Trends in Queen Triggerfish abundance at the Mona Island Marine Reserve

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Introduction and Methodology

Mona and Monito Islands are part of the Puerto Rico territory are in the Mona Passage between the Dominican Republic and western Puerto Rico. Mona Island (67.89 W; 18.09 N) is surrounded by an insular platform of approximately 81.6 km^2 and is separate from nearby smaller Monito Island by depths of 400 m yet isolated from other larger islands by at least 40 nautical miles, hence limited immigration of post-settlement coral reef fish is expected as evidenced for corals (Baums et al. 2006). Given this geographical context sampling all the habitats around Mona Island provides a reliable estimate of the habitat use patterns of coral reef fishes, except for submerged mangroves that are landlocked.

The insular platform of both islands has been part of a marine protected area (MPA) Mona and Monito Natural Reserve including 1,512.7 km^2 of the marine jurisdiction up to 9 Nm from shore since 1997 (Aguilar-Perera et al. 2006). The shallower areas up to half (0.5) nautical miles around both islands were designated as a no-take zone marine reserve (NTMR) within the larger Natural Reserve under Fisheries Regulation # 6768 (2004). The boundaries of the NTMR were modified to the limit of the insular platform, defined as 100 fathoms in depth, except for a swath on the west side of Mona, as per Fisheries Regulation Amendment # 7326 (2007). Later the NTMR boundary was extended to one nautical mile surrounding each island (Figure 1), as per Fisheries Regulation # 7949 (2010). Mona Island provides a relatively less-fished area for comparison of coral reef fishes to Puerto Rico since it is isolated, uninhabited except for limited ranger and biologist staff and sporadically groups of campers and hunters and considered the largest MPA in the US Caribbean (Schärer-Umpierre et al. 2014).

Sampling at Mona Island was performed with diver-based, visual census methods throughout the shallow (< 30 m) habitats during three independent research projects. Sampling of reef fishes was conducted by counting and estimating the fork length of each individual fish and classifying into 5-cm size bins within belt transects (30 x 2 m) in three separate time periods over 13 years after designation of the NTMR. The first set of samples were collected between

October 2005 and June 2006 with only one replicate transect per site, distributed throughout all habitat types after the inception of a NTMR designated in 2004 (Schärer-Umpierre 2009). The second sampling effort was conducted only in coral reef habitat types during 2009 and 2010 with one replicate per site after the spatial configuration of the NTMR was changed to include all habitats up to 0.5 Nautical mile from shore (Mateos-Molina et al. 2014). The final sampling in coral reef habitat types only during 2017 included two transects per site the first from June 8-28, 2017, and the second replicate from December 11-14, 2017. During the 2017 sampling period the NTMR included all the habitats on the insular platform up to 1 Nm from shore (Olson et al. 2019). It is important to note that the island was impacted by swells generated by Hurricane María during September of 2017, between the two replicate samplings of that year.

Sampling at Mona Island conducted in 2005 included the full range of coral reef associated habitats as per a benthic habitat map digitized at 100 m^2 minimum mapping unit (MMU) based on NOAA (2001) aerial georeferenced photography (Schärer 2009). Sites within all habitat types located in less than 30 m depth were selected randomly to establish seascape effects on the ontogenetic distribution of reef fish in 2005 (Table 2). For the purposes of the index presented in this report only coral reef and colonized hardbottom habitats were included in the 'delta-lognormal' analysis, as subsequent time periods (2010 and 2017) sampled in a subset of habitat types (Table 3). Depths between 10 and 20 m were sampled in 2010 and 5 to 25 m in 2017, but only depths of stations where *B. vetula* occurred are included in the delta-lognormal analysis; and replicate samples in 2017 were summed by station.

The delta-lognormal index of relative abundance (I_y) as described by Lo *et al*. (1992) is estimated as

$$(5) \qquad I_y = c_y p_y,$$

where c_y is the estimate of mean CPUE for positive catches only for year y; p_y is the estimate of mean probability of occurrence during year y. Both c_y and p_y are estimated using generalized linear models. Data used to estimate abundance for positive catches (c) and probability of occurrence (p) are assumed to have a lognormal distribution and a binomial distribution, respectively, and modeled using the following equations:

(6) $$\ln(\mathbf{c}) = \mathbf{X\beta} + \boldsymbol{\varepsilon}$$

and

(7) $$\mathbf{p} = \frac{e^{\mathbf{X\beta}+\boldsymbol{\varepsilon}}}{1+e^{\mathbf{X\beta}+\boldsymbol{\varepsilon}}}$$, respectively,

where **c** is a vector of the positive catch data, **p** is a vector of the presence/absence data, **X** is the design matrix for main effects, **β** is the parameter vector for main effects, and **ε** is a vector of independent normally distributed errors with expectation zero and variance σ^2. Therefore, c_y and p_y are estimated as least-squares means for each year along with their corresponding standard errors, SE (c_y) and SE (p_y), respectively. From these estimates, I_y is calculated, as in equation (5), and its variance calculated as

(8) $$V(I_y) \approx V(c_y)p_y^2 + c_y^2 V(p_y) + 2c_y p_y \mathrm{Cov}(c,p),$$

where

(9) $$\mathrm{Cov}(c,p) \approx \rho_{c,p}\left[\mathrm{SE}(c_y)\mathrm{SE}(p_y)\right],$$

and $\rho_{c,p}$ denotes correlation of c and p among years.

The MIXED procedure in SAS (v. 9.1, 2004) was used to develop the binomial and lognormal submodels. Similar covariates were considered for both submodels: year, water depth, habitat type, and the interaction of water depth and habitat type. Model performance was evaluated using AUC (Area Under Curve) methodology presented by Steventon *et al*. (2005) and residual analyses. A backward selection procedure was used to determine which variables were to be included into the lognormal submodel based on type 3 analyses with a level of significance for inclusion of $\alpha = 0.05$. If year was not significant then it was forced into each submodel in order to estimate least-squares means for each year, which are predicted annual population margins (i.e., they estimate the marginal annual means as if over a balanced population). The fit of the lognormal submodel was evaluated using the AIC statistics and residual analyses.

Results and Discussion

Throughout the coral reef and associated habitats at Mona Island 218 *B. vetula* were observed in 879 transects over the three time periods. Colonized pavement with sand channels and colonized pavement were the habitats with highest presence of *B. vetula* followed by spur and groove reef, colonized bedrock and uncolonized pavement. Table 3 summarizes the habitat types sampled in 2010 and 2017 and used in delta-lognormal analysis.

All variables were retained in the binomial submodel (Table 4), with the resulting index, based on frequency of occurrence listed in Table 5. The binomial submodel had an AUC = 0.791 (Figure 2). The AUC statistic provides information on the model's lack-of-fit, and in this case, it means that in 79 out of 100 instances, a station selected at random from those with queen triggerfish had a higher predicted probability of queen triggerfish being present than a station randomly selected from those that had no queen triggerfish. The results of type 3 analyses for the lognormal submodel are summarized in Table 6. For the lognormal submodel, only the variables for year and habitat type were retained. Figure 3 indicates the approximately normal distribution of the residuals of the lognormal submodel.

Index values indicate an increase in *B. vetula* density at Mona Island, Puerto Rico between the second (2010) and third (2017) sampling periods. Table 7 and Figure 4 summarize indices of density (number per m^2) developed from the delta-lognormal model. This increase is consistent with that observed for other small reef fishes, like the Coney (*Cephalopholis fulva*) at Mona Island, as well as the Yellowtail snapper (*Ocyurus chrysurus*) and *C. fulva* at La Parguera Natural Reserve, off southwestern Puerto Rico (Olson et al. 2019), that could be attributed to recruitment and not an MPA effect per se. Further analysis of the length distribution of the *B. vetula* sampled at Mona Island may shed light on the potential explanation for the increased abundance index.

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Table 1. Summary of sampling effort and number of *B. vetula* observed per time period for 2005-06, 2010 and 2017.

Time period	**Number of transects**	**Sum of *B. vetula***
Sampling 2005	*611*	*91*
Replicate 1	611	91
Sampling 2010	*108*	*33*
Replicate 1	108	33
Sampling 2017	*160*	*94*
Replicate 1	80	57
Replicate 2	80	37
Grand Total	**879**	**218**

Table 2. Summary of sampling effort and number of *B. vetula* observed per habitat type for 2005, based on benthic habitat maps created by Schärer-Umpierre (2009).

Labels	**Number of transects**	**Sum of *B. vetula***
Colonized Bedrock	28	5
Colonized Pavement	86	37
Colonized Pavement & Sand	41	21
Shallow Coral	121	1
Linear Reef	31	0
Patch Reef	24	0
Rubble	22	0
Scattered Coral % Rock	4	7
Seagrass	16	0
Seagrass & Patches	37	0
Seagrass & Rubble	23	0
Spur & Groove	89	17
Uncolonized Bedrock	54	0
Uncolonized Pavement	35	3
Grand Total	**611**	**91**

Table 3. Habitat types sampled in 2010 and 2017 and used in delta-lognormal analysis, based on benthic habitat maps created by Schärer-Umpierre (2009).

Habitat types
coral reef-patch reef
coral reef-linear reef
coral reef-spur and groove
colonized hardbottom-bedrock
colonized hardbottom-pavement with sand
colonized hardbottom-pavement

Table 4. LR Statistics for Type 3 Analysis For Binomial Sub-model

Source	*DF*	*Chi-Square*	*Pr > ChiSq*
year	2	44.97	<.0001
depth	1	18.29	<.0001
type	5	21.09	0.0008
*depth*type*	5	11.49	0.0424

Table 5. Binomial index values for *B. vetula* density at Mona Island, Puerto Rico.

Year	*Modeled Proportion Positive*	*CV*	*LCL*	*UCL*
2005	0.11	0.31	0.06	0.21
2010	0.20	0.34	0.10	0.39
2017	0.51	0.21	0.34	0.77

Table 6. LR statistics for Type 3 Analysis for lognormal submodel for *B. vetula* density at Mona Island, Puerto Rico.

Source	*DF*	*Chi-Square*	*Pr > ChiSq*
year	2	107.34	<.0001
type	5	53.67	<.0001

Table 7. Delta-lognormal index values for *B. vetula* density at Mona Island, Puerto Rico.

Year	*Index*	*CV*	*LCL*	*UCL*
2005	0.024	0.36	0.01	0.05
2010	0.059	0.44	0.03	0.14
2017	0.48	0.27	0.29	0.81

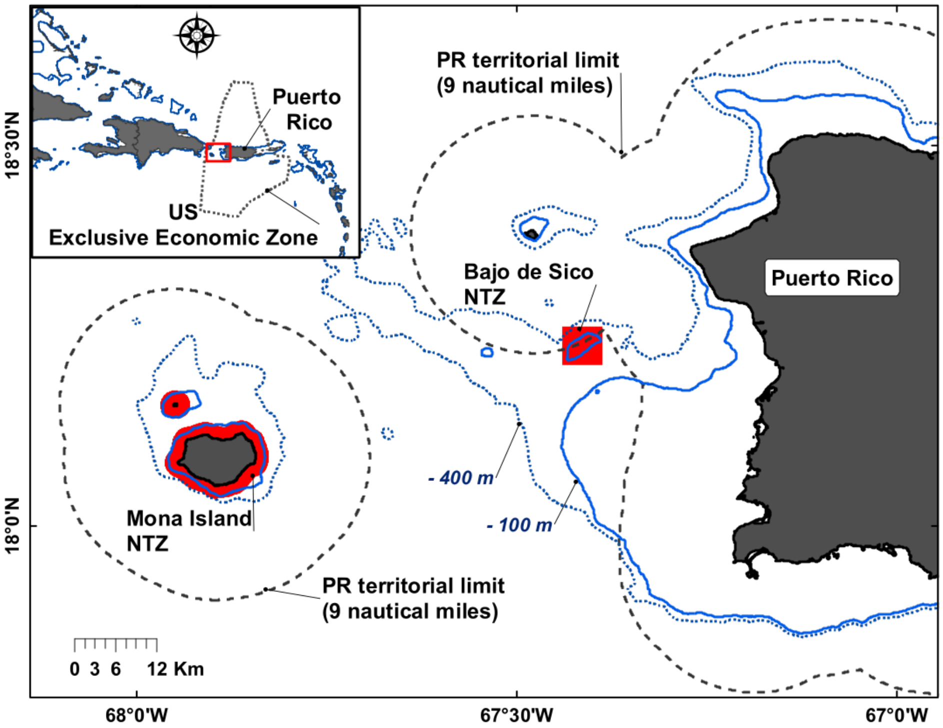

Figure 1. Mona Island no-take zone up to one Nautical mile of Mona and Monito Islands.

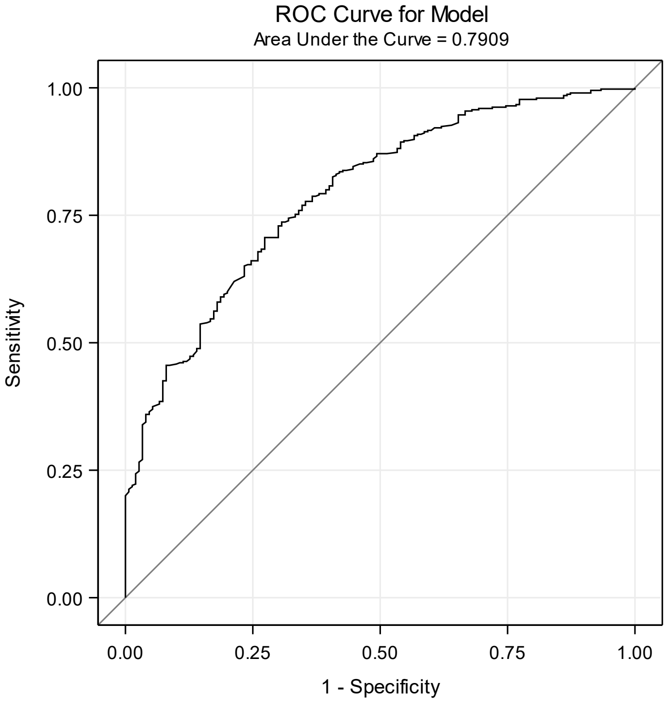

Figure 2. ROC curve for binomial model diagnostics.

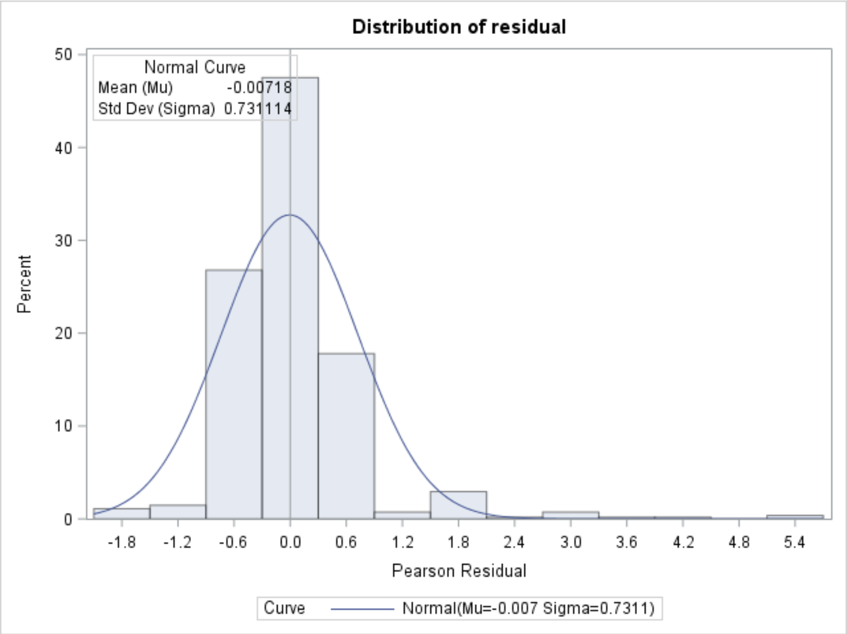

Figure 3. Plot of residuals for the lognormal submodel.

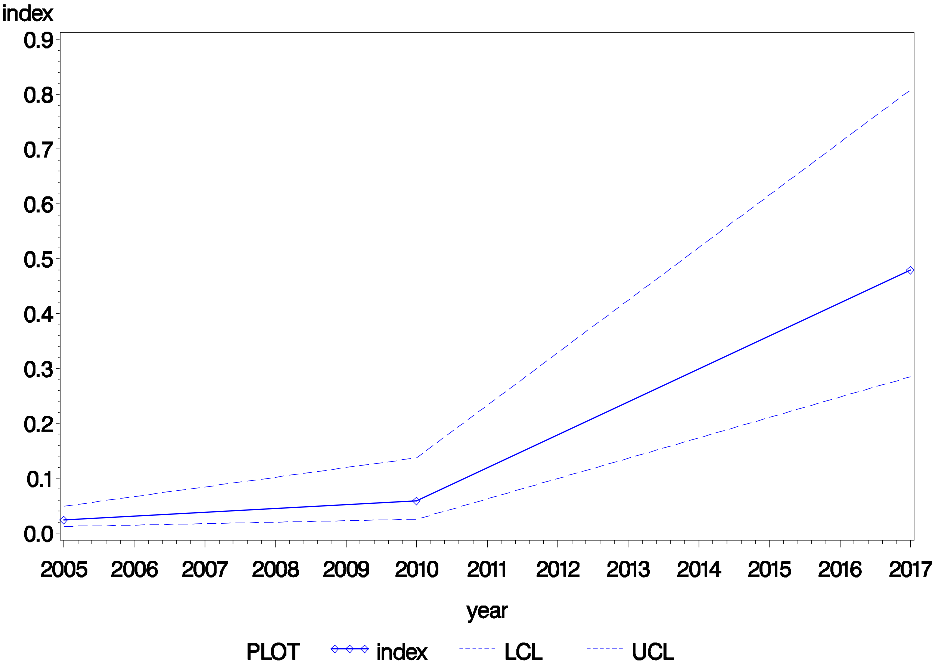

Figure 4. Plot of delta-lognormal index with 95% confidence intervals.

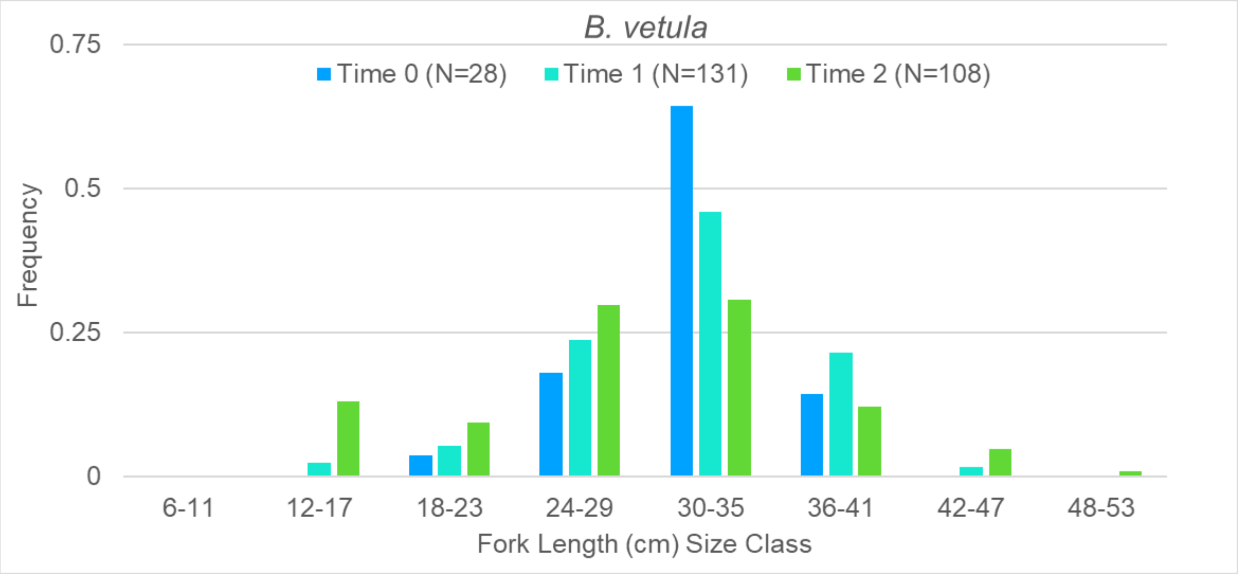

Figure 5. Fork length (cm) size class distribution of *B. vetula* per sampling time.