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Genome Report

Whole genome assembly and annotation of the endangered Caribbean coral *Acropora cervicornis*

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Coral species in the genus *Acropora* are key ecological components of coral reefs worldwide and represent the most diverse genus of scleractinian corals. While key species of Indo-Pacific *Acropora* have annotated genomes, no annotated genome has been published for either of the two species of Caribbean *Acropora*. Here we present the first fully annotated genome of the endangered Caribbean staghorn coral, *Acropora cervicornis*. We assembled and annotated this genome using high-fidelity nanopore long-read sequencing with gene annotations validated with mRNA sequencing. The assembled genome size is 318 Mb, with 28,059 validated genes. Comparative genomic analyses with other *Acropora* revealed unique features in *A. cervicornis*, including contractions in immune pathways and expansions in signaling pathways. Phylogenetic analysis confirms previous findings showing that *A. cervicornis* diverged from Indo-Pacific relatives around 41 million years ago, with the closure of the western Tethys Sea, prior to the primary radiation of Indo-Pacific *Acropora*. This new *A. cervicornis* genome enriches our understanding of the speciose *Acropora* and addresses evolutionary inquiries concerning speciation and hybridization in this diverse clade.

Keywords: *Acropora cervicornis*; acroporidae; scleractinia; de novo assembly; comparative genomics; time-calibrated phylogeny

Introduction

The *Acropora* are one of the most speciose and important genera of reef-building scleractinian corals globally (Wallace 1999). The genus *Acropora* are divided into multiple speciose Indo-Pacific clades and a single depauperate Caribbean clade (Wallace 1999). The two sister species of Caribbean *Acropora*—the Staghorn coral *A. cervicornis* and Elkhorn coral *A. palmata*—and their hybrid—called *A. prolifera* (Vollmer and Palumbi 2002) are thought to have diverged from the Indo-Pacific *Acropora* during the late Eocene after the closure of the western Tethys Sea prior to the rapid diversification in the Indo-Pacific *Acropora* (Wallace 1999; Wallace and Portell 2022). To date, all 16 published de novo assembled and annotated *Acropora* genomes are of Indo-Pacific species (Shinzato et al. 2011, Ying et al. 2019; Fuller et al. 2020; Shinzato et al. 2021; López-Nandam et al. 2023).

Acropora, like all corals, are severely threatened by anthropogenic climate change leading to elevated water temperatures that can cause acute bleaching and subsequently death (Hughes et al. 2018). The Caribbean *Acropora* are also experiencing a secondary range-wide pressure in the form of White Band Disease, which has resulted in ~95% population losses of both species Caribbean wide and is the direct cause of their listing on the Endangered Species List (Aronson and Precht 2001; National Marine Fisheries Service 2006). Because these two species are such important foundational species in the Caribbean reef ecosystem, these losses have likely had tremendous unknown effects on higher order taxa which depend on *Acropora* dominant reefs for survival.

Here we present the first fully annotated genome for the endangered Caribbean staghorn coral *Acropora cervicornis*, importantly representing the first Caribbean species of this diverse clade. This genome was assembled using a combination of long-read nanopore and short-read shotgun sequences and annotated and validated using mRNA sequencing. This reference genome will accelerate genomic research on this endangered coral and address fundamental evolutionary questions about speciation and hybridization in the speciose Acroporids.

Materials and methods

Sample collection and sequencing

High molecular weight genomic DNA was extracted in June 2021 from adult tissue of the K2 genotype maintained in the Coral Restoration Foundation (CRF) Key Largo, Florida nursery. Three libraries were prepared using Oxford Nanopore Technologies (ONT) kit SQK-LSK112. Two libraries were not size selected while the third included 20+kb PippenPrep size-selection. All ONT prepared libraries were sequenced separately on three Minion flow cells (FLO-MIN112). High-quality base-calling was performed using Guppy v6.1.7 (ONT).

Four additional Illumina PCR-free shotgun libraries were constructed using the Discovar protocol to produce libraries with fragments between 400 and 600 bp (Love et al. 2016). KAPA PCR-free library kits were leveraged with the addition of a second round of 0.7× Agencourt AmPure XP SPRI bead cleanup post-adapter ligation. Libraries were multiplexed and sequenced on a single rapid-run HiSeq 2500 flowcell with 250 bp paired-end sequencing. Additionally, a library of paired 150 bp reads was prepared using the Illumina DNA Prep kit and sequenced as part of a NovaSeq S4 run.

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