

MITOGENOME ANNOUNCEMENT

**The complete mitochondrial DNA of endemic Eastern Pacific coral
(*Porites panamensis*)**Miguel A. Del Río-Portilla¹, Carmen E. Vargas-Peralta¹, David A. Paz-García^{2,3}, Fabiola Lafarga De La Cruz¹, Eduardo F. Balart³, and Francisco J. García-de-León²

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Abstract

The mitogenome of the endemic coral *Porites panamensis* (Genbank accession number KJ546638) has a total length of 18,628 bp, and the arrangement consist of 13 protein-coding genes, 2 ribosomal RNA (rRNA) genes and 2 transfer RNA (tRNA) genes. Gene order was equal to other scleractinian coral mitogenomes.

Keywords

Mitochondrial genome, *Porites panamensis*, scleractinian coral

History

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Porites panamensis is one of the most important endemic coral reef builders with wide distribution (from 31 °N in Mexico to Isla Gorgona (3 °N), Colombia) in the Eastern Pacific (Glynn & Ault, 2000; Saavedra-Sotelo et al., 2013). This coral grows under extreme environmental conditions for coral development (low pH waters, high levels of temperature and nutrient stress) and may serve as a natural model of coral reef development in an environment modified by projected climate change (Halfar et al., 2005; Manzello et al., 2008). Despite of its physiological resistance, this species is vulnerable to local impact due to its genetic structuration and limited capacity of dispersion (Paz-García et al., 2012; Saavedra-Sotelo et al., 2013). For example, this species disappeared almost completely from coral communities of Central America after massive mortalities cause by ENSO 1982–1983 event (Guzmán et al., 1987).

Here, we sequenced the completed mitochondrial genome of *Porites panamensis* (Genbank accession number KJ546638) from Bahía de Los Angeles (28 °N), Mexico. One small fragment (~3 cm²) from the center of the colony was collected on July 2011 (sampling permit DGOPA.05356.140710.3457) and preserved in salt-saturated DMSO buffer (Seutin et al., 1991).

The DNA libraries were constructed by shearing the DNA on a Bioruptor Illumina TruSeq (Illumina, San Diego, CA) compatible adapters with custom indexes added using Kapa BioSciences library (Kapa Biosystems, Woburn, MA) preparation kits, checked for quality, normalized, pooled and run an Illumina

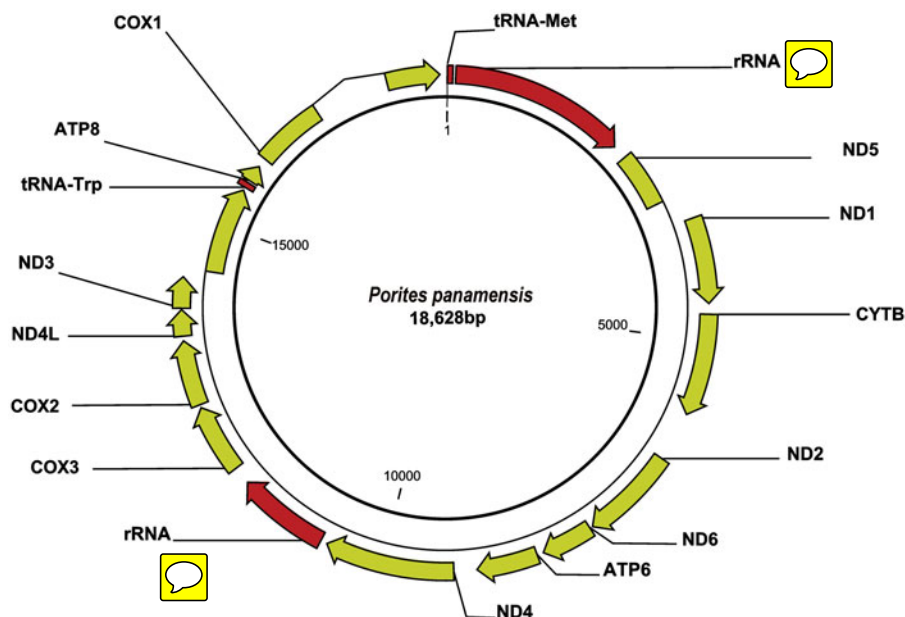
MiSeq (paired-end 250 reads, Illumina, San Diego, CA) at the Georgia Genomics Facility (University of Georgia). Reads were assembled using CLC-Genomics Workbench 6.5 in two ways: (a) with no reference and (b) mapping to the complete mt genome of Caribbean coral *Porites porites* as reference (GeneBank accession number NC_008166.1), but no nucleotide difference was found between both assembling options. Gene annotation was carried out using DOGMA (Wyman et al., 2004) and MITOS (Bernt et al., 2013) software. However, these programs annotated several tRNA, which were then checked with tRNAscan-SE (Lowe & Eddy, 1997) and RFam (Griffiths-Jones et al., 2003) programs.

Porites panamensis mitogenome has a total length of 18,628 bp (50.1 average coverage), the base composition of the genomes was as follow: A (26.0%), T (37.7%), C (13.3%) and G (23.0), which demonstrated an A+T (63.7%) rich feature, similar to other scleractinian coral mitogenomes. Dogma and Mitos produced five and eight possible tRNA, but only two were annotated with tRNAscan-SE and RFam, which is consistent with *Porites okinawensis* (Lin et al., 2011), but not with *P. porites*, which has only one tRNA (Medina et al., 2006). The *P. panamensis* mitochondrial genome arrangement consists of 13 protein-coding genes, 2 ribosomal RNA (rRNA) genes and two transfer RNA (tRNA) genes (tRNA-M and tRNA-W). Gene order is the same as in other scleractinian corals (Figure 1). The mitochondrial structure is similar to *Porites* species (Lin et al., 2011; Medina et al., 2006) and other corals such as Indo-Pacific genus *Pocillopora* (Flot & Tillier, 2007) and Atlantic genus *Orbicella* (“*Montastraea*” *annularis* complex) (Fukami & Knowlton, 2005).

This mitochondrial genome will provide useful information to posterior phylogenetic and population analyses in the genus *Porites*.

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Figure 1. Mitogenome gene order of the endemic coral *Porites panamensis*.



Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. Support was provided by CICESE and CIBNOR through the Subsistema Nacional de Recursos Genéticos Acuáticos, SUBNARGENA, of the Secretaría de Ganadería, Agricultura, Desarrollo Rural, Pesca y Alimentación, SAGARPA. Funding was provided project by CONACYT (grant 157993) to EFB. DAPG is recipient of student fellowships from CONACYT (160065).

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