chemnitzii* to the sum total of naticid drilling predation was likely small.

As reported by Smith and Dietl [10], *N. chemnitzii* are also relatively uncommon in the active cheniers. No *N. chemnitzii* were found at Isla Montague, compared to 947 *N. reclusiana*. In the active chenier at Las Isletas, 80 *N. chemnitzii* were found. By comparison, 1,581 *N. reclusiana* were collected in the same sampling effort, suggesting a recent arrival of *N. chemnitzii* and no more than a minor contribution to predator-prey dynamics at Las Isletas [10]. Similarly, no *N. chemnitzii* have been collected from Campo don Abel, whereas 20 *N. reclusiana*

were collected in the samples used in this study. These collections from Isla Montague and Las Isletas are a combination of bulk and target sampling, which accounts for the differences in sample sizes. In target sampling, the entire outcrop is scanned for species of interest and all are collected regardless of preservational quality [14]. Bulk sampling is restricted to a defined volume from a few locations on the outcrop [15]. Considering only bulk samples from Isla Montague (n=15), 97 *N. reclusiana* were found and for Las Isletas (n=6) there were 241 *N. reclusiana* and seven *N. chemnitzii*, or a ratio of 35:1. Any contribution from *N. chemnitzii*—which is rare compared to *N. reclusiana* and would have been restricted to <25% of the prey individuals—to the sum total of naticid drilling predation would have been small and cannot explain the north-south trend in prey preference.

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