

Supplementary Materials for

A portfolio of climate-tailored approaches to advance the design of marine protected areas in the Red Sea

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Data sources

Population density (2020 estimate) was based on the Gridded Population of the World v4.11 (Center for International Earth Science Information Network - CIESIN, 2018) and displayed on Figure 1.

Environmental variables for the Red Sea

Bathymetry data were acquired from Amante and Eakins (2009). We considered the 100-m bathymetric contour to define the shelf edge in the Red Sea on Figure 2. Coastline data were obtained from Wessel and Smith (1996).

Eddies in the Red Sea were visualized using sea surface height anomaly (SSHA) data from the Ssalto/Duacs altimeter products on Figure 2, which were produced and distributed by the Copernicus Marine and Environment Monitoring Service (CMEMS) (marine.copernicus.eu). We also plotted the mean SSHA during 2017.

Tidal range in the Red Sea was based on the M2 tide from the FES2004 model (Lyard, Lefevre, Letellier, & Francis, 2006).

Thermal regions

Sea surface temperature (SST) data were acquired from Coral Reef Watch's CoralTemp1.0 SST product (Liu et al., 2014). We defined “hot” regions as those with maximum monthly mean (MMM) greater than 31.25 °C. Additionally, the upwelling zone is where the climatological minimum daily mean SST in July is less than the climatological maximum daily mean SST in June (Churchill, Bower, McCorkle, & Abualnaja, 2014; DeCarlo et al., 2021). The “cool” zone has $MMM < 28$ °C, and the “warm” zone is all areas with 28 °C $< MMM < 31.25$ °C.

Coral bleaching history

The history of coral bleaching was compiled from the literature (DeVantier, Turak, Al-Shaikh, 2000; Furby, Bouwmeester, & Berumen, 2013; Monroe et al., 2018; Osman et al., 2018). We considered a bleaching event “severe” if it affected greater than or equal to 30% of corals, and “minor” if an event affected 1-30% of corals. We did not include the 2007 bleaching in Egypt since it was attributed to extreme low tides (causing sub-aerial exposure of corals living on reef flats) and not a thermally induced bleaching event. Additionally, we included minor bleaching events in 1982 that were detected in coral skeletal cores from the NCS region (Fig. 2) and the Farasan Banks in the SCS region (Fig. 2) (DeCarlo et al., 2020).

Genetic connectivity

The genetic connectivity was compiled from 16 studies on genetic connectivity that contained data from at least in two sites in the Red Sea and that presented results of pairwise

genetic distance tables (*i.e.*, fixation indices) with associated significant level. These studies were conducted on 22 fishes including eight butterflyfishes (*Chaetodon melannotus*, *C. austriacus*, *C. fasciatus*, *C. larvatus*, *C. mesoleucos*, *C. paucifasciatus*, *C. semilarvatus*, and *C. trifascialis*) (DiBattista et al., 2017, 2020), one surgeonfish (*Ctenochaetus striatus*) (DiBattista et al., 2020), one wrasse (*Larabicus quadrilineatus*) (Froukh & Kochzius, 2007), three groupers (*Plectropomus areolatus*, *P. pessuliferus marisrubri*, and *Cephalopholis hemistiktos*) (Priest et al., 2016; Wilson, 2017), one clownfish (*Amphiprion bicinctus*) (Nanninga et al., 2014; Saenz-Agudelo et al., 2015), four damselfishes (*Dascyllus aruanus*, *D. marginatus*, *D. trimaculatus*, and *Chromis viridis*) (Froukh, 2007; Robitzch, 2017; Salas, Bernardi, Berumen, Gaither, & Rocha, 2019), one sea goldie (*Pseudanthias squamipinnis*) (Froukh, 2007), one goatfish (*Mulloidichthys flavolineatus*) (Fernandez-Silva et al., 2015), one snapper (*Lutjanus kasmira*) (DiBattista et al., 2017), and one angelfish (*Pomacanthus maculosus*) (Torquato et al., 2019). We were also able to retrieve genetic distance data from two corals (*Pocillopora verrucosa*, and *Seriatopora hystrix*) (Maier, Tollrian, Rinkevich, & Nürnberger, 2005; Robitzch, Banguera-Hinestroza, Sawall, Al-Sofyani, & Voolstra, 2015), three anemones (*Heteractis magnifica*, *Stichodactyla mertensii*, and *Entacmaea quadricolor*) (Emms et al., 2020), and one sponge (*Stylissa carteri*) (Giles et al., 2015).

The GPS location of all studied sites (used in pairwise comparisons) were plotted using thin black lines and then grouped per region (seven regions in total). If the value of the fixation index between two regions was high and significant, this indicates strong genetic differentiation (*i.e.*, very little genetic exchange). In contrast, if the value of the fixation index was small and not significant, this implied little genetic differentiation (*i.e.*, high genetic exchange). A “significant difference” designation between two regions was only assigned if >50% of sites from one region

were significantly different from >50% of sites from the second region. These results are presented in the pie charts color-coded in Figure 2.

Mangrove coverage, seagrass distribution, and blue carbon

Mangrove areas in the Red Sea were based on data from Almahasheer et al. (2016). The seagrass observations (transformed as presence and absence data) plotted on the map was derived from Bruckner et al. 2012, Jayathilake & Costello, 2018, and Qurban et al., 2019.

The values of the carbon stock sediments (Almahasheer et al., 2016; Arshad, Alrumman, & Eid, 2018; Eid, El-Bebany, & Alrumman, 2016; Eid et al., 2020; Eid & Shaltout, 2016; Garcias-Bonet et al., 2019; Qurban et al., 2019; Serrano, Almahasheer, Duarte, & Irigoien, 2018; Shaltout, Ahmed, Alrumman, Ahmed, & Eid, 2020) (megagram of organic carbon per hectare; Mg ha^{-1}) were plotted per site and represented by a line on Figure 2. These data have also been standardized over a depth of 10 cm that roughly corresponds to 50 years of accumulation. The carbon stock value in sediments were then averaged and represented per region.

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