Bull Mar Sci. 99(2):119–136. 2023
https://doi.org/10.5343/bms.2022.0064

research tools in marine science

Acropora cervicornis Data Coordination Hub, an open access database for evaluating genet performance

Patrick M Kiel [1, 2, 3 *]
Nathan Formel [1, 2, 4]
Mike Jankulak [1, 2]
Andrew C Baker [3]
Ross Cunning [5]
David S Gilliam [6]
Carly D Kenkel [7]
Chris Langdon [3]
Diego Lirman [3]
Caitlin Lustic [8]
Kerry Maxwell [9]
Alison L Moulding [10]
Amelia Moura [11]
Erinn M Muller [12]
Stephanie Schopmeyer [13]
R Scott Winters [11]
Ian C Enochs [1]

[1] *Ocean Chemistry and Ecosystem Division, Atlantic Oceanographic and Meteorological Laboratory, NOAA, 4301 Rickenbacker Cswy, Miami, Florida 33149*

[2] *Cooperative Institute for Marine and Atmospheric Studies, University of Miami, 4600 Rickenbacker Cswy, Miami, Florida 33149*

[3] *Department of Marine Biology and Ecology, University of Miami, 4600 Rickenbacker Cswy, Miami, Florida 33149*

[4] *Biology Department, Woods Hole Oceanographic Institution, 266 Woods Hole Rd, Woods Hole, Massachusetts 02543*

[5] *Daniel P Haerther Center for Conservation and Research, John G. Shedd Aquarium, 1200 South Lake Shore Dr, Chicago, Illinois 60605*

[6] *Halmos College of Arts and Sciences, Nova Southeastern University, 8000 North Ocean Dr, Dania Beach, Florida 33004*

[7] *Department of Biological Sciences, University of Southern California, 3616 Trousdale Pkwy, Los Angeles, California 90089*

[8] *The Nature Conservancy, Florida Keys, 29547 Saratoga Ave, Big Pine Key, Florida 33043*

[9] *Florida Fish and Wildlife Research Institute, Fish and Wildlife Conservation Commission, 2796 Overseas Hwy, Suite 119, Marathon, Florida 33050*

Continued on next page

ABSTRACT.—Once one of the predominant reef-building corals in the region, *Acropora cervicornis* is now a focal species of coral restoration efforts in Florida and the western Caribbean. Scientists and restoration practitioners have been independently collecting phenotypic data on genets of *A. cervicornis* grown in restoration nurseries. While these data are important for understanding the intraspecific response to varying environmental conditions, and thus the potential genetic contribution to phenotypic variation, in isolation these observations are of limited use for large-scale, multi-institution restoration efforts that are becoming increasingly necessary. Here, we present the *Acropora cervicornis* Data Coordination Hub, a web-accessible relational database to align disparate datasets to compare genet-specific performance. In this data descriptor, we release data for 248 genets evaluated across 38 separate traits. We present a framework to align datasets with the ultimate goal of facilitating informed, data-driven restoration throughout the Caribbean.

[10] *Protected Resources Division, Southeast Regional Office, NOAA National Marine Fisheries Service, 263 13th Ave S, St. Petersburg, Florida 33701*

[11] *Coral Restoration Foundation, 89111 Overseas Hwy, Tavernier, Florida 33070*

[12] *Mote Marine Laboratory, 1600 Ken Thompson Pkwy, Sarasota, Florida 34241*

[13] *Florida Fish and Wildlife Research Institute, Fish and Wildlife Conservation Commission, 100 8th Ave SE, St. Petersburg, Florida 33701*

** Corresponding author email: <patrick.kiel@noaa.gov>*

Date Submitted: 13 December, 2022.
Date Accepted: 23 March, 2023.
Available Online: 24 March, 2023.

Corals build structurally complex reef frameworks, which support the greatest concentration of marine biodiversity and provide goods and services to a large portion of the global population (Moberg and Folke 1999). Climate change and local stressors have, however, greatly diminished the capacity of corals to maintain and build new habitat (Hoegh-Guldberg et al. 2007, Donovan et al. 2021).

This is especially true in the Caribbean, where coral cover has declined to less than half of what it was in the 1970s (Jackson et al. 2014). The historically dominant ecosystem engineers of Caribbean reefs, *Acropora* spp., have seen some of the largest declines due to coastal development, multiple disease outbreaks, and repeated mass bleaching events (Aronson and Precht 2001, Cramer et al. 2020). With the loss of the acroporids, most Caribbean reefs are now below an accretionary threshold, threatening the economic and ecological services provided by reefs throughout the region (Alvarez-Filip et al. 2009, Perry et al. 2013).

In response to the widespread declines in coral reef ecosystem health, active restoration is now recognized as an integral component of coral reef management (Kleypas et al. 2021, Knowlton et al. 2021). In the Caribbean, restoration practitioners leverage the fast growth rate and natural asexual reproduction of *Acropora cervicornis* to accelerate reef recovery and recoup lost ecosystem services (Young et al. 2012). Today, over 100 restoration programs in Florida and the western Caribbean outplant thousands of *A. cervicornis* colonies every year. Genetic analyses of these corals have revealed marked diversity, with genets varying in their phenotypic responses under differing environmental scenarios (Drury et al. 2017, Lohr and Patterson 2017). This genotypic diversity may also contribute to community disease resistance (Brown et al. 2022), underscoring the need for restoration practitioners to not solely focus on individual genet identities, but instead, on propagating diverse populations. Coral

reef resilience, in the face of changing environmental conditions, will require the maintenance of sufficient genetic variation for adaptive evolution. Thus, genetic rescue principles, which seek to match this phenotypic diversity with select environmental stressors (e.g., heat tolerance, disease resistance) to increase the rate of adaptation, pose practitioners a two-fold challenge of maintaining genetic diversity and increasing stress tolerance (Whiteley et al. 2015, Baums et al. 2022).

The success of restoration programs lies in their ability to balance these two goals and establish genetically diverse, self-sustaining populations that can recover ecosystem structure and function while climate change is systematically addressed. One path to realize these restoration goals is to propagate multiple genets that collectively confer resistance and resilience to a multitude of current and future stressors. Accordingly, the systematic identification of genet-specific performance and tradeoffs among phenotypes under targeted stressors is paramount for informed restoration (Baums et al. 2019). However, identifying the genetic contribution to phenotypic variation remains difficult due to extensive genotype by environment interactions (O'Donnell et al. 2018, Drury and Lirman 2021, Million et al. 2022). Therefore, large datasets with coupled experimental and environmental metadata are necessary to parse the genotypic influences on a coral's phenotype across a matrix of environments and stressors.

Restoration practitioners and researchers have been independently collecting phenotypic data of *A. cervicornis* to identify genet-specific growth rates (Lirman et al. 2014, Lohr and Patterson 2017), disease susceptibility (Muller et al. 2018), and bleaching resistance (Cunning et al. 2021). While individually valuable for research on intraspecific variation, the application of these findings to inform coral reef restoration is limited by the spatial and temporal extent and the number of genets analyzed within each study.

The alignment of these datasets in a single database will enable comparisons of genet-specific physiology and foster restoration success. The National Academies of Sciences, Engineering, and Medicine (2019) is in agreement with this goal and has called for a publicly available database.

Here, we present the *Acropora cervicornis* Data Coordination Hub (AcDC — accessible at https://www.coral.noaa.gov/AcDC/). AcDC is an Open Science Framework to federalize disparate datasets, standardize measurements and methodologies, and enable comparisons of genet performance. We describe the structure of the relational database and the graphical user interface and release 23 datasets from restoration and research partnerships in Florida to showcase AcDC's capabilities (Fig. 1). Our continued goals are to grow the database and increase genotypic, temporal, and spatial coverage across the Caribbean to enable data-driven restoration throughout the region.

Description of Research Tool

The *Acropora cervicornis* Data Coordination Hub is hosted at NOAA's Atlantic Oceanographic and Meteorological Laboratory. AcDC has two main components: (1) a relational database that stores the data, and (2) a graphical user interface that allows individuals to access and visualize the data.

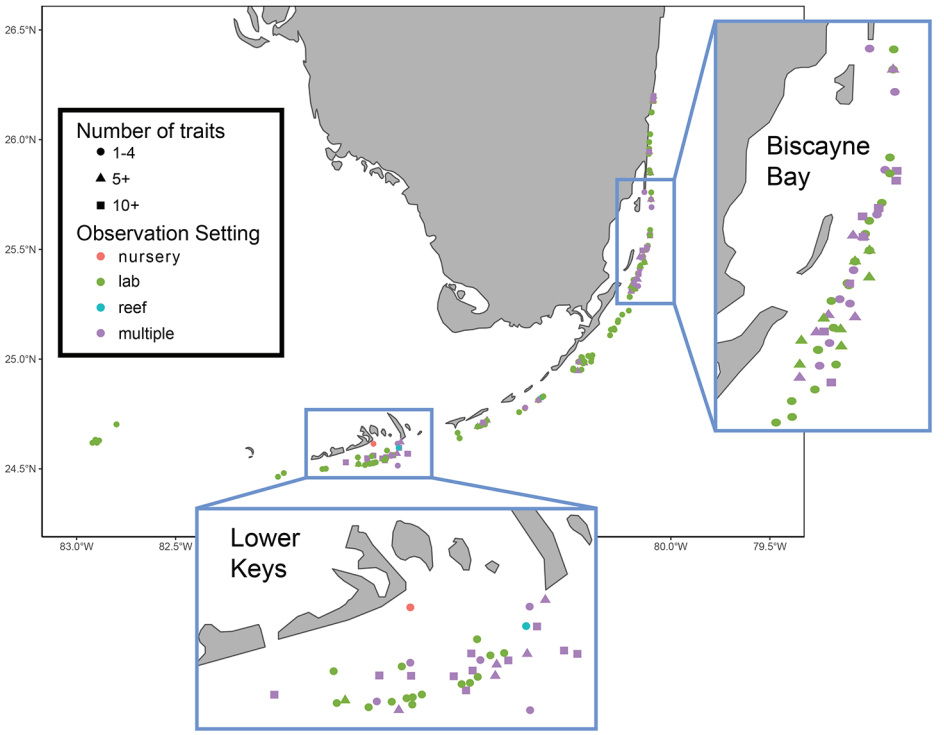

Figure 1. Geographic distribution of the data across south Florida and the Florida Keys. The two inset regions highlight areas where genets have been intensively studied, showcasing the capabilities of the *Acropora cervicornis* Data Coordination Hub to connect datasets from both researchers and restoration partners. Individual points represent donor colony source locations. Shapes denote the number of unique traits available, and colors denote the type of location where the observation was made, termed observation setting.

Database Design.—AcDC was built as a relational database with the open-source fork of MySQL, MariaDB v10.6.5 (MariaDB Foundation 2021). The database uses the Observation and Measurement Ontology for Ecological Data (Madin et al. 2007) to dynamically link observations and measurements. Observations identify the genet, record the location, cite the data source, and group simultaneously recorded measurements for discrete ramets. Measurements are the individual qualitative and quantitative assessments of a coral's phenotype. Each contains a value, a trait, a standard, and a method. Here, traits are defined as organismal or contextual measurements. Organismal traits are assessments for a particular coral phenotype, and contextual traits describe the time or environment of the observation. This ontology is supplemented with a calculated measurements table that aggregates and standardizes performance metrics from the raw measurements.

AcDC has ten tables that are grouped into primary core tables and secondary lookup tables (Fig. 2). Core tables hold the phenotypic data and contextual metadata and include the measurements, observations, and calculated measurements tables. Secondary lookup tables store the repeated, categorical reference data and include the datasets, filters, genets, locations, methods, standards, and traits tables. A brief description of each table and the available fields are outlined below (Table 1). Fields

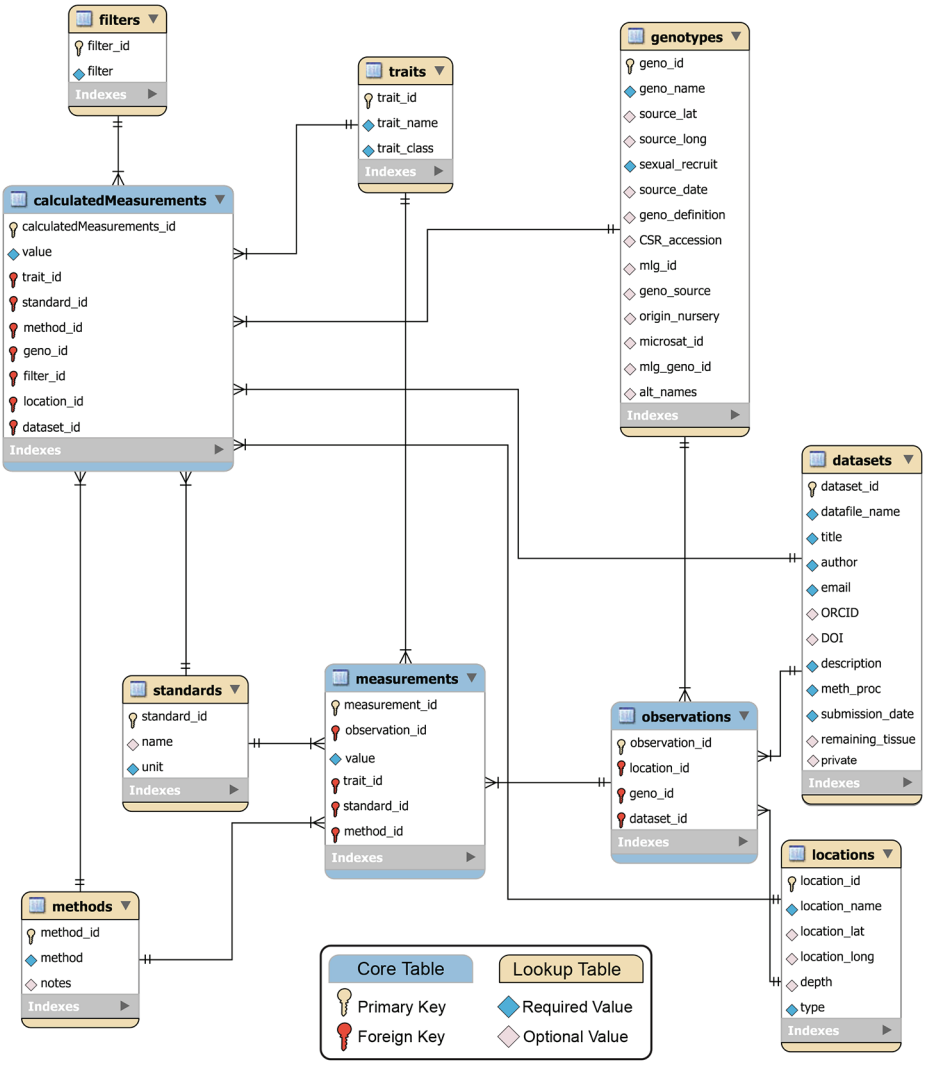

Figure 2. Schematic of database structure and data relationships. The relational database connects the standardized performance metrics with the raw phenotypic data and the corresponding metadata. Core tables (blue) store the bulk of the data and rely on the secondary lookup tables (yellow) to contextualize measurements. A brief description of each table and all its variables is provided in the text.

that have value constraints and must contain specific values are parenthetically defined with the accepted values in the value constraints column.

Genet Identification and Cross-Database Connections.—Clonal organisms such as corals can asexually reproduce and create multiple ramets (i.e., fragments) of the same genet (i.e., genetically unique coral colony originating from a distinct sexual reproductive event; Baums et al. 2019). AcDC uses three genet definitions to classify genetically identical ramets that can be traced back to a single parent colony. The first and default definition is the putative genet, which adopts

Table 1. Description of database tables and fields. The value constraints column denotes the accepted values for the respective field if any constraints exist.

Table/Field	Description	Value Constraints
Datasets	Stores data source and author metadata	- - -
dataset_id	Primary key identifier	- - -
datafile_name	Short descriptive identifier	- - -
title	Full title of publication	- - -
author	Corresponding author's name	- - -
email	Corresponding author's email	- - -
ORCID	Corresponding author's ORCID	- - -
DOI	Publication DOI	- - -
description	Short description provided by author or mined from abstract	- - -
methods_procedures	Short overview of methods provided by author or mined from methods section	- - -
submission_date	Date of upload to database	- - -
private	Binary identifier of private data status	(0,1)
remaining_tissue	Binary identifier of collaboration status	(0,1)
Filters	Stores shorthand filter logic for graphical user interface queries	- - -
filter_id	Primary key identifier	- - -
filter	Unique shorthand filter character string	- - -
Genets	Stores colony collection metadata and cross-database interfacing keys	- - -
geno_id	Primary key identifier	- - -
geno_name	Given name by the restoration program	- - -
source_lat	Latitude of the original donor colony	- - -
source_long	Longitude of the original donor colony	- - -
sexual_recruit	Binary identifier of lab grown genet	(0,1)
source_date	Date the original donor colony was sampled	- - -
geno_definition	The methodology used to determine putative genet	(unique coordinates, genetic analysis)
CSR_accesion	Accession number for matching genet from Coral Sample Registry database (Moura et al. 2021)	- - -
mlg_id	Multilocus genotype id from STAGdb (Kitchen et al. 2020)	- - -
mlg_geno_id	STAGdb (Kitchen et al. 2020) foreign key identifier	- - -
geno_source	Character string to identify where genet data is sourced	(e.g., other database, contributed collection data, publication)
origin_nursery	Restoration program that originally sampled donor colony	- - -
microsat_id	Genotype id from microsatellite loci (Baums et al. 2009)	- - -
alt_names	Alternative naming conventions of the genet	- - -
Locations	Stores observation setting metadata	- - -
location_id	Primary key identifier	- - -
location_name	Name of the location	- - -
location_lat	Latitude of the location	- - -
location_long	Longitude of the location	- - -
depth	Approximate water depth of the location	- - -
type	Description of location	reef = outplant data collected in the field; ln = nursery data collected from a line nursery, including all mid-water propagation techniques; bn = nursery data collected; lab = data collected from colonies as part of an ex-situ experiment from a block nursery, including all fixed-to-benthos propagation techniques;

Table 1. *Continued.*

Table/Field	Description	Value Constraints
Methods	Stores specific techniques and practices used to record measurements	- - -
method_id	Primary key identifier	- - -
method	Name of method	- - -
notes	Miscellaneous notes	(e.g., DOI of method publication, SOP link)
Standards	Stores units of the measurements	- - -
standard_id	Primary key identifier	- - -
name	Naming convention of a unit	(e.g., g cm^{-3} is density)
unit	Unit of measurement	(e.g., g cm^{-2})
Traits	Stores measurement type identification and classification	- - -
trait_id	Primary key identifier	- - -
trait_name	Name of trait	- - -
trait_class	Class of trait	(organismal, contextual)
Observations	Identifies the genet, location, and data source	- - -
observation_id	Primary key identifier	- - -
location_id	Foreign key from locations table	- - -
geno_id	Foreign key from genets table	- - -
dataset_id	Foreign key from datasets table	- - -
Measurements	Stores assessment of coral phenotype and contextual data and identifies observation, trait, standard, and method	- - -
measurement_id	primary key identifier	- - -
observation_id	Foreign key from observations table, groups related measurements	- - -
value	A nominal, ordinal, or interval value	- - -
trait_id	Foreign key from traits table	- - -
standard_id	Foreign key from standards table	- - -
method_id	Foreign key from methods table	- - -
Calculated Measurements	Stores standardized data for performance comparisons and identifies the trait, standard, method, genet, data filters, location, and data source	- - -
calculatedMeasurements_id	Primary key identifier	- - -
value	A nominal, ordinal, or interval value	- - -
trait_id	Foreign key from traits table	- - -
standard_id	Foreign key from standards table	- - -
method_id	Foreign key from methods table	- - -
geno_id	Foreign key from genets table	- - -
filter_id	Foreign key from filters table	- - -
location_id	Foreign key from locations table	- - -
dataset_id	Foreign key from datasets table	- - -

the nomenclature and genet identity from the restoration program that originally sampled the parent colony. The second definition is the Coral Sample Registry accession number, which is inherited from the Coral Restoration Foundation's Coral Sample Registry database (Moura et al. 2021). The Coral Sample Registry database aggregates coral sampling metadata to account for overlapping sampling efforts and sharing of coral colonies among restoration programs. With this definition, genets are identified by a unique string of 36 alphanumeric characters and represent ramets traced to distinct colony sampling events. The final definition is the multi-locus genotype identifier inherited from STAGdb (Kitchen et al. 2020), which

analyzes bi-allelic single nucleotide polymorphism markers to genetically identify unique colonies. With this definition, genets are uniquely named with four numeric characters. The multi-locus genotype definition, which incorporates genetic analyses, may aggregate putative genets and their phenotypic data. By maintaining genet identifiers used by the restoration programs and complementary coral restoration databases, AcDC inherits already accepted naming conventions and permits users to aggregate phenotypic data with their chosen definition.

New genets are added to the database as phenotypic data are submitted. As part of the data submission metadata form, contributors can include the genet's STAGdb multi-locus genotype identifier and the Coral Sample Registry accession id. If included in a submission, genet metadata can be directly pulled from the two databases, thus minimizing data entry and creating community-wide data consistency. Contributors are further encouraged to submit all applicable metadata, including donor colony location, date of donor colony sampling, name of the restoration program that originally sampled the parent colony, and any known alternative naming conventions. These data are maintained in the genets table.

In addition to the metadata collected from data contributors, genet metadata are downloaded from the corresponding restoration databases. For the Coral Sample Registry database, a custom script with an OAUTH API access token directly downloads the data. For the STAGdb, a custom script queries reports from the publicly accessible website and scrapes the corresponding metadata. The metadata submitted by data contributors are checked against the metadata collected from STAGdb and the Coral Sample Registry database, and any discrepancies are automatically flagged by the script for manual quality control. Metadata originating from the initial donor colony sampling event, such as that submitted to the Coral Sample Registry database, are adopted in case of metadata discrepancies.

Traits of Interest.—AcDC incorporates phenotypes proposed to be important under current and predicted environmental stress, including wound healing rates, growth rates, bleaching resistance, disease resistance, and sexual reproductive output (Baums et al. 2019). These phenotypes are tied to colony morphology, coral-host physiology, and *Symbiodiniaceae* densities, where available. Traits that track a singular phenotype are grouped together and classified as a trait family. For example, the growth-rate family has a total of 13 assessments of coral growth, each operating at different timescales, measuring different forms of colony growth, and employing different methodologies. The seven trait families include biomechanical properties, bleaching resistance, coral-host physiology, disease resistance, growth rates, sexual reproduction, and wound healing (Fig. 3; Online Fig. S1). This architecture groups together similar traits and is adaptable to the inclusion of new metrics and methods, which may be added to the database when new data is submitted.

Traits are further distinguished as single point observations or repeated observations. Point observations describe the density or count of an individual phenotype; examples include oocyte volume, bundle sperm density, and skeletal bulk density. Repeated observations are traits that require multiple, related assessments of discrete ramets to calculate a rate of change; examples include multiple measurements of total linear extension to calculate a linear growth rate and multiple measurements of fluorometry to calculate a rate of coral bleaching. Repeated observations must contain a contextual measurement termed "tag" to group related observations and

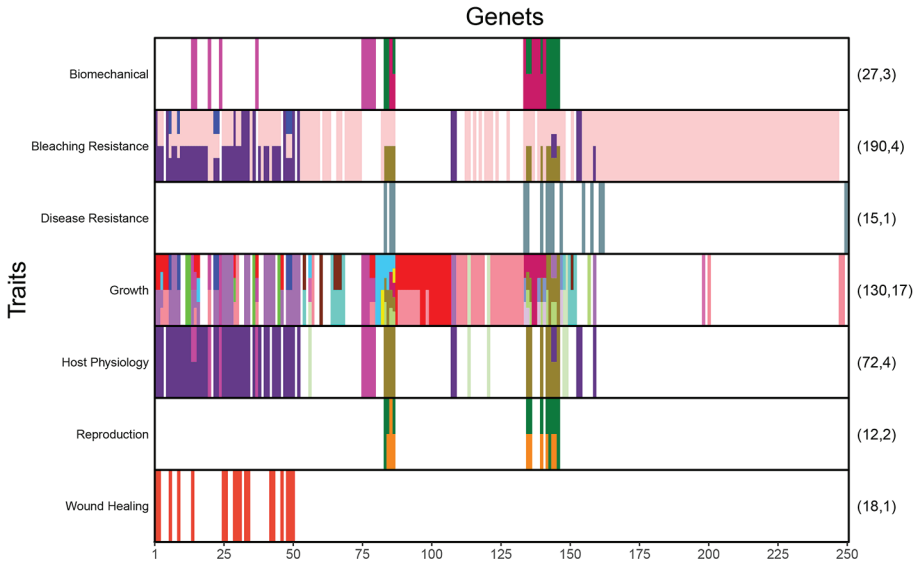

Figure 3. Trait by genet matrix illustrating the genet coverage. The matrix identifies data currently available in the *Acropora cervicornis* Data Coordination Hub and helps direct future lines of research to fill in gaps. Colored cells depict data available for a genet and correspond to a unique dataset. The color key is presented in Online Figure S2, and the corresponding metadata can be found in Online Table S1 by referencing the dataset's short name. Numbers in parentheses denote the number of genets available followed by the number of datasets for each trait family. Genets are arranged along the horizontal axis by the genet's database id, which can be referenced in the Genotypes table within the Online Supplementary Material.

enable the calculation of comparable performance metrics. Each component observation within a set of grouped observations must contain the tag measurement, and the tag measurement must be unique within a given dataset.

Standardization and Calculation of Traits.—Prior to the calculation of individual ramet traits, data are systematically checked for quality control and assurance in addition to the duplicate measurements check that occurs during data ingress and is described in the Technical Validation section below. For all growth data, a cumulative maximum function is run to ensure data are monotonically increasing. Negative growth data, which indicate a fragmented colony or partial mortality and are therefore not indicative of a true growth rate, are thereby eliminated. Coral bleaching metrics undergo a similar check with a cumulative minimum function to ensure data are monotonically decreasing. This constrains these metrics to the bleaching process and eliminates data that might indicate recovery. The removal of broken branches and thermally recovered fragments precludes data that are likely confounded by nongenotype effects and ensures the summary statistics presented in the graphical user interface are reflective of the genet's average performance. While eliminated data are not considered in the calculation of standardized performance metrics, all raw data are retained in the database and can be queried through the Raw Data tab on the graphical user interface.

Growth rates of *A. cervicornis* nonlinearly vary with respect to colony age and size, due in part to the branching nature of the species. Changes in growth standardized to time may therefore not be directly comparable between colonies of different ages.

To address this and facilitate maximum data comparability, growth data metrics are defined for 6-mo and annual intervals and standardized to initial size. Data within one month of the target interval are included in the calculations. For 6-mo metrics, this includes data between 5 and 7 mo, and for annual metrics, this includes data from 11 to 13 mo. If multiple data points exist within the window around the target interval, the data point closest to the target (182 d for 6-mo and 365 d for 12-mo) is chosen for calculations. The difference in growth from final and initial value of linear, volumetric, interstitial space, and calcification data are standardized to initial value and total number of days, resulting in a proportionate measurement of the ramet's daily growth to its initial size termed *productivity* (Eq. 1; Lirman et al. 2014):

$$productivity = \frac{\frac{metric_f - metric_i}{metric_i}}{days} \quad \text{Eq. 1}$$

where *metric* is the type of growth metric measured, *days* are the total number of days elapsed between the final and initial observations, and subscripts *f* and *i* denote the final and initial values, respectively. Productivity is expressed as linear growth rates, volumetric growth rates, interstitial space growth rates, and mass normalized daily calcification depending on the type of growth metric used for the calculation. Equation terms and subscripts are maintained throughout, unless otherwise noted.

Calcification data are additionally standardized to surface area, if available, and represent the average mass in milligrams of calcium carbonate precipitated each day per square centimeter of coral tissue. Linear, volumetric, and interstitial space data are further used to calculate specific growth rates using an exponential growth model denoting percent increase in size per day (Eq. 2; Crane et al. 2019). This metric was calculated to include all growth data, some of which was filtered from the productivity measurements due to the monitoring intervals not fitting within the defined 6-mo or annual time-point windows.

$$specific\ growth\ rate = 100 * \left(\left(\frac{metric_f}{metric_i} \right)^{\frac{1}{days}} - 1 \right) \quad \text{Eq. 2}$$

Multiple bleaching metrics are held within the database, including photochemical efficiency (Ralph et al. 2015), R-color score (Winters et al. 2009, DeMerlis et al. 2022), and Coral Color Reference Card values (Siebeck et al. 2006). The ratio of the final to the initial bleaching metric is first exponentiated by the reciprocal of the number of degree heating days (DHD), defined as the time-integrated bleaching stress above the regional maximum of the monthly-mean taken as 30.5 °C (Eq. 3 and 4; Podesta and Glynn 1997, Manzello et al. 2007). This value is then subtracted by 1 and multiplied by 100 to give units of percent change in bleaching metric per DHD,

$$bleaching\ rate = 100 * \left(\left(\frac{metric_f}{metric_i} \right)^{\frac{1}{DHD}} - 1 \right) \quad \text{Eq. 3}$$

$$DHD = \sum_{d=1}^{d=n} T - 30.5 \quad \text{Eq. 4}$$

where d is the day of the experiment, n is the total number of days, and T is the temperature the corals were exposed to on day d for all days where the temperature is greater than 30.5 °C. Bleaching rates, therefore, are negative values denoting the percent decay in the bleaching metric, with increased magnitude indicating reduced bleaching resistance.

Wound healing is defined as the percent closing of lesions where 100% is completely healed and 0% denotes no observable healing (Kaufman et al. 2021). The rate of wound healing is calculated as the proportion of recovery standardized to the initial wound area and total number of days required to reach maximum percent healed (Eq. 5),

$$wound\ healing\ rate = \frac{\frac{\%healed}{wound\ area_i}}{healing\ days} \quad \text{Eq. 5}$$

where wound area is expressed in units of square centimeters.

Point measurements do not undergo calculations and instead rely on commonly accepted standardized metrics. These metrics include Bayesian Relative Risk for disease assessment (Muller et al. 2018), effective dose of heat stress required to reduce photochemical efficiency by 50% (Voolstra et al. 2020, Evensen et al. 2021), and gross photosynthesis and respiration measurements (Muller et al. 2021). All associated metadata are included in the database with these point measurements and are used to facilitate quality control and apply data filters.

Following the calculation of individual measurements, contextual filters are appended to the calculated measurements record as shorthand strings, which can be queried upon in the graphical user interface. The script identifies all applicable filters by querying the corresponding metadata stored in the measurement and observation records. If a filter applies to any of the component observations within a set of grouped observations, then the calculated measurements record will receive the corresponding filter. Filter options include stress hardening type, bleaching stress, ambient temperature, ocean acidification stress, ambient pH, and seasonal filters. Stress hardening is defined as the variable exposure to elevated temperatures to improve a coral's thermal stress response (DeMerlis et al. 2022). The stress hardening filter is applied if a contextual trait named "stress hardening" exists for an observation. The bleaching stress filter is applied if any of the measurement records for temperature are greater than 30.5 °C; otherwise, the ambient temperature filter is applied. The ocean acidification stress filter is applied if any of the measurement records for pH are less than 7.9; otherwise, the ambient pH filter is applied. Finally, the seasonal filter checks if all data were exclusively collected from the first of May to the first of November and applies a wet season filter if these conditions are met. If data were exclusively collected between 1 November and 1 May, then a dry season filter is applied. With this temporal filter, the total length of repeated observations must be less than or equal to six months to unambiguously fit within a single defined season. Otherwise, no seasonal filter is applied.

Applicable filters are concatenated into a single string. All possible unique combinations of filters are held within the secondary lookup filters table (Fig. 2), and the calculated measurements record holds the corresponding foreign key containing the appropriate contextual filter.

Composite Performance Indices for Trait Families.—AcDC aligns metrics within a trait family to assess relative genet performance across multiple traits and methodologies using standardized composite indices. Composite scores are calculated with data from the standardized traits. Currently, composite indices exist for the growth rates and bleaching resistance trait families. These indices more effectively communicate genet performance and predominantly serve as benchmarking tools for the coral restoration community and should not be mistaken as absolute scores (Nardo et al. 2008, Charles et al. 2022).

For the composite growth index, standardized 6-mo and 12-mo linear growth and volumetric growth, mass normalized daily calcification, and total alkalinity anomaly incubation metrics are included for their overlap among all represented genets and independence among each individual trait. First, outliers are identified and removed using modified z-scores where the median value for the trait is subtracted from each value, and then the difference is scaled by the median of the absolute deviations about the median multiplied by the constant 1.486 to approximate a standard deviation under a normal distribution. We use the commonly accepted threshold of 3.5 to identify outliers, which are then removed and not included in the composite score calculations (Iglewicz and Hoaglin 1993, Nardo et al. 2008). Standardized measurements that were filtered, however, are reflected in individual trait summary statistics and are only excluded from the composite growth score calculations. Then, the remaining standardized measurements are converted into standard z-scores within their respective metrics, and an average linear extension and calcification score is calculated. Linear extension traits include linear growth and volumetric growth metrics, and calcification traits include mass normalized daily calcification and the total alkalinity anomaly incubation metrics. The average of these standard scores is taken as the final composite growth index for the genet. Genets with scores greater than 0 denote above average growth, while scores below 0 denote below average growth. Composite performance scores are reactive to data filtration and data updates, and therefore, composite scores represent the best estimate of a genet's average performance given the available data and applied filters. Composite scores should be analyzed in conjunction with the individual traits to understand potential tradeoffs among the component traits and across multiple trait families.

For the composite bleaching resistance index, a similar approach is employed using the CBASS ED50, bleaching R-score, bleaching color score, and bleaching photochemical efficiency metrics. Outliers are identified and removed when modified z-scores are greater than 3.5, and the remaining values are converted to standard z-scores. The average of these standard scores is taken as the final composite bleaching resistance index for the genet with positive scores indicating above average bleaching resistance and negative scores indicating below average bleaching resistance.

Technical Validation.—During data ingress, the data import script flags potential duplicate observations by checking for matching measurement, trait, location,

and genet values. Flagged records are manually checked and are discarded if uniqueness cannot be confirmed.

Consistent genet identification and quality control were established by integrating the complementary Coral Sample Registry and STAGdb databases as described above. Further, the standardized performance metrics ensure quality control by checking for a monotonic growth or stress response prior to its calculation. The details of this QA/QC check are described above.

Data Collection and Analyses

Phenotypic data were sourced from the science and restoration communities through the collection of published data and unpublished nursery evaluation data from restoration programs in Florida (Coral Restoration Foundation, Florida Fish and Wildlife Research Institute, Mote Marine Laboratory, The Nature Conservancy, Nova Southeastern University, and the University of Miami).

First, a literature review was conducted using the search terms "*Acropora cervicornis* AND genet" on the Google Scholar and Clarivate's Web of Science databases. An additional search of grey literature was conducted on NOAA's National Centers for Environmental Information database with the same search terms. The corresponding authors were contacted directly for data submission when the data were not publicly available.

Then, the program manager at each coral restoration program in Florida was contacted to access internal stock evaluation and monitoring datasets. These data were assessed for the standard quality control and completeness outlined above. Due to program-specific differences in monitoring efforts and stock evaluation, not all collected data could be cast into the database. A complete collection of all contributed data at the time of publication is presented in Online Table S1.

Current and Future Applications

Graphical User Interface.—To communicate genet performance data, we developed a graphical user interface in R v4.1.2 using the rShiny package (Chang et al. 2021). The goal of the interface is to complement quantitative metrics with intuitive graphical data representations. The interface has three core tools: (1) Trait Analysis, (2) Genet Report, and (3) Genet Comparison.

Each tool shares common features with one another and is directly hyperlinked, permitting users to navigate between tools for multiple use-cases. Quantitative tables contain descriptive statistics for each genet, including the number of observations, minimum and maximum values, average, standard deviation, and number of assimilated datasets. These descriptive statistics are augmented with graphical displays of genet performance including a stoplight indicator with red, yellow, and green values, respectively denoting first, middle, and third tercile performance and a modified boxplot juxtaposing a genet's average value and one standard deviation above the entire sampled population's minimum and maximum values along with the population's average and one standard deviation. The modified boxplot's color scheme places the genet in the context of the sampled population, with red indicating the genet's average is greater than one SD below the population average, yellow indicating the genet's average is within one SD of the population average, and green

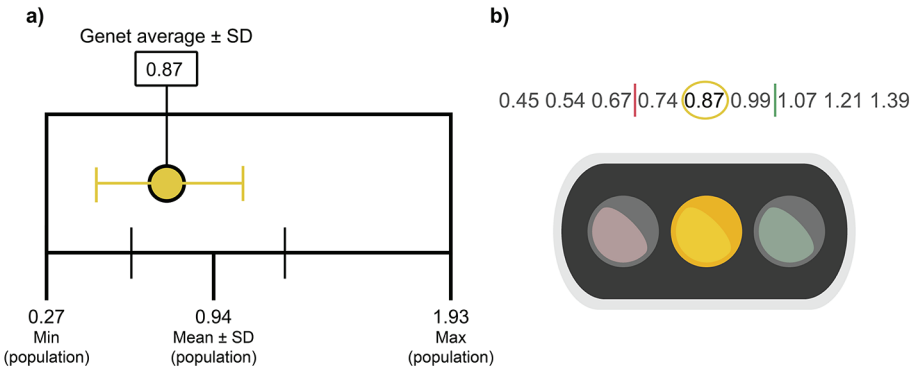

Figure 4. Graphical depictions of relative genet performance. Graphical displays of genet performance complement descriptive statistics. The representative example includes (A) a modified boxplot juxtaposing the genet average and one standard deviation (SD) above the population average and one SD, minimum, and maximum values. The color scheme denotes the genet average relative to the population average, with red indicating the genet average is greater than one SD below the population average, yellow indicating the genet average is within one SD of the population average, and green indicating the genet average is greater than one SD above the population average. (B) The global stoplight rankings provide a complementary quick, inline estimation of relative genet performance compared to ambient, unfiltered values with red indicating performance in the first tercile, yellow indicating performance in the middle tercile, and green indicating performance in the third tercile. The numbers above the stoplight indicator illustrate an example where a genet's average is placed in the middle tercile when compared to other genets.

indicating the genet's average is greater than one SD above the population average (Fig. 4). Further, users may download all summary tables and raw data directly from the web application. The packaged download will include a second table providing the citations for the aggregated datasets. Users must agree to cite the datasets in all resulting products prior to downloading the data.

The Trait Analysis tool allows users to investigate a trait family of interest, apply data filters, and identify the relative performance of genets within the trait family. Users can filter by the observation's geographic location, observation setting, applicable experimental attributes, or season. It is important to note that the global rank and summary statistics are a representation of all currently available data and will be subject to change with the inclusion of new data and more genets.

The Genet Report tool allows users to view all phenotypic data for a given genet and the available metadata. If available in the database, the genet overview table provides hyperlinks to the genet's record on STAGdb (Kitchen et al. 2020) and the Coral Sample Registry (Moura et al. 2021).

The Genet Comparison tool builds upon the individual Genet Report and Trait Analysis tools and allows users to select multiple genets and apply data filters. This tool was built for users to generate custom genet evaluation reports. Genets can be selected by one of the three genet definitions used in the database, the donor colony source location, or the restoration program that originally sampled the donor colony.

Data and Code Availability.—Data released as part of this manuscript and data from future contributions are made directly available to download using the graphical user interface. Under the Raw Data tab, users may query all publicly available data to analyze independently, including data that is not presented in the three

core tools described above. These include mortality data that is not directly tied to physiology, data that were rejected due to QA/QC concerns, and all measurements underlying the standardized performance metrics. As part of this data export, a packaged file containing all suggested citations will be exported as described previously.

The code for the RShiny graphical user interface, SQL database, standardized trait calculations and filters, composite indices, and cross-database integration are additionally available in the Online Supplementary Material and on the AcDC GitHub repository (https:\\github.com/pkiel/AcDC).

Usage Notes.—The static release of phenotypic data in the Online Supplementary Material or on the AcDC GitHub repository may not contain the complete data available on AcDC. To access the most up to date and available data, please navigate to AcDC (https://www.coral.noaa.gov/AcDC/).

Data contributors must choose an appropriate data license at the time of submission. License options include the Creative Commons 1.0 Universal public domain dedication (CC0), the Creative Commons Attribution 4.0 International license (CC BY 4.0), and a nonlicensed Internal Use Only designation. For data submitted under the Internal Use Only designation, raw data are not downloadable. These data, however, are still used to calculate summary statistics, which are viewable to the public with the graphical user interface. This designation is intended as a temporary status while publications are under peer-review. Contributors are encouraged to choose one of the license options or submit an updated metadata form if they originally submitted data under an Internal Use Only designation during the peer-review process. Following a three-year designation as Internal Use Only, a CC BY 4.0 license is applied to the contribution and raw data is made publicly accessible.

Acknowledgments

AcDC was developed by NOAA AOML's Coral Program with funds from NOAA's Coral Reef Conservation Program, Project #31254. The authors are grateful for the researchers who originally collected the data including M D'Alessandro, A DeMerlis, C Drury, K Haider, C Hankins, D Hesley, K Johnson-Sapp, R Karp, M Kaufman, A Kirkland, H Koch, I Kuffner, K Lohr, W Million, K O'Donnell, B Paradis, J Patterson, N Rivas, and J Unsworth. The authors would additionally like to thank the working groups whose feedback greatly enhanced AcDC's capabilities and was provided by NOAA Fisheries' *Acropora* Recovery Implementation Team and the Florida Department of Environmental Protection's Stony Coral Tissue Loss Disease Restoration Team.

Literature Cited

Alvarez-Filip L, Dulvy NK, Gill JA, Côté IM, Watkinson AR. 2009. Flattening of Caribbean coral reefs: region-wide declines in architectural complexity. Proc R Soc B. 276:3019–3025. https://doi.org/10.1098/rspb.2009.0339

Aronson RB, Precht WF. 2001. White-band disease and the changing face of Caribbean coral reefs. Hydrobiologia. 460:25–38. https://doi.org/10.1023/A:1013103928980

Baums IB, Baker AC, Davies SW, Grottoli AG, Kenkel CD, Kitchen SA, Kuffner IB, LaJeunesse TC, Matz MV, Miller M, et al. 2019. Considerations for maximizing the adaptive potential of restored coral populations in the western Atlantic. Ecol Appl. 29(8):1–23. https://doi.org/10.1002/eap.1978

Baums IB, Chamberland VF, Locatelli NS, Conn T. 2022. Maximizing genetic diversity in coral restoration projects. *In:* van Oppen, MJH, Aranda Lastra, M, editors. Coral reef conservation and restoration in the Omics Age. Cham, Switzerland: Springer. p. 35–53. https://doi.org/10.1007/978-3-031-07055-6_3

Brown AL, Anastasiou D-E, Schul M, MacVittie S, Spiers LJ, Meyer JL, Manfrino C, Frazer TK. 2022. Mixtures of genotypes increase disease resistance in a coral nursery. Sci Rep. 12(1):19286. https://doi.org/10.1038/s41598-022-23457-6

Chang W, Cheng J, Allaire J, Sievert C, Schloerke B, Xie Y, Allen J, McPherson J, Dipert A, Borges B. 2021. Shiny: web application framework for R. Available from: https://cran.r-project.org/package=shiny

Charles V, Gherman T, Emrouznejad A. 2022. The role of composite indices in international economic diplomacy. *In:* Charles V, Emrouznejad A, editors. Modern indices for international economic diplomacy. Cham, Switzerland: Palgrave Macmillan. p. 1–17.

Cramer KL, Jackson JBC, Donovan MK, Greenstein BJ, Korpanty CA, Cook GM, Pandolfi JM. 2020. Widespread loss of Caribbean acroporid corals was underway before coral bleaching and disease outbreaks. Sci Adv. 6(17):eaax9395. https://doi.org/10.1126/sciadv.aax9395

Crane DP, Ogle DH, Shoup DE. 2019. Use and misuse of a common growth metric: guidance for appropriately calculating and reporting specific growth rate. Rev Aquac. 12(3):1542–1547. https://doi.org/10.1111/raq.12396

Cunning R, Parker KE, Johnson-Sapp K, Karp RF, Wen AD, Williamson OM, Bartels E, D'Alessandro M, Gilliam DS, Hanson G, et al. 2021. Census of heat tolerance among Florida's threatened staghorn corals finds resilient individuals throughout existing nursery populations. Proc R Soc B. 288:20211613. https://doi.org/10.1098/rspb.2021.1613

DeMerlis A, Kirkland A, Kaufman ML, Mayfield AB, Formel N, Kolodziej G, Manzello DP, Lirman D, Enochs IC. 2022. Pre-exposure to a variable temperature treatment improves the response of *Acropora cervicornis* to acute thermal stress. Coral Reefs. 41:435–445. https://doi.org/10.1007/s00338-022-02232-z

Donovan MK, Burkepile DE, Kratochwill C, Shlesinger T, Sully S, Oliver TA, Hodgson G, Freiwald J, van Woesik R. 2021. Local conditions magnify coral loss after marine heatwaves. Science. 372(6545):977–980. https://doi.org/10.1126/science.abd9464

Drury C, Lirman D. 2021. Genotype by environment interactions in coral bleaching. Proc Biol Sci. 288:20210177. https://doi.org/10.1098/rspb.2021.0177

Drury C, Schopmeyer S, Goergen EA, Bartels E, Nedimyer K, Johnson ME, Maxwell K, Galvan V, Manfrino C, Lirman D. 2017. Genomic patterns in *Acropora cervicornis* show extensive population structure and variable genetic diversity. Ecol Evol. 7(16):6188–6200. https://doi.org/10.1002/ece3.3184

Evensen NR, Fine M, Perna G, Voolstra CR, Barshis DJ. 2021. Remarkably high and consistent tolerance of a Red Sea coral to acute and chronic thermal stress exposures. Limnol Oceanogr. 66(5):1718–1729. https://doi.org/10.1002/lno.11715

Hoegh-Guldberg O, Mumby PJ, Hooten AJ, Steneck RS, Greenfield P, Gomez E, Harvell CD, Sale PF, Edwards AJ, Caldeira K, et al. 2007. Coral reefs under rapid climate change and ocean acidification. Science. 318:1737–1742. https://doi.org/10.1126/science.1152509

Iglewicz B, Hoaglin DC. 1993. How to detect and handle outliers. Milwaukee, Wisconsin: American Society for Quality Control, Statistics Division.

Jackson JBC, Donovan MK, Cramer KL, Lam V. 2014. Status and trends of Caribbean oral reefs: 1970–2012. Gland, Switzerland: Global Coral Reef Monitoring Network, International Union for the Conservation of Nature.

Kaufman ML, Watkins E, van Hooidonk R, Baker AC, Lirman D. 2021. Thermal history influences lesion recovery of the threatened Caribbean staghorn coral *Acropora cervicornis* under heat stress. Coral Reefs. 40(2):289–293. https://doi.org/10.1007/s00338-020-02025-2

Kitchen SA, Von Kuster G, Kuntz KLV, Reich HG, Miller W, Griffin SP, Fogarty ND, Baums IB. 2020. STAGdb: a 30K SNP genotyping array and Science Gateway for *Acropora*

corals and their dinoflagellate symbionts. Sci Rep. 10:12488. https://doi.org/10.1038/s41598-020-69101-z

Kleypas J, Allemand D, Anthony KRN, Baker AC, Beck MW, Hale LZ, Hilmi N, Hoegh-Guldberg O, Hughes T, Kaufman L, et al. 2021. Designing a blueprint for coral reef survival. Biol Conserv. 257:109107. https://doi.org/10.1016/j.biocon.2021.109107

Knowlton N, Grottoli AG, Kleypas J, Obura D, Corcoran E, de Goeij JM, Felis T, Harding S, Mayfield A, Miller M, et al. 2021. Rebuilding coral reefs: a decadal grand challenge. International Coral Reef Society and Future Earth Coasts. https://doi.org/10.53642/nrky9386

Lirman D, Schopmeyer S, Galvan V, Drury C, Baker AC, Baums IB. 2014. Growth dynamics of the threatened Caribbean staghorn coral *Acropora cervicornis*: influence of host genotype, symbiont identity, colony size, and environmental setting. PLOS ONE. 9:e107253. https://doi.org/10.1371/journal.pone.0107253

Lohr KE, Patterson J. 2017. Intraspecific variation in phenotype among nursery-reared staghorn coral *Acropora cervicornis* (Lamarck, 1816). J Exp Mar Biol Ecol. 486:87–92. https://doi.org/10.1016/j.jembe.2016.10.005

Madin JS, Bowers S, Schildhauer M, Krivov S, Pennington D, Villa F. 2007. An ontology for describing and synthesizing ecological observation data. Ecol Inform. 2(3):279–296. https://doi.org/10.1016/j.ecoinf.2007.05.004

Manzello DP, Berkelmans R, Hendee JC. 2007. Coral bleaching indices and thresholds for the Florida Reef Tract, Bahamas, and St. Croix, US Virgin Islands. Mar Pollut Bull. 54(12):1923–1931. https://doi.org/10.1016/j.marpolbul.2007.08.009

MariaDB Foundation 2021. MariaBD Server: The open source relational database. v10.6.5. Available from: https://mariadb.org

Million WC, Ruggeri M, O'Donnell S, Bartels E, Conn T, Krediet CJ, Kenkel CD. 2022. Evidence for adaptive morphological plasticity in the Caribbean coral, *Acropora cervicornis*. Proc Natl Acad Sci USA. 119(49):e2203925119. https://doi.org/10.1073/pnas.2203925119

Moberg F, Folke C. 1999. Ecological goods and services of coral reef ecosystems. Ecol Econ. 29(2):215–233. https://doi.org/10.1016/S0921-8009(99)00009-9

Moura A, Beck B, Duffey R, Mceachron LL, Miller M, Moore J, Moulding AL, Winters RS. 2021. Integrating coral restoration data with a novel coral sample registry. Front Mar Sci. 8:700172. https://doi.org/10.3389/fmars.2021.700172

Muller EM, Bartels E, Baums IB. 2018. Bleaching causes loss of disease resistance within the threatened coral species *Acropora cervicornis*. eLife. 7:e35066. https://doi.org/10.7554/eLife.35066

Muller EM, Dungan AM, Million WC, Eaton KR, Petrik C, Bartels E, Hall ER, Kenkel CD. 2021. Heritable variation and lack of tradeoffs suggest adaptive capacity in *Acropora cervicornis* despite negative synergism under climate change scenarios. Proc R Soc B. 288:20210923. https://doi.org/10.1098/rspb.2021.0923

Nardo M, Saisana M, Saltelli A, Tarantola S, Hoffmann A, Giovannini E. 2008. Handbook on constructing composite indicators: methodology and user guide. Paris, France: OECD publishing.

National Academies of Sciences, Engineering, and Medicine. 2019. A decision framework for interventions to increase the persistence and resilience of coral reefs. Washington, DC: The National Academies Press. https://doi.org/10.17226/25424

O'Donnell KE, Lohr KE, Bartels E, Baums IB, Patterson J. 2018. *Acropora cervicornis* genet performance and symbiont identity throughout the restoration process. Coral Reefs. 37(4):1109–1118. https://doi.org/10.1007/s00338-018-01743-y

Perry CT, Murphy GN, Kench PS, Smithers SG, Edinger EN, Steneck RS, Mumby PJ. 2013. Caribbean-wide decline in carbonate production threatens coral reef growth. Nat Commun. 4:1402. https://doi.org/10.1038/ncomms2409

Podestá GP, Glynn PW. 1997. Sea surface temperature variability in Panamá and Galápagos: extreme temperatures causing coral bleaching. J Geophys Res. 102:15749–15759. https://doi.org/10.1029/96JC03557

Ralph PJ, Hill R, Doblin MA, Davy SK. 2015. Theory and application of pulse amplitude modulated chlorophyll fluorometry in coral health assessment. *In:* Woodley CM, Downs CA, Bruckner AW, Porter JW, Galloway SB, editors. Diseases of coral. Hoboken: John Wiley & Sons, Inc. p. 506–523. https://doi.org/10.1002/9781118828502.ch38

Siebeck UE, Marshall NJ, Klüter A, Hoegh-Guldberg O. 2006. Monitoring coral bleaching using a colour reference card. Coral Reefs. 25(3):453–460. https://doi.org/10.1007/s00338-006-0123-8

Voolstra CR, Buitrago-López C, Perna G, Cárdenas A, Hume BCC, Rädecker N, Barshis DJ. 2020. Standardized short-term acute heat stress assays resolve historical differences in coral thermotolerance across microhabitat reef sites. Glob Change Biol. 26(8):4328–4343. https://doi.org/10.1111/gcb.15148

Whiteley AR, Fitzpatrick SW, Funk WC, Tallmon DA. 2015. Genetic rescue to the rescue. Trends Ecol Evol. 30(1):42–49. https://doi.org/10.1016/j.tree.2014.10.009

Winters G, Holzman R, Blekhman A, Beer S, Loya Y. 2009. Photographic assessment of coral chlorophyll contents: implications for ecophysiological studies and coral monitoring. J Exp Mar Biol Ecol. 380(1–2):25–35. https://doi.org/10.1016/j.jembe.2009.09.004

Young CN, Schopmeyer SA, Lirman D. 2012. A review of reef restoration and coral propagation using the threatened genus *Acropora* in the Caribbean and western Atlantic. Bull Mar Sci. 88(4):1075–1098. https://doi.org/10.5343/bms.2011.1143