The complete mitochondrial genome of the lobe coral *Porites lobata* (Anthozoa: Scleractinia) sequenced using ezRAD

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**ABSTRACT**

The complete mitochondrial genome of the coral *Porites lobata* was sequenced using ezRAD. The assembled genome consists of 18,647 bp, including 13 protein-coding genes, two ribosomal RNA genes and two transfer RNA genes. The gene arrangement was consistent with other scleractinian coral mitochondrial genomes. The sequence was strikingly similar to *Porites okinawensis*, indicating the necessity for further systematic work to resolve phylogenetic relationships in the genus *Porites*.

*Porites lobata* (Dana 1846) is one of the most well-known, ecologically important reef building coral species in the world (Veron 2013); its geographic distribution extends from the Red Sea to the Eastern Pacific (Veron 2000), and colonies can live up to 1000 years (Brown et al. 2009), contributing substantially to the formation and maintenance of coral reefs (Baums et al. 2012). In Hawaii, *P. lobata* represents one of the most dominant coral species (Franklin et al. 2013). Although well studied, the taxonomy of *Porites* is highly contentious owing to phenotypic variation, plasticity and cryptic species as revealed by genetic and morphometric studies (e.g. Forsman et al. 2009; Prada et al. 2014; Forsman et al. 2015).

The mitochondrial genomes of animals share great similarity (e.g. Boore 1999), and highly conserved regions, such as the cytochrome c oxidase subunit I gene (COI), have been useful for a wide range of conservation, ecological, evolutionary and systematic studies (e.g. Hebert et al. 2003). The mitochondrial genome of scleractinian corals, however, is known to evolve extremely slowly (Shearer et al. 2002), and in many genera, including *Porites*, short mitochondrial markers such as COI have not been useful for closely related species. Therefore, sequencing the complete mitochondrial genome of *P. lobata* will enhance our understanding of the evolutionary relationships within the genus *Porites*.

Here we present the complete mitochondrial genome of *P. lobata* (GenBank access no. KU572435), assembled using next-generation sequencing. Small fragments of *P. lobata* samples were collected from Oahu, Hawaii (China Walls, Maunalua Bay: 21.261°N, 157.7115°W, Site N, Maunalua Bay: 21.2765–21.2782°N, 157.7112–157.7116°W, Kewalo Basin: 21.9606°N, 157.8611°W and Lanikai: 21.3931°N 157.7149 W). DNA libraries were constructed using the Illumina TruSeq Nano DNA kit, following the ezRAD Protocol modified from Toonen et al. (2013). Individually barcoded samples were pooled, quality-checked and sequenced on an Illumina MiSeq Analyzer at the Evolutionary Genetics Core Facility (Hawaii Institute of Marine Biology [HIMB], Kaneohe, HI). Quality-filtered reads were assembled to the mitochondrial genome of *Porites okinawensis* (GenBank access no. NC015644) using Geneious v.6.0.5 (Biomatters Ltd. Auckland, New Zealand), as well as BWA v.0.7.12 (Li & Durbin 2009) to ensure the assembly quality and base calls. A consensus sequence was called using 0% majority option for coverage greater than 3 × (average 126 ×). Consensus sequences for 11 individuals were also called separately, which assembled 82.5–99.1% of the genome. Gene annotation was done using DOGMA (Wyman et al. 2004) and MITOS (Bernt et al. 2013), with additional verification of transfer RNA (tRNA) by trNAscan-SE (Schattner et al. 2005) and RFam ( Nawrocki et al. 2015).

The length of *P. lobata* mitochondrial genome was 18,647 bp, the same length as that of *P. okinawensis*, with the base composition of A (22.2%), T (41.1%), C (12.9%) and G (23.7%), consistent with other scleractinian mitochondrial
genomes that are A + T rich (Del Río-Portilla et al. 2016). The genome includes 13 protein-coding genes, two ribosomal RNA genes and two tRNA genes (tRNA-M and tRNA-W). The gene arrangement follows the same order as those of other Porites and scleractinian coral species (Lin et al. 2011; Del Río-Portilla et al. 2016). The pairwise sequence identity of P. lobata mitochondrial genome to P. okinawensis was 99.9%, well within the sequence variability of the mitochondrial genome observed among the 11 P. lobata individuals; approximately 99.8% (only 35 out of 18,647 of the sites were polymorphic). This highlights the need for further systematic work to determine species boundaries and geographic distributions of this recalcitrant group (Forsman et al. 2009).

The phylogenetic tree (Figure 1) was constructed by the Bayesian and the maximum-likelihood methods using complete mitochondrial genomes of 15 scleractinian species. The tree supports clear phylogenetic relationships at the genus level. This mitochondrial genome (P. lobata) represents the fifth mitochondrial genome to be published for Porites, and provides additional insight into evolutionary relationships within the genus.

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**Disclosure statement**

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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![Figure 1](image-url)
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