

Supplementary Information for

Climate drives the geography of marine consumption by changing predator communities

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Other supplementary materials for this manuscript include the following:

Movies S1

Fig. S1. Patterns of consumer (A) species richness, (B) diversity expressed as the number of equally abundant species needed to produce observed values of Hurlburt's probability of interspecific encounter **(1)**, (C) density, and (E) biomass across mean annual sea surface temperature. Lines are LOESS curves (with shaded 95% confidence intervals) independently fitted within each habitat (green=seagrass, gold=unvegetated sediments). Note that density and biomass (C,D) are shown on a log scale.

Fig. S2. Relationships between consumption rate and (A) latitude and (B) mean annual sea surface temperature (SST) along the coastlines for which we have sufficient data to test for the presence and shape of latitudinal gradients. Solid lines show logistic regressions with quadratic terms for Latitude or SST, and dashed lines show logistic regressions with linear predictor terms only. Note that while the Eastern North Pacific follows trends in the Southern Hemisphere well, we do not discuss this case specifically in the text because we lack sufficient sampling towards warmer, low latitude environments.

Fig. S3. Bivariate relationships among consumption rate and explanatory variables. (A) Water temperature measured at the time of feedings assays tended to exceed long-term average sea surface temperature, as most studies took place during the summer. Differences between mean annual and measured water temperature decreased toward the warmest sites, but variance was highest between 15 and 25℃. The red line shows predictions from local regression (LOESS) and the black line is the 1:1 line. (B) Correlations between mean annual SST, the proportion of active foraging consumer taxa, consumer functional richness measured from all scored traits, an index of multivariate consumer composition (PCoA axis 1 from Fig. 2), the abundance of consumers (log-transformed) identified using ordination constrained to consumption rates, and consumption rates (logit-transformed). Red lines within the scatterplots below the diagonal show predictions from LOESS, panels along the diagonal show the frequency and density of each variable, and numbers above the diagonal show Spearman rank correlation coefficients.

Fig. S4. Relationships between consumption rate and community-level weighted trait means for six traits relevant to feeding and locomotion. Traits means are based on presence-absence data of consumers from seines and videos for all traits except length, which we weighted by abundance and restricted to seining data. Points represent mean consumption rate for communities in each site and habitat combination. The x-axis in the upper-left panel reflects whether the dominant consumer is an active swimming forager (1) or not (0). Body size in total length for fish and carapace width for crabs.

Fig. S5. Distribution of presences (1) and absences (0) for selected taxonomic families across latitude. Solid black lines are predicted values from a quadratic logistic model and the dotted lines are local regression (LOESS) curves. Shown are the 13 families with the strongest positive correlation with consumption, the 6 families with strongest negative correlation with consumption rate, and wrasses (Labridae).

Fig. S6. Consumption rate estimates within each habitat at every site. Filled symbols show rate estimates from individual assays in seagrass (green) and unvegetated (gold) habitats and are semi-transparent to show overlapping estimates. Open black symbols show the mean consumption rate in each habitat. Note the different scale of the y-axis in each panel, which span the range of observed consumption rates at each site.

Fig. S7. Histogram of parameter estimates from linear models of consumption rate as a function of habitat (seagrass vs. unvegetated sediments), independently-fitted for each site. Estimates above zero mean that consumption rate was higher in seagrass than unvegetated sediments. Sites in the extreme bins of the histogram are labelled. At NSW1, for example, all squid bait were consumed after one hour in seagrass, while just over 40% were consumed in one hour in unvegetated sediments, representing a change in consumption rate of nearly 0.6 hr-1. Estimates for 20 of 38 within-site comparisons fell within the range -0.02 to 0.02.

Table S1. Correlations between the presence of predator families and consumption rate based on canonical correspondence analysis of predator taxonomic composition. Correlation is derived from the first axis of the constrained ordination of family composition as a function of consumption rate. Also displayed are the number of morphospecies in each family, the number of sites in our dataset where each family was observed, and patterns of presence and absence in seagrass and unvegetated habitats. Families marked with an asterisk were observed to attack or remove the squid bait from at least one of the 10 sites with video data (Table S3).

Table S2. Predator taxa observed to strike and remove bait from squidpops in video footage taken during assays. Taxa that were identified in the video footage but not observed to attack squidpops are not included. The order of fish taxa reflects the clades of bony fishes proposed by Hughes et al. 2018 **(2)**. We have included a short clip of one video from Italy in Movie S1.

Table S3. List of all sites and habitat types used in consumption assays. We report the date of the first assay in each habitat, the geolocations of sites, and the range of squidpop numbers used in each assay.

Movie S1 (separate file). Example of fish feeding behavior in a seagrass meadow (*Posidonia oceanica*) from Italy showing attacks on a squidpop. Later in the video a moray eel appears and strikes at one of the smaller fish. This movie illustrates the complex ecological interactions that can take place in seagrass meadows.

SI References

Sample References:

- 1. J. M. Chase, T. M. Knight, Scale-dependent effect sizes of ecological drivers on biodiversity: why standardised sampling is not enough. *Ecol. Lett.* **16**, 17–26 (2013).
- 2. L. C. Hughes, *et al.*, Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data. *Proc. Natl. Acad. Sci.* **115**, 6249–6254 (2018).