



Acropora palmata, conocido como coral *cuerno de alce*, es una de las principales especies constructoras de arrecifes en el mar Caribe.

 Acropora presenta dos tipos de reproducción:
Asexual por fragmentación: se generan nuevas colonias con la misma información genética (clones).



Sexual: Acropora es una especie hermafrodita, es decir, que produce ambos gametos, óvulos y espermatozoides.

Cada año en verano ocurre el desove, en el cual los gametos son liberados al mar. Para lograr la fecundación se requiere de al menos dos colonias con información genética diferente (genotipos diferentes) y generar nuevos individuos con una identidad genética única.



La reproducción sexual aumenta la diversidad genética de la especie.

INAPESCA

Por esta razón en la restauración de arrecifes es importante conocer los genotipo de las colonias para el trasplante y conocer la diversidad genética de la población de corales.







Population genomics of natural and restored populations of the Elkhorn coral in northern Quintana Roo, Mexico

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Introduction

Acropora palmata is listed as critically endangered by the IUCN Red List of Threatened Species, and subject to special protection in Mexico. As a response to this decline, restoration programs have been developed. However, genomics

Results and Discussion

Results from ~ 7000 Single Nucleotide Polymorphisms (SNPs) indicate high gene flow among populations ($F_{ST} = 0.009 - 0.085$), suggesting the presence of a single panmictic population, even when we include restored populations (Fig. 3 and 4). Our results differ from previous studies that suggest that gene flow is restricted and structured populations (Devlin-Durante y Baums 2017; Baums et al., 2010; Hemond & Vollmer, 2010 and others).

studies have not been fully integrated into restoration initiatives fully. Therefore, we studied genome-wide variation of *A. palmata* in six natural populations and one population that has been restored (Cuevones Reef) through clonal propagation and sexual recruitment (Fig. 1).

Methods

107 individuals in northern Quintana Roo, Mexico were collected, over 100 km. Two to thirty fragments of different colonies were randomly collected from each sampling site (Fig. 2). The genomic DNA from coral fragments was extracted, WGS libraries were constructed and sequences on the Illumina HiSeq 1000 platform, using a low-coverage Whole Genome Sequencing (lc-WGS) approach. Genetic diversity and structure were assessed through fixation index (F_{ST}), Principal Component Analysis (PCA) and Discriminant Analysis of PC (DAPC) in R software.





Figure 1. A donor colony and

fragments transplanted in

Cuevones Reef.



AK BN CA CU FA IX LI

Figure 3. Principal Component Analysis based on SNP markers, indicate a panmictic population at northern Quintana Roo. Sites: Akumal (AK), Bajito Nizuc (NA), Cadenita (CA), Cuevones (CU), Farito (FA), Ixlache (IX), Limones (LI).

Figure 4. Compositebarplot ofDAPCprobabilityofeachindividualbelongingtoeach

population.



Figure 2. Study area in the Mexican Caribbean north of Quintana Roo, which is a part of Mesoamerican Reef.

Bioinformatic workflows



Population genetic analysis



Our results provide evidence that the strategy of including asexual and sexual reproduction for reef restoration at Cuevones, increases genetic diversity values (H = 3.46) and is comparable to that of natural populations (H = 1.79-3.29). The maximum value of expected heterozygosity was found at Ixlache (He = 0.17), followed by the restored reef Cuevones (He = 0.16), and the lowest value was found at Bajito Nizuc (He = 0.12) (Fig. 2).

Conclusion

These results demonstrate that restoration efforts in Quintana Roo, Mexico, adequately capture natural genetic diversity by including generation of sexual recruits and clonal propagation, that maintain healthy levels of genetic variation in restored reefs. In addition, the presence of gene flow among reefs in the area is crucial to restoring and conservation of *Acropora* species in the Caribbean.



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