

Supplementary Materials for **Genomic models predict successful coral adaptation if future ocean warming rates are reduced**

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The PDF file includes:

- appendix S1. Description of the individual-based model.
- fig. S1. Comparison of probabilistic and individual-based models.
- fig. S2. Sensitivity to choice of climate model.
- fig. S3. Demographic impacts of migration.
- fig. S4. Results of simulations for determining the width of the survival function.
- fig. S5. Effects of the chosen quantile for the calculation of scaling factor (S) between degrees Celsius SST and T_{prop} .

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/3/11/e1701413/DC1)

- table S1 (Microsoft Excel format). Source data

appendix S1. Description of the individual-based model.

Purpose

We developed a model to examine the potential for adaptation of reef-building corals to projected increases in sea surface temperature through the year 2100. Specifically, we ask whether the rate of adaptation from standing genetic variation is sufficient to keep up with the rate of ocean warming.

State variables and scales

Each individual is characterized by the fraction of loci, T_{prop} , (out of a possible 114) at which the allele associated with heat tolerance is present. The genetic architecture of thermal tolerance was determined from our previous study (Bay & Palumbi 2014). The environment is characterized by temperature. Collectively, all individuals comprise a single population which is summarized by population size and average T_{prop} . Each time-step represents a single year, reflecting annual reproduction dynamics. The simulations run for 85 time-steps, representing the years 2015-2100.

Process overview and scheduling

Each year, the following processes occur: selection-based mortality, reproduction, settlement. First, all individuals are subject to mortality based on T_{prop} , with the optimal T_{prop} (T_{opt}) determined by the current temperature (see submodel for conversion). Remaining individuals randomly mate, creating a larval pool and individuals are randomly selected from that larval pool for settlement. The fraction of the larval pool allowed to settle is density dependent.

Design concepts

Fitness is modelled explicitly as separate survival and reproduction processes. While all individuals have the same probability of reproduction, survival varies. The probability of survival depends on the fraction of thermal tolerance alleles T_{prop} in relation to environmental temperature, which sets the optimal T_{prop} . Fitness varies over time as ocean temperature changes. Adaptation is therefore observed as a shift in the average T_{prop} for the population. Because genetic drift can be a strong driver of shifts in allele frequencies, especially when population sizes are small, stochasticity is integrated by using probabilistic binomial draws for mortality and settlement.

Initialization

Input parameters are a combination of literature values and empirical estimates. We used a growth rate from recolonization estimates ($r_{max}=0.38$) and an initial population size of 1000, which is also considered the carrying capacity. A total of 114 thermal tolerance loci were genotyped in the Rarotonga population using RNA-Seq data. We calculated allele frequencies for each of the 114 thermal tolerance loci, then simulated a starting population using binomial genotype draws based on those allele frequencies. Warming scenarios for Rarotonga were based on the sea surface temperature model output from the NOAA Geophysical Fluid Dynamics Laboratory Earth System Model 2M. We used projected temperatures from four representative

concentration pathways (RCPs). The temperature of the warmest month for each year was translated into an optimal T_{prop} value.

Submodels

Selection-based mortality – The survival probability of colony j at time i is modelled using a Gaussian distribution with the mean at the optimal T_{prop} value (T_{opt}), based on current environmental temperature

$$ProbSurv(j,i) = \exp(-[T_{prop}(j) - T_{opt}(i)]^2 / 2 * \sigma^2)$$

We used a $\sigma^2=0.16$ which in preliminary simulations best maintained both population size and genetic variance.

Reproduction and settlement – The size of the larval pool is the number of surviving individuals multiplied by r_{max} . Each larvae in this pool gets genotypes from two parents, selected randomly from surviving colonies and assuming no linkage between loci. The probability of settlement is equal across all larvae and is determined using the following equation for density dependence

$$R_i = r_{max} * (N_i - D_i) * (K - N_i + D_i) / K.$$

Where R_i is the number of recruits, N_i is the number of colonies at the beginning of the year, D_i is the number of colonies that died, and K is the carrying capacity. The probability of settlement is therefore R_i divided by the size of the larval pool.

Settling larvae are determined by a binomial draw.

Temperature dynamics

Temperature projections from four RCP scenarios are used to calculate T_{opt} (optimal T_{prop}) for each year. Initially, T_{opt} is set to the mean T_{prop} observed for Rarotonga individuals, reflecting the assumption that the population is currently adapted to the environment. The baseline SST is calculated as the mean of the warmest months from 2005-2015. The change in SST is calculated from the warmest month for each year and converted to an optimal T_{opt} using a scaling value of $S=1.02$, based on the relationship between temperature and T_{prop} from our previous study (Bay & Palumbi 2014):

$$\Delta T_{opt}(i) = S * \Delta SST_i$$

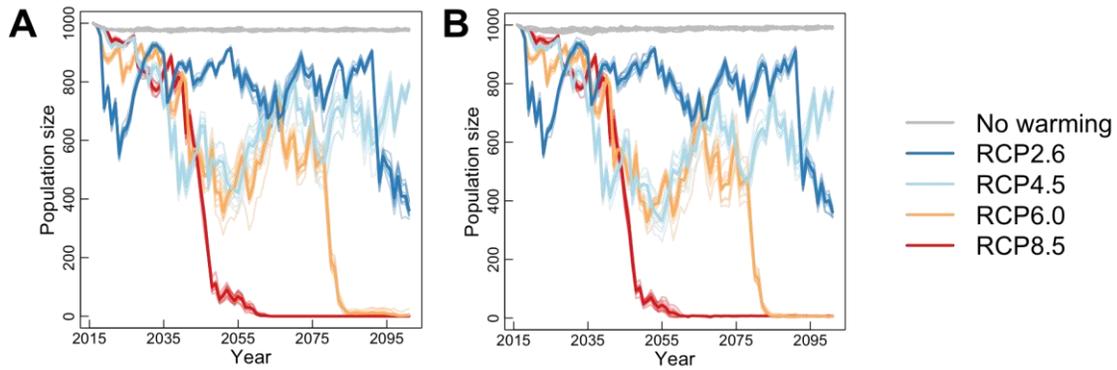


fig. S1. Comparison of probabilistic and individual-based models. Little difference between probabilistic (**A**) vs. fully individual-based (**B**) models. Thin lines show individual simulation runs (10 per scenario) and scenario means are shown with thicker lines. This simulation was based on 114 thermal tolerance loci and a growth rate of $r_{max}=0.38$.

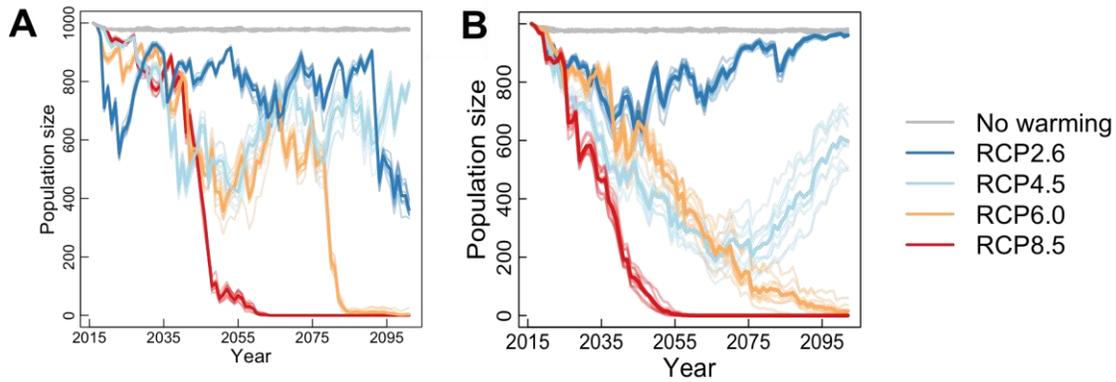


fig. S2. Sensitivity to choice of climate model. Evolutionary outcomes using the ESM2M model (A) compared to using the mean across 35 IPCC class GCM models used in AR5 (B). Thin lines show individual simulation runs (10 per scenario) and scenario means are shown with thicker lines. This simulation was based on 114 thermal tolerance loci and a growth rate of $r_{max}=0.38$.

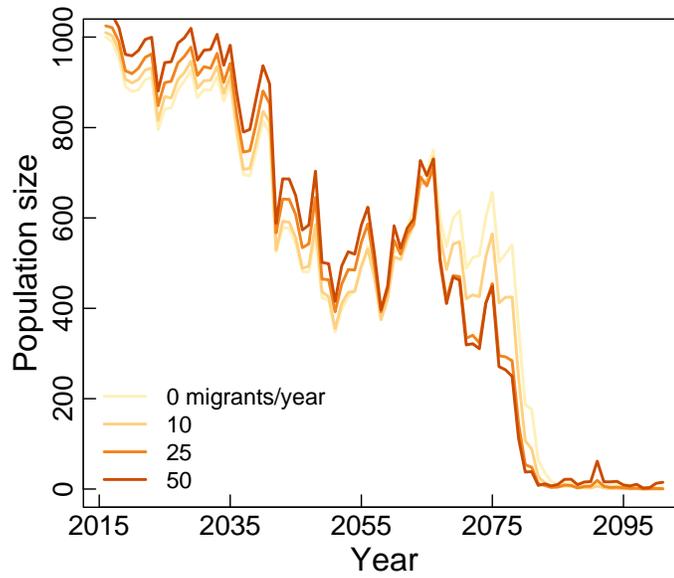


fig. S3. Demographic impacts of migration. Individuals simulated based on initial Rarotonga frequencies were added to the population at different rates, showing the demographic results of adding non-tolerance individuals.

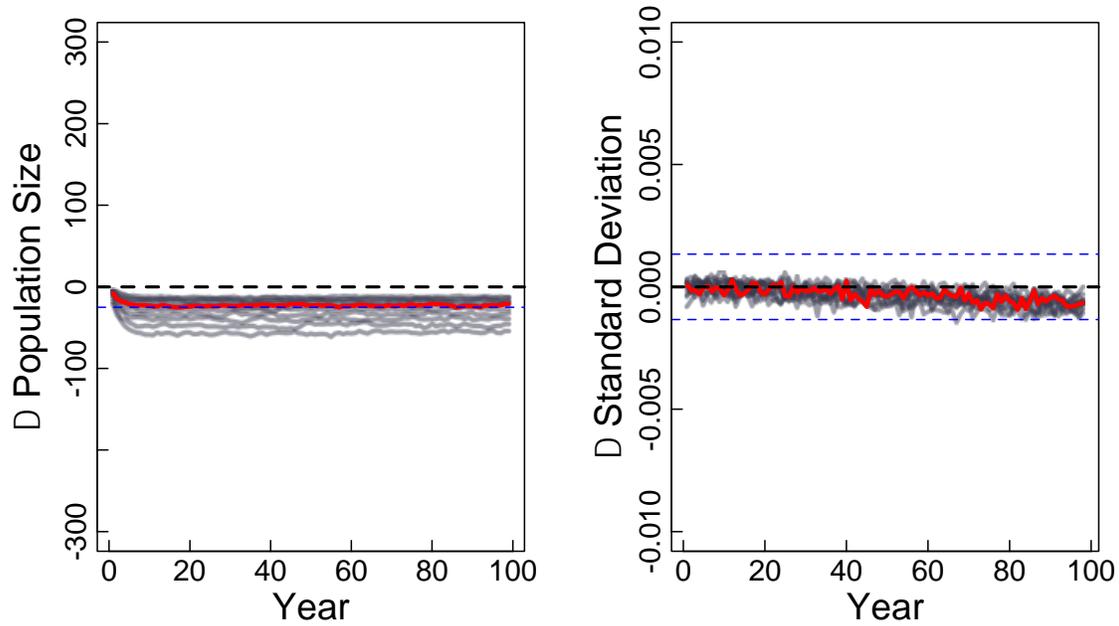


fig. S4. Results of simulations for determining the width of the survival

function. Each line shows simulation under a different value for the standard deviation of the survival curve. The left plot shows the change in population sizes and the white plot shows the standard deviation for $T_{prop.}$ Ultimately, we used a value of 0.16, highlighted in red, which is consistent with the distribution of allele frequencies found in Rarotonga.

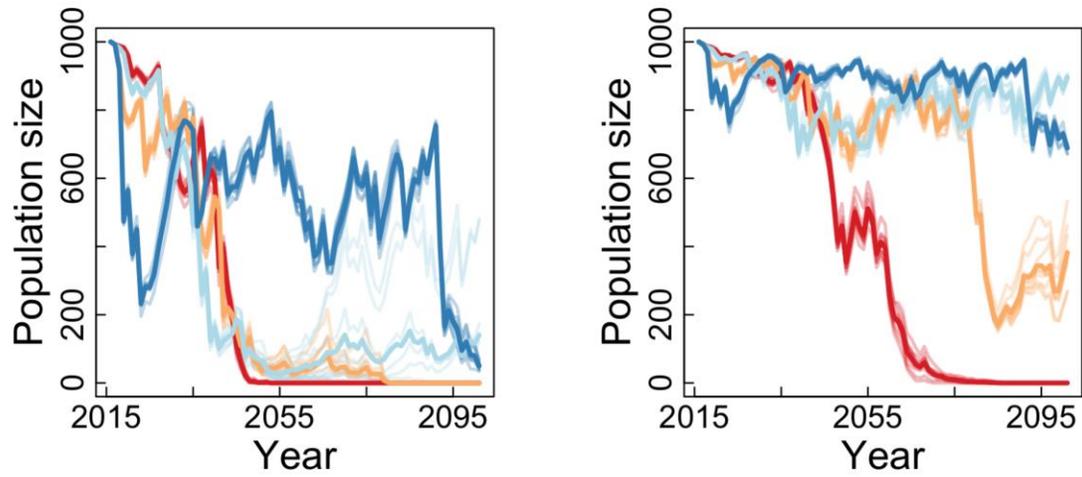


fig. S5. Effects of the chosen quantile for the calculation of scaling factor (S) between degrees Celsius SST and T_{prop} . In the main text, we used the difference between 99th quantile temperatures from the HV and MV pools in Ofu. Here, we show the results, based on 114 SNPs and $r_{max}=0.38$, using scaling factors based on the 98th quantile (left) and the 99.9th quantile (right).