



Mitochondrial DNA Part A

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MITOGENOME ANNOUNCEMENT

Description of the mitochondrial genome of the tree coral *Dendrophyllia arbuscula* (Anthozoa, Scleractinia)

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Abstract

Dendrophylliidae is one of the few monophyletic families within the Scleractinia that embraces zooxanthellate and azooxanthellate species represented by both solitary and colonial forms. Among the exclusively azooxanthellate genera, *Dendrophyllia* is reported worldwide from 1 to 1200 m deep. To date, although three complete mitochondrial (mt) genomes from representatives of the family are available, only that from *Turbinaria peltata* has been formally published. Here we describe the complete nucleotide sequence of the mt genome from *Dendrophyllia arbuscula* that is 19069 bp in length and comprises two rDNAs, two tRNAs, and 13 protein-coding genes arranged in the canonical scleractinian mt gene order. No genes overlap, resulting in the presence of 18 intergenic spacers and one of the longest scleractinian mt genome sequenced to date.

Keywords

Dendrophyllia arbuscula, mitochondrial genome, Scleractinia

History

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Introduction

Comprising nearly 1500 recent species (Cairns, 1999), scleractinians are one of the main framework builders in marine ecosystems. Morphologically, the order is separated into 31 families of which, molecularly, are divided into three main clades – ‘‘Basal’’, ‘‘Complex’’, and ‘‘Robust’’ (Kitahara et al., 2010; Romano & Palumbi, 1996; Stolarski et al., 2011). Within the ‘‘Complex’’ clade, the Dendrophylliidae comprises 20 genera and 166 species (Cairns, 1999, 2001, 2007) embracing zooxanthellate, azooxanthellate, and facultative representatives reported to shallow and deep waters. Although capturing the full spectrum of polyp integration, ranging from exclusively solitary to colonial representatives, complete mitochondrial (mt) sequence has been formally published for only one representative of the family, the zooxanthellate *Turbinaria peltata* (Shi et al., 2014). Using scleractinian mt universal primers (Lin et al., 2011) in addition to the development of five specific primers, here we present the complete mt sequence of *D. arbuscula* van der Horst, 1922. Colony was sampled from Seto (33°41'25"N/135°20'16"E), Japan. Sequences were edited using Sequencher v. 5.1 (Sinauer Associates, Inc., Sunderland, MA) (Gene Codes) and verified under Blast search. The position of the protein-coding, rDNAs, and tRNAs genes were determined through comparison with the available homologous sequences in GenBank, and also using the Dual Organelle Genome Annotator (Wyman et al., 2004).

The entire mt genome from *D. arbuscula* is 19069 bp in length (GenBank KR824937), and consists of two rRNAs

(rnl and rns), two tRNAs (trnM and trnW), and 13 protein-coding genes (*ND1-6*, *ND4L*, *ATP6*, *ATP8*, *COB*, and *COI-3*) all arranged in the canonical scleractinian mt gene order (see Chen et al., 2008; Kitahara et al., 2014; Lin et al., 2014) and encoded on the same strand. No genes overlap, resulting in 18 intergenic spacers totaling 2611 bp. All protein-coding genes but *ND5*, *ND6*, *ND4L*, and *ND3* use methionine (ATG) as the translation initiation codon. *ND6* uses isoleucine (ATA) and *ND5*, *ND4L*, and *ND3* use valine (GTG). TAA or TAG was verified as complete stop codons for each protein-coding gene. The sense strand of the mt genome of *D. arbuscula* is composed of 25.4% A, 13.6% C, 23.7% G, and 37.3% T. At 62.7% the (A + T)-content is within the ‘‘average’’ observed for ‘‘Complex’’ scleractinians, but ranges from 43.7% for trnM to 69.7% for *ND4L*. The genes *ND5* and *COI* are interrupted by group-I introns, of which that of *ND5* is 11299 bp long and engulf 11 genes, and that of *COI* extends for 964 bp and contains a LAGLI-DADG motif that potentially codes for a homing endonuclease.

Nucleotide sequences of all protein-coding genes from 39 scleractinians representing the ‘‘Basal’’ (1), ‘‘Complex’’ (25), and ‘‘Robust’’ (13) clades, in addition to sequences from 12 Corallimorpharia, two Actiniaria, one Antipatharia, and two Octocorallia were used to reconstruct the Anthozoa evolutionary history (Figure 1). Final alignment total is 11339 bp of which 7545 are phylogenetically informative. Topology resulting from maximum likelihood analysis using PhyML (Sinauer Associates, Inc., Sunderland, MA) (Guindon et al., 2010) under the GTR + I + G nucleotide evolutionary model, follows the three main scleractinian clades, and places the dendrophylliids as sister group to poritids, in the ‘‘Complex’’ clade.

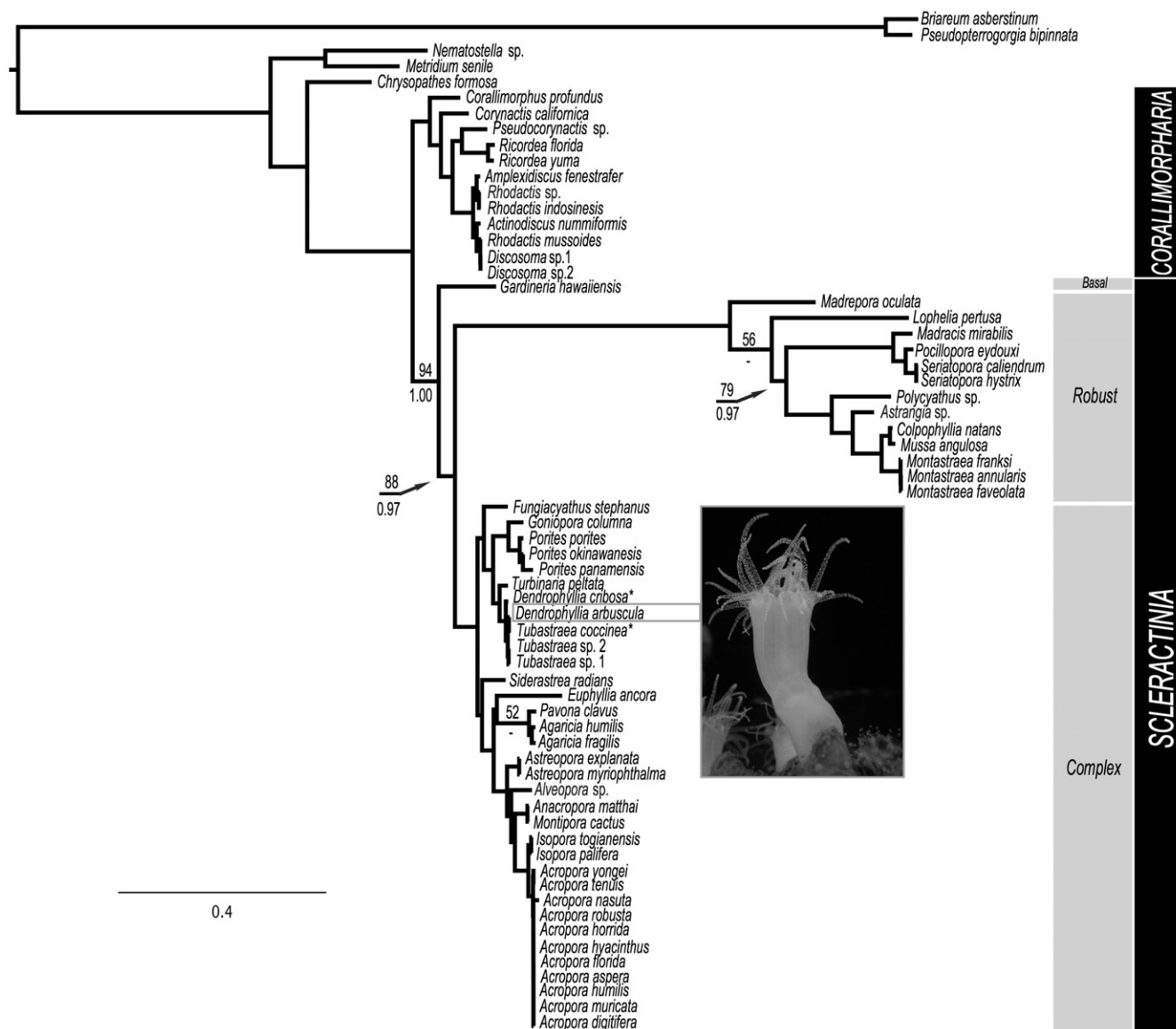


Figure 1. ML phylogeny of scleractinian corals based on all mitochondrial protein-coding genes. ML bootstrap (upper) and Sh-Like (lower) node support values are shown at each; nodes without support numbers indicate bootstrap and Sh-Like support over ≥ 98 . An asterisk following species name indicate that its sequence has not been formally published yet.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. The authors would like to thank the São Paulo Research Foundation for funding the present study (# 2012/21583-1 to Alvaro E. Migotto; # 2012/01771-8 to SNS).

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