**Sala & Giakoumi 2017 - No-take marine reserves are the most effective protected areas in the ocean**

**Supplemental Online Material**

**Methods**

Lester & Halpern (2008) conducted a meta-analysis using data from studies where no-take marine reserves, partially protected MPAs and open access areas were in the vicinity. They pooled all 20 studies in a single meta-analysis. Sciberras and colleagues (Sciberras et al., 2013; Sciberras et al., 2015) conducted a more thorough meta-analysis considering many factors including taxonomic resolution of the data, size and age of the reserves at the time of surveys. However, disaggregation of the data resulted in low number of studies per case. For this essay, we conducted a comprehensive survey of peer-reviewed scientific literature to compile a database of studies documenting and comparing the biomass of whole fish assemblages of no-take marine reserves, partially-protected marine protected areas (MPAs), and open access areas, all within the same vicinity (to avoid biogeographic confounding). We chose total fish biomass because it is positively correlated to abundance of top predators, food chain length, and negatively correlated with turnover rate; hence it is the best single indicator of the successional state – maturity – of the fish assemblage [e.g., (Sandin et al., 2008; Sandin and Sala, 2011)].

Our dataset included only studies which provided data for the biomass of fish assemblages in fully protected areas, partially protected areas, and open access areas. We used data from (Friedlander and DeMartini, 2002), (Claudet et al., 2008), (Harmelin-Vivien et al., 2008), (Aburto-Oropeza et al., 2011), (Garcia-Rubies et al., 2013), (Rife et al., 2013), (Friedlander et al., 2014), Friedlander et al. (unpublished data), and Giakoumi et al. (in review).

To quantify the effect of protection, we calculated the effect size using the log-response ratio ln (*XT/Xc*), where *XT* and *Xc* are the mean values of biomass inside (treatment site) and outside the MPA (control site), respectively. The variance associated with the effect size (*ve*) is:

*ve*= + (1)

where *ST* and *NT* are the standard deviation and sample size of the variable estimated inside the MPA and *SC*and *NC*the standard deviation and sample size outside the MPA.

Effect sizes for fish assemblages were estimated both for no-take vs. fished areas, partially protected vs. fished areas, and no-take vs. partially protected.

Effect sizes were weighted to ensure greater contribution of the most robust studies. We used the inverse of the sum of the within study variances (*wi*) with the among-study variance:

(2)

The overall effect size (*E*) was calculated as:

(3)

The variance of *E* was calculated as

(4)

and its 95% confidence interval as

(5)

where *t* is a critical value determined from the *tn-1*distribution. The effect sizes were considered to be significantly different from zero if their confidence interval did not overlap zero.

To detect whether there was a significant heterogeneity in the effect sizes, we calculated the total heterogeneity (QT)

(6)

QT was tested against a distribution with n-1 degrees of freedom. A significant deviation from the null hypothesis that all *ei* are equal indicated that there is potentially some structure in the data.

We then built mixed-effects models to account for random variation as well as the variation within and between studies. We calculated an estimate of the pooled study variance

(7)

And weights for the mixed effects model were calculated as

(8)

and re-calculated the overall effect size (*E*) and associated 95% confidence interval using .

The mean values and confidence intervals of effect sizes estimated by the mixed-effects models were used for further analyses and are presented in Figure 1.