Mutations at microsatellite loci of Acropora palmata in the Caribbean and North-West Atlantic from 2015-2016 (Coral Hybridization project)

Website: https://www.bco-dmo.org/dataset/666321
Data Type: Other Field Results
Version: 2
Version Date: 2017-10-19

Project
» Collaborative research: Is hybridization among threatened Caribbean coral species the key to their survival or the harbinger of their extinction? (Coral Hybridization)

Contributors	Affiliation	Role
Baums, Iliana B.	Pennsylvania State University (PSU)	Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Somatic mutations that occurred at 5 microsatellite loci in Acropora palmata collected throughout the Caribbean. These data were deposited in DRYAD: http://dx.doi.org/10.5061/dryad.f6600 and published in the paper Devlin-Durante et al, Mol Ecol. (2016).

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Coverage

Spatial Extent: **N**:26.7075 **E**:-64.677 **S**:12.0831 **W**:-88.199

Methods & Sampling

Adult Acropora palmata colonies were sampled (1 cm2) with hammer and chisel and tissues were preserved in 96% non-denature Ethanol. DNA was extracted using the DNEasy tissue kit (Qiagen) following manufacturer's instructions. Two multiplex Polymerase Chain Reactions (PCR) were performed per sample using fluorescently labeled primers to assay five loci containing AAT repeats. These five microsatellite loci have previously been demonstrated to be mendelian and coral-specific using controlled crosses (Baums et al., 2005). PCR products were visualized with an automated sequencer (ABI 3730). An internal size standard (Gene Scan 500-Liz, Applied Biosystems CA) ensured accurate sizing. Electropherograms were analyzed with GeneMapper Software 3.0 (Applied Biosystems, CA). Alleles were scored as PCR product size.

Data Processing Description

Electropherograms of microsatellite alleles were scored for allele sizes (basepairs) in Genemapper vers. (Applied Biosystems) and transferred to spreadsheets.

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- nd (no data) was entered into all blank cells
- replaced spaces and / with underscores
- sorted records by region

VERSIONS: 2017-10-26: Replaced version 1 (2016-11-30) with version 2 (2017-10-19). Some latitudes and longitudes were added to allow visualization of the data on the mapserver.

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Data Files

File	
Apalmata_mutations_sort.csv	(Comma Separated Values (.csv), 25.80 KB) MD5:4bd4ffe8e62b446059d18a1613959e94
Primary data file for dataset ID 666321	

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Related Publications

Baums, I. B., Devlin-Durante, M. K., & LaJeunesse, T. C. (2014). New insights into the dynamics between reef corals and their associated dinoflagellate endosymbionts from population genetic studies. Molecular Ecology, 23(17), 4203–4215. doi:10.1111/mec.12788
General

Baums, I., Hughes, C., & Hellberg, M. (2005). Mendelian microsatellite loci for the Caribbean coral Acropora palmata. Marine Ecology Progress Series, 288, 115–127. doi:10.3354/meps288115
Methods

Devlin-Durante, M. K., Miller, M. W., Precht, W. F., & Baums, I. B. (2016). How old are you? Genet age estimates in a clonal animal. Molecular Ecology, 25(22), 5628–5646. doi:10.1111/mec.13865
Results

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Related Datasets

IsRelatedTo

Baums, I. B. (2021) **Multilocus microsatellite genotypes of Acropora palmata from the Caribbean and North-West Atlantic from 2015-2016 (Coral Hybridization project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-11-30 doi:10.26008/1912/bco-dmo.666350.1 [view at BCO-DMO]

Different Version

Devlin-Durante, M. K., Miller, M. W., Caribbean Acropora Research Group, Precht, W. F., and Baums, I. B. (2017). Data from: How old are you? Genet age estimates in a clonal animal (Version 2) [Data set]. Dryad Digital Repository. https://doi.org/10.5061/dryad.f6600

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Parameters

Parameter	Description	Units
region	sampling region	unitless
reef	the sampling reef	unitless
database_id	Baums lab sample Database ID (unique for each sample)	unitless
locus	the microsatellite locus that had a mutated allele (166; 181; 182; 192;207)	basepairs
ancestral_allele_1	the first ancestral alleles of the genet	basepairs
ancestral_allele_2	the second ancestral alleles of the gene	basepairs
allele_3	any additional alleles detected	basepairs
allele_4	any additional alleles detected	basepairs
origin_allele_3	designation of origin of how additional allele 3 arose (i.e from ancestral Allele 1 or Allele 2). Sometimes one ancestral allele mutated twice giving rise to Alleles 3 and 4.	basepairs
origin_allele_4	designation of origin of how additional allele 4 arose (i.e from ancestral Allele 1 or Allele 2). Sometimes one ancestral allele mutated twice giving rise to Alleles 3 and 4.	basepairs
mutation_step_allele_3	Count of mutation steps from ancestral allele to mutated allele. Each mutation step is an addition or loss of 3 bp.	basepairs
mutation_step_allele_4	Count of mutation steps from ancestral allele to mutated allele. Each mutation step is an addition or loss of 3 bp.	basepairs
mutational_change_allele_3_bp	Mutational Change Allele 3 (bp) The mutational change (in bp) from the ancestral alleles to the new allele is given.	basepairs
mutational_change_allele_4_bp	Mutational Change Allele 4 (bp) The mutational change (in bp) from the ancestral alleles to the new allele is given.	basepairs
sample_count_for_genet	Genets had from 2 to 94 samples (sample count for genet)	samples
genet_id	Genets are identified by their Genet ID	unitless
full_mutation	Sometimes ancestral alleles were no longer detected (full mutations)	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees

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Instruments

Dataset-specific Instrument Name	automated sequencer (ABI 3730)
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	ABI 3730
Generic Instrument Name	Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

Baums_Carib

Website	https://www.bco-dmo.org/deployment/666348
Platform	Penn_State_U
Start Date	2015-10-01
End Date	2016-10-26
Description	genetics studies

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Project Information

Collaborative research: Is hybridization among threatened Caribbean coral species the key to their survival or the harbinger of their extinction? (Coral Hybridization)

Coverage: Caribbean and North-West Atlantic

NSF Award Abstract:
Reef-building acroporid corals form the foundation of shallow tropical coral communities throughout the Caribbean. Yet, the once dominant staghorn coral (Acropora cervicornis) and the elkhorn coral (A. palmata) have decreased by more than 90% since the 1980s, primarily from disease. Their continuing decline jeopardizes the ability of coral reefs to provide numerous societal and ecological benefits, including economic revenue from seafood harvesting and tourism and shoreline protection from extreme wave events caused by storms and hurricanes. Despite their protection under the U.S. Endangered Species Act since 2006, threats to the survival of reef-building acroporid corals remain pervasive and include disease and warming ocean temperatures that may lead to further large-scale mortality. However, hybridization among these closely related species is increasing and may provide an avenue for adaptation to a changing environment. While hybrids were rare in the past, they are now thriving in shallow habitats with extreme temperatures and irradiance and are expanding into the parental species habitats. Additional evidence suggests that the hybrid is more disease resistant than at least one of the parental species. Hybridization may therefore have the potential to rescue the threatened parental species from extinction through the transfer of adapted genes via hybrids mating with both parental species, but extensive gene flow may alter the evolutionary trajectory of the parental species and drive one or both to extinction. This collaborative project is to collect genetic and ecological data in order to understand the mechanisms underlying increasing hybrid abundance. The knowledge gained from this research will help facilitate more strategic management of coral populations under current and emerging threats to their survival. This project includes integrated research and educational opportunities for high school, undergraduate and graduate students, and a postdoctoral researcher. Students in the United States Virgin Islands will take part in coral spawning research and resource managers will receive training on acroporid reproduction to apply to coral restoration techniques.

Current models predict the demise of reefs in the next 200 years due to increasing sea surface temperatures and ocean acidification. It is thus essential to identify habitats, taxa and evolutionary mechanisms that will allow some coral species to maintain their role as foundation fauna. Hybridization can provide an avenue for adaptation to changing conditions. Corals hybridize with some frequency and results may range from the introduction of a few alleles into existing parent species via introgression, to the birth of a new, perhaps better adapted genetic lineage. The only widely accepted coral hybrid system consists of the once dominant but now threatened Caribbean species, Acropora cervicornis and A. palmata. In the past, hybrid colonies originating from natural crosses between elkhorn and staghorn corals were rare, and evidence of hybrid reproduction was limited to infrequent matings with the staghorn coral. Recent field observations suggest that the hybrid is increasing and its ecological role is changing throughout the Caribbean. These hybrids appear to be less affected by the disease that led to the mass mortality of their parental species in recent decades. Hybrids are also found thriving in shallow habitats with high temperatures and irradiance suggesting they may be less susceptible to future warming scenarios. At the same time, they are expanding into the deeper parental species habitats. Preliminary genetic data indicate that hybrids are now mating with each other, demonstrating the potential for the formation of a new species. Further, hybrids appear to be capable of mating with both staghorn and elkhorn coral, perhaps leading to gene flow between the parent species via the hybrid. Research is proposed to address how the increase in hybridization and perhaps subsequent introgression will affect the current ecological role and the future evolutionary trajectory of Caribbean acroporids. Specifically, this collaborative project aims to answer the following questions: 1) What is the historic rate, direction, and degree of introgression across species ranges and genomes? Linkage block analysis based on genome-wide SNP genotyping across three replicate hybrid zones will answer this question. 2) What is the current extent and future potential of later generation hybrid formation? Morphometric and genetic analyses combined with in vitro fertilization assays will be used. 3) What mechanisms allow hybrids to thrive in hot, shallow waters? A series of manipulative in situ and ex situ experiments will determine whether biotic or abiotic factors favor hybrid survival in shallow waters. 4) Are hybrids more disease resistant than the parentals species? Disease transmission assays in reciprocal transplant experiments and histological analysis to determine the extent of disease will be conducted. A multidisciplinary approach will be taken that combines traditional and cutting edge technology to provide a detailed analysis of the evolutionary ecology of Caribbean corals.

Note: PI Nicole Fogarty's original award OCE-1538469 was issued while at Nova Southeastern University. This was replaced by OCE-1929979 upon moving to the University of North Carolina Wilmington.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1537959

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