



Supporting Online Material for
**Projecting Coral Reef Futures Under Global Warming and Ocean
Acidification**

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This PDF file includes:

Figs. S1 and S2

References

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Table S1

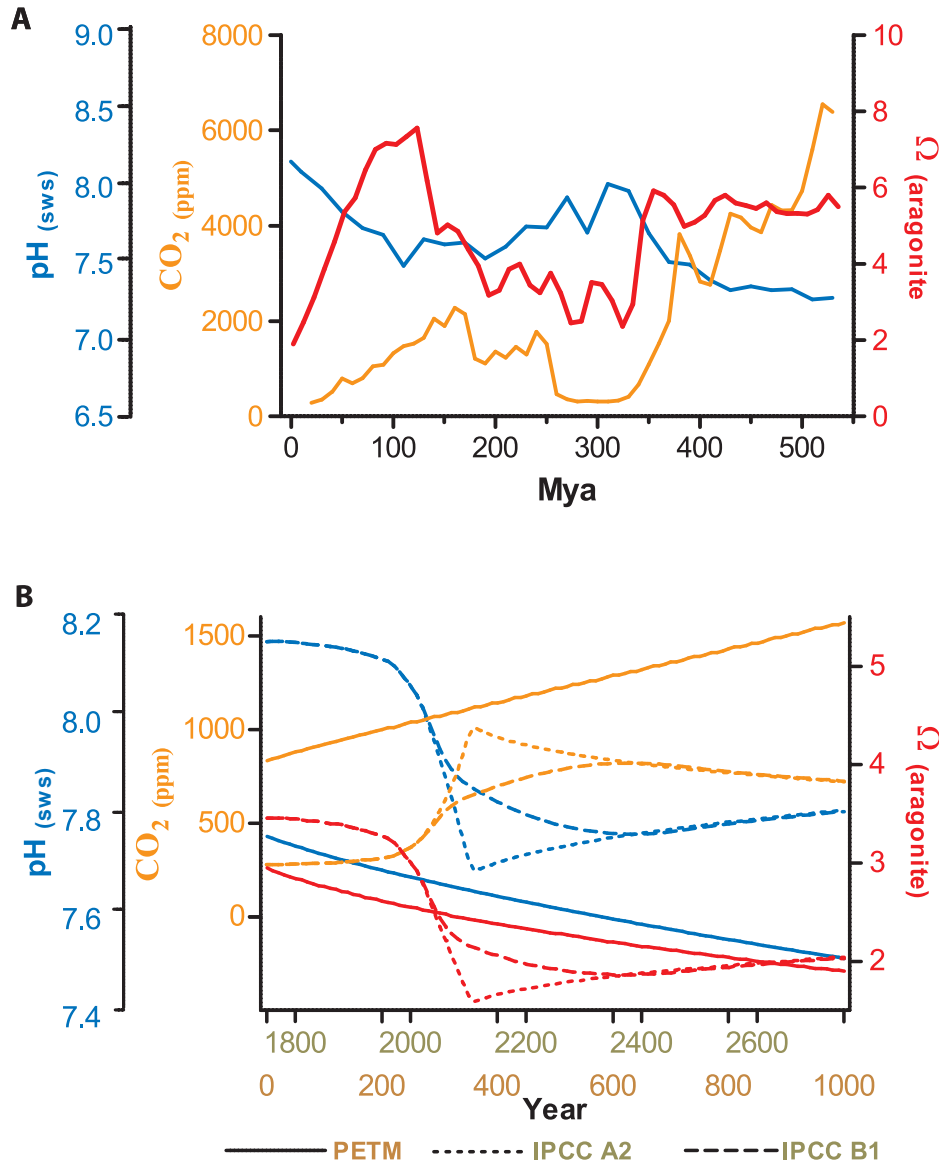


Fig. S1. Coupling of CO₂, Ω_{arag}, and pH over long and short geological time scales. (a) Over the past 550 million years, CO₂(95) and pH(96) are negatively correlated, but modeled Ω_{arag}(97) often varies independently. (b) During the PETM and under modern IPCC scenarios for rapid CO₂ change, CO₂, modeled Ω_{arag}, and pH are tightly coupled (model results from(98)). Note that Ω_{arag} shows a clear negative relationship with CO₂ under fast change, but no consistent relationship with CO₂ under slow change conditions in the geological past. Indeed, high Ω_{arag} occurred in association with the highest historical CO₂ levels from 550 to 350 mya. Estimation of Ω_{arag} in the deep geological past is based on a stoichiometric equilibrium model assuming constant 15°C SST, CO₂ values from the GEOCARB III model, estimated

values of Ca, Mg, K, and SO_4^{2-} , estimated DIC based on a previous correlation established for pCO_2 and HCO_3^- for the past 100 myr (then extrapolated from this correlation using GEOCARB III(1)), and assumed present-day values for other major ions (details in(97) and references therein).

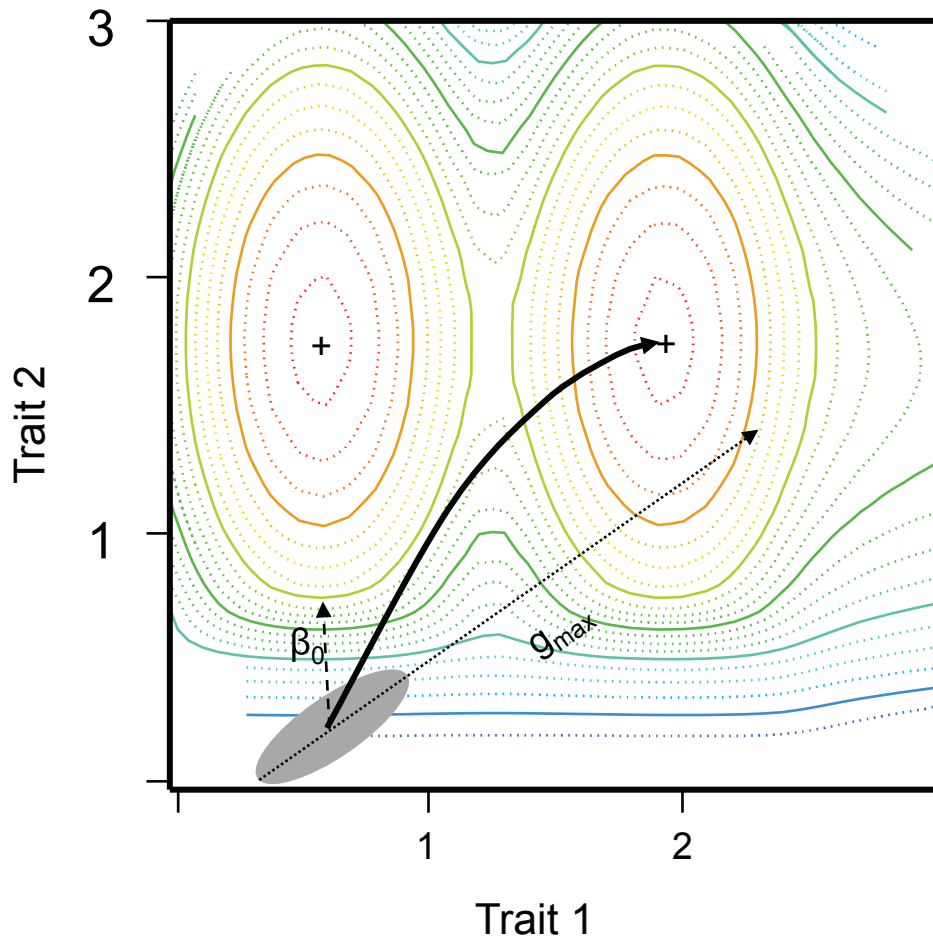


Fig. S2. The adaptive potential of coral reef organisms. Estimating additive genetic variation in traits associated with climate change, and correlations between those and other traits provide key insights into the paths of least genetic resistance, and thus the evolutionary potential of coral reef organisms. Some studies have examined the heritability of traits involved with coping with climate change in coral reef organisms(99, 100) but, crucially, these studies estimate ‘broad sense’ rather than ‘narrow sense’ heritability, so may not predict the evolutionary responses of the focal organisms over time(101). The figure above (adapted from (101)) illustrates how genetic correlations between traits can bias evolutionary trajectories such that evolution does not follow the initial direction of selection (denoted by β_0) but rather is biased initially along the genetic line of least resistance. In the figure, the filled circle depicts the initial mean phenotype of the population and the solid line depicts the path of the mean over subsequent generations. The dotted line represents the direction of

maximum genetic variance within the population (g_{\max} ; for an example of how to estimate g_{\max} among stressful environments, see(102)) and the dashed line represents the initial direction of selection. Thus, despite selection for a slight decrease in trait 1, the combination of the adaptive landscape and direction of maximum genetic variance results in an increase in trait 1 as evolution in trait 2 occurs.

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78. Consider a simple modification to the two-species Lotka-Volterra competition model to incorporate density-independent mortality from bleaching: $dN_i/dt = r_i N_i (K_i - N_i - \alpha_{ij} N_j) / K_i - B c_i N_i$, where N_i , r_i , and K_i represent the abundance, intrinsic growth rate, and carrying capacity of species i ($i = 1, 2$) and α_{ij} , the relative competitive effect of species j on species i . B represents bleaching severity, and c_i is a coefficient relating bleaching severity to the species-specific mortality rate induced by bleaching. Species 2 increases in abundance as bleaching intensity increases if $r_2/r_1 > c_2 K_2 / (c_1 \alpha_{21} K_1)$. Species 2 can increase in abundance as bleaching intensity increases if it has a sufficiently greater ability to rapidly exploit available space (i.e., it has a sufficiently higher r), relative to its relative bleaching susceptibility (c_2/c_1). This occurs because increased bleaching mortality has two effects on a species: It directly reduces a species' abundance, but it also increases available space for colonization because of increased mortality of the species' competitor.
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