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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 19,069 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.

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 divides 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 forms, 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 Sequencer 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 19,069 bp in length (GenBank KR824937), and consists of two rDNAs (ml and mns), two tRNAs (trnM and trnW), and 13 protein-coding genes (ND1-6, ND4L, ATP6, ATP8, COB, and CO1-3) 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 CO1 are interrupted by group-I introns, of which that of ND5 is 11,299 bp long and engulf 11 genes, and that of CO1 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 11,339 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.

Keywords

Dendrophyllia arbuscula, mitochondrial genome, Scleractinia

History

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Declaration of interest
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References


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.