UNDERSTANDING LOCAL ADAPTATION IN FLORIDA'S STAGHORN CORALS

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PROJECT SUMMARY

OVERVIEW

Staghorn coral (*Acropora cervicornis*), a major reef builder in the Caribbean, is known to provide complex habitat for multiple reef-associated organisms and is the fastest growing coral in the Caribbean. However, over the past four decades stressors such as White Band Disease have caused a massive decline in the species, with abundance declining over 95% in some regions. Consequently, staghorn corals are frequently targeted for use in active coral reef restoration efforts with the goal of revitalizing coral cover that will persist in the face of climate change and other stressors. The long-term persistence of populations in the face of these stressors lies in their resistance and resilience to disturbance. Recruitment and genetic connectivity between populations are key to restoring resistant and resilient staghorn corals by generating the high standing genetic diversity necessary to precipitate adaptive potential.

Restoration efforts informed by high resolution knowledge on staghorn coral population structure, connectivity, diversity, and the adaptive potential will be more successful in creating natural aggregations with high adaptive potential. Previous studies have shown high population structure over regional scales and limited larval dispersal over distances greater than 500 km. While the Florida region itself has relatively high gene flow compared with other regions of the Caribbean, higher resolution data show patchiness in flow and subtle genetic structure between populations and individual reefs. We hypothesize that patchiness in gene flow and population structure is correlated to habitat heterogeneity and that population structure may result from adaptive processes. Population differentiation between geographically-close staghorn outcrops can have major implications in the sourcing of transplanted corals for these regions and underline the importance of using high-resolution genomic data to inform restoration efforts.

INTELLECTUAL MERIT

The proposed study will provide much needed data on the extent of genetic structure among and between *A. cervicornis* populations, the effect of habitat heterogeneity on population structure, and the key biological functions that differentiate populations in the Florida Reef Tract. Information on genetic diversity between and among *A. cervicornis* populations is needed to inform the sourcing of transplanted corals so as to avoid the effects outbreeding depression and maximize adaptive potential

BROADER IMPACTS

Raw sequencing data for the proposed research will be submitted to the National Center for Biotechnology Information as a Sequence Read Archive (SRA). Additionally, the results of this study will be published in an open-access journal and step-by-step instructions for genomic analyses will be made publicly available within a GitHub repository. The findings of this study will be presented to restoration practitioners, managers, and other scientists during the Coral Restoration Consortium. In addition to providing open access of all protocols and results of this study the principle investigator will also recruit undergraduates and local high-schoolers in under-represented groups to intern with the lab. These students will be mentored by the PI and will be able to obtain hands-on experience in fieldwork, and data collection analysis. Students will also have the opportunity to conduct related independent research and present their findings at the university's poster presentation.

Coral reefs are known to provide numerous ecosystem services including provisioning of food and complex habitat for commercially and recreationally important fish and invertebrates, shoreline protection, and tourism and consequently carry heavy intrinsic societal value (Costanza et al., 1997). In the Caribbean, staghorn coral (*Acropora cervicornis*) is a dominant reef-building species, providing three-dimensional habitat for a multitude of other species in the region, thus increasing interspecific biodiversity (Agudo-Adriani, Cappelletto, Cavada-Blanco, & Croquer, 2016). However, during the past four decades staghorn corals have experienced extensive die-off in their Caribbean range, with some populations declining by greater than 95% (Miller, Bourque, & Bohnsack, 2002). This massive die-off has been contributed to a combination of multiple interacting natural and anthropogenic stressors including White Band Disease, eutrophication, overfishing, climate change, storm damage, grazer die-off (Drury et al., 2018; Kitchen et al., 2019; Vollmer & Palumbi, 2006). The staghorn coral's rapid decline in in the Caribbean, coupled with its intrinsic ecological and societal value led the United States government to list it as a threatened species under the U.S. Endangered Species Act in 2006 (Hogarth, 2006).

Due to the species' ecological significance, rapid growth rates, potential for asexual reproduction, and recent population decline, staghorn corals are frequently targeted by restoration practitioners for coral gardening. In this restoration technique, fragments of coral are collected and raised in nurseries until they reach a sufficient size for translocation. They are then transported and affixed to reefs that require new growth with the goal of revitalizing healthy coral cover on the reef that will persist in the face of climate change and other stressors (Epstein, Bak, & Rinkevich, 2001; Rinkevich, 2005). The long-term persistence of staghorn corals lies in their resistance and resilience to disturbance, which are dependent on multiple factors. Successful restoration staghorn corals in their Caribbean range requires maintenance of their current abundance and distribution (Cowen & Sponaugle, 2009; T. P. Hughes & Tanner, 2000; Munday et al., 2009), recolonization of devasted areas (Connell, 1997; Gilmour, Smith, Heyward, Baird, & Pratchett, 2004; Szmant, 1986), and maintenance of high standing genetic diversity, which is necessary to generate adaptive potential (Ayre & Hughes, 2000; Hughes, Inouye, Johnson, Underwood, & Vellend, 2008). Thus, in-depth knowledge of staghorn coral genomic structure, connectivity, diversity, and the adaptive potential is necessary to inform effective restoration of the species.

Research on genetic connectivity of staghorn corals in the Caribbean by Vollmer and Palumbi (2006) showed high population structure over regional scales and limited larval dispersal over distances greater than 500 km. While the Florida region itself has relatively high gene flow compared with other regions of the Caribbean, higher resolution data show patchiness in flow and subtle genetic structure between populations and individual reefs (Drury et al., 2016; Drury et al., 2017; Hemond & Vollmer, 2010). A study on genomic patterns of staghorn populations in the Florida Reef Tract revealed higher-than-expected population structure in Broward county reefs (Drury et al., 2017). We hypothesize that patchiness in gene flow and population structure is correlated to habitat heterogeneity and that population structure may result from adaptive processes. Population differentiation between geographically-close staghorn outcrops can have major implications in the sourcing of transplanted corals for these regions so as to avoid decreased fitness in restored populations due to outbreeding depression (Baums, 2008). The proposed research includes two aims to elucidate potential local adaptation of corals in the Florida Reef Tract:
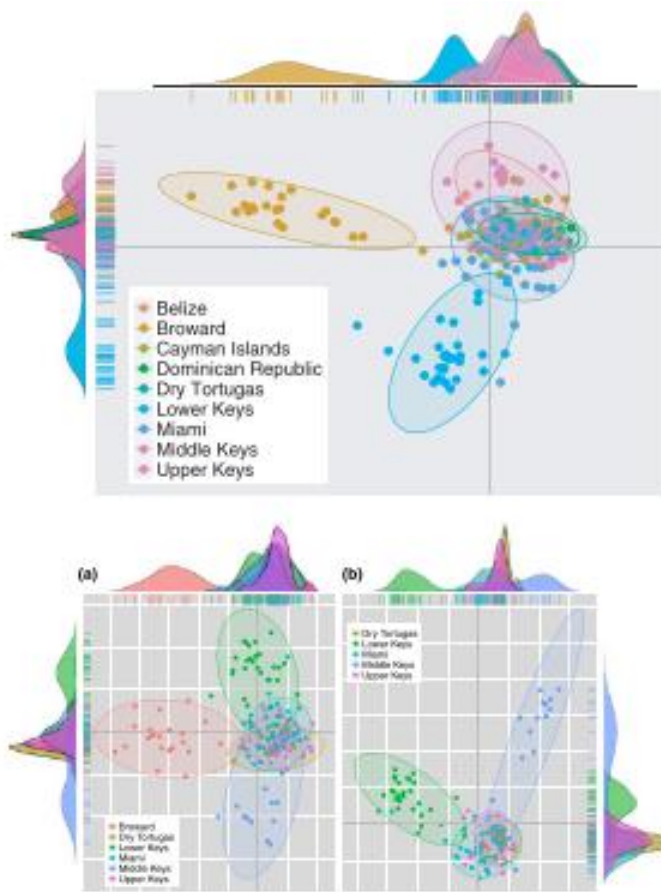
Aim 1: To identify population differentiation in the genome due to habitat heterogeneity in the Florida Reef Tract.

Aim 2: To identify the biological processes, molecular functions and cellular components under natural selection within staghorn populations in the Florida Reef Tract.

PROPOSED RESEARCH

Staghorn coral nubbins will be collected from sites from the Broward county region, and the lower and middle keys, regions that were shown to have higher differentiation in the Drury et al. 2017 paper. Two reefs will be sampled from each region, and five corals will be sampled at random in each reef to capture the mean expected heterozygosity of that location (Drury et al., 2017). DNA will be extracted from the corals for ezRAD sequencing. This method of sequencing was chosen for its feasibility, its preclusion for PCR bias. Although it is relatively more expensive than other sequencing methods, the number of samples to be analyzed is relatively small.

Figure 1. a) Discriminant analysis of principal components for all populations. Colors assigned by population for Broward, Miami- Dade, Upper Keys, Middle Keys, Lower Keys, Dry Tortugas, Belize, Cayman Islands, and Dominican Republic. Top density plot represents Discriminant Function 1, and side density plot represents Discriminant Function 2. b) DAPC for (a) Florida Populations and (b) Florida Populations without Broward. Colors assigned in both plots by population for Broward, Miami- Dade, Upper Keys, Middle Keys, Lower Keys, Dry Tortugas. Top density plot represents Discriminant Function 1, and side density plot represents Discriminant Function 2. (Taken from Drury et al., 2017)

In order to investigate population structure correlations with habitat we propose an environmental associations analysis. Environmental data such as water temperature, salinity, pH, alkalinity and other water quality parameters will be collected from long-term National Oceanic and Atmospheric Association buoys and water samples will be collected during coral sampling. BAYENV, Bayescan, and PCAdapt will be used to identify outlier SNPs. Only SNPs identified by more than two methods will be kept for further analysis. Gene ontology will be used to identify the biological processes, molecular functions and cellular components in outlier SNPs and putatively adaptive SNPs.
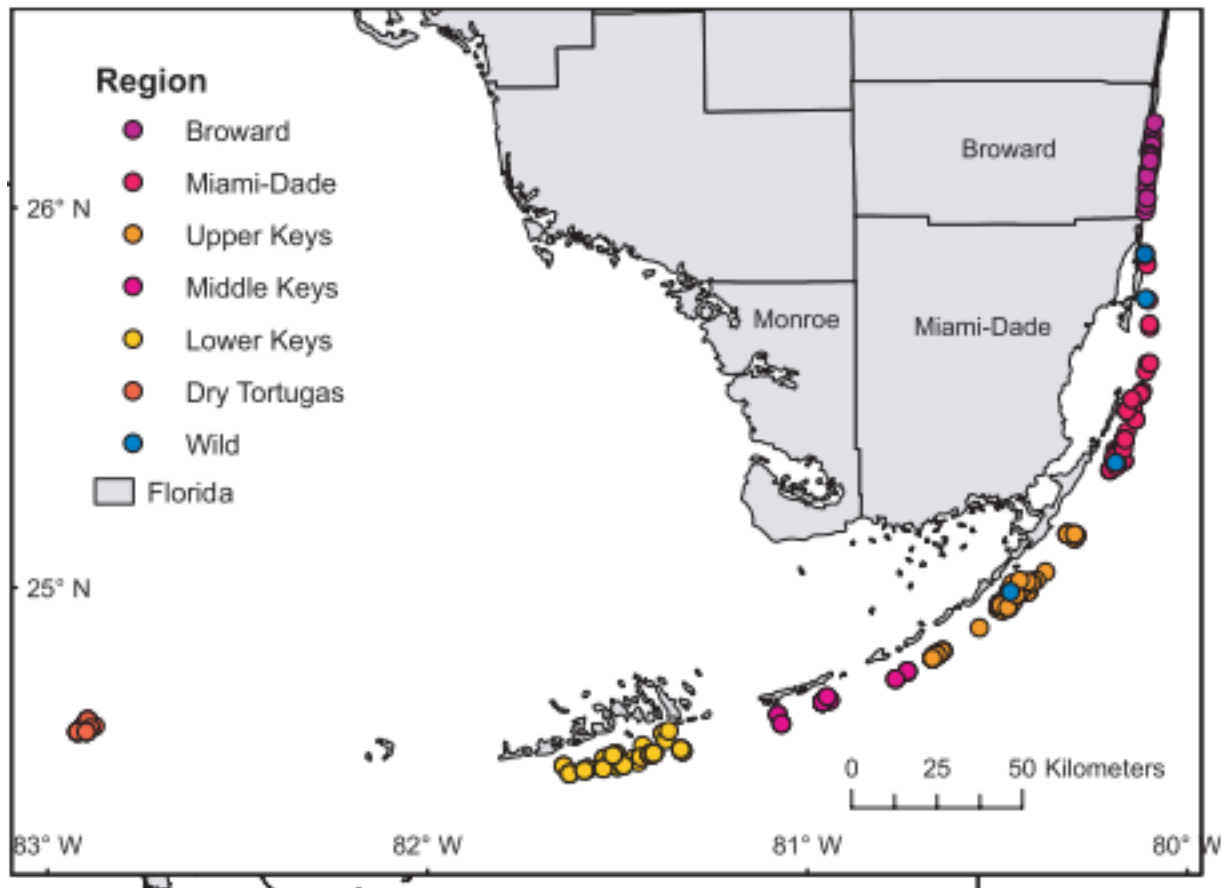
Figure 2. Map of collection locations from the Drury et al. 2017 paper. Map shows locations of Florida collections, color coded by regional population. "Wild" collections within Florida (n = 4) and the Dominican Republic (n = 2) are locations where multiple samples were collected from individual reefs, represented by blue dots. (Taken from Drury et al., 2017).

INTELLECTUAL MERIT

The proposed study will provide much needed data on the extent of genetic structure among and between *A. cervicornis* populations, the effect of habitat heterogeneity on population structure, and the key biological functions that differentiate populations in the Florida Reef Tract. Information on genetic diversity between and among *A. cervicornis* populations is needed to infer resilience and resistance to natural and anthropogenic stressors. This information can be utilized by restoration practitioners to better inform management decisions.

BROADER IMPACTS

Raw sequencing data for the proposed research will be submitted to the National Center for Biotechnology Information as a Sequence Read Archive (SRA). Additionally, the results of this study will be published in an open-access journal and step-by-step instructions for genomic analyses will be made publicly available within a GitHub repository. The findings of this study will be presented to restoration practitioners, managers, and other scientists during the Coral Restoration Consortium. In addition to providing open access of all protocols and results of this study the principle investigator will also recruit undergraduates and local high-schoolers in under-represented groups to intern with the lab. These students will be mentored by the PI and will be able to obtain hands-on experience in fieldwork, and data collection analysis. Undergraduate students will also have the opportunity to conduct related independent research

and present their findings at the university's poster presentation as part of a university fellowship program.

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