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MITOGENOME ANNOUNCEMENT



Complete mitochondrial genome of *Callogorgia* cf. *gracilis* (Octocorallia: Calcaxonia: Primnoidae)

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ABSTRACT

We report the first complete mitochondrial genome of *Callogorgia*. *Callogorgia* cf. *gracilis* isolate DFH32_518B was collected by a remotely operated vehicle at 98 m on McGrail Bank (27.9840725°N, 92.604242°W). The complete mitogenome is 18,937 bp (27.8% A, 18.3% C, 19.8% G, and 34.1% T) and has the ancestral octocoral gene order for its 14 protein-coding genes, two rRNA genes, and one tRNA gene. It is sister to and ~96.6% similar (uncorrected) to *Narella hawaiiensis*, the only other complete mitogenome reported for Primnoidae. The *cox1* + *igr1* + *mtMutS* region differs by two base pairs (0.12%) from the only reported *C. gracilis* haplotype.

ARTICLE HISTORY

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KEYWORDS

Mesophotic coral ecosystem; Cnidaria; Gulf of Mexico

Callogorgia consists of 27 valid species (Cairns et al. 2018), four of which occur in the northwestern Gulf of Mexico (Cairns and Bayer 2002; Etnoyer and Cairns 2017): *C. americana*, *C. delta*, *C. gracilis*, and *C. linguimaris*. *C. gracilis* is the only one reported shallower than 180 m (Quattrini et al. 2013; Etnoyer and Cairns 2017) and is distinguishable by its stiff, straight main stem, cylindrical (vs. clavate) polyps, number of sclerites, and unique mitochondrial molecular barcode (*cox1*+*igr1*+*mtMutS*) (Cairns and Bayer 2002; Quattrini et al. 2013). The collected specimen is morphologically consistent with *C. gracilis* but differs by two base pairs (0.12%) from the single *cox1*+*igr1*+*mtMutS* haplotype reported in Quattrini et al. (2013) for *C. gracilis* (DOI: 10.6084/m9.figshare.6998459). Because additional specimens are required to delineate species within the *C. gracilis* complex (see Cairns and Bayer 2002), we assigned this specimen to *C. cf. gracilis*.



The specimen was collected by remotely operated vehicle (SubAtlantic Mohawk 18 operated by University of North Carolina – Wilmington, Undersea Vehicles Program) at 98 m on McGrail Bank (27.9840725°N, 92.604242°W) on 24 September 2017. DNA was extracted with GeneJET Genomic DNA Purification Kit (ThermoFisher Scientific Waltham, MA) per manufacture's protocol and submitted to Biopolymers Facility at Harvard Medical School for library preparation and next-generation sequencing (NextSeq 500). Trimmed reads (Trimmomatic-0.32, Bolger et al. 2014) were assembled *de novo* with SPAdes (Bankevich et al. 2012) on the University of New Hampshire Bioinformatics Core facility on server. After circularizing and editing overlapping ends of the SPAdes contig in Geneious R10.2.6 (Kearse et al. 2012), trimmed reads (BBduk v. 37.25) were mapped to the resulting reference sequence to generate a consensus sequence. Genes were

annotated by manually adjusting *Narella hawaiiensis* (NC026192) annotations mapped to the consensus sequence. The complete mitogenome was aligned with default MUSCLE (Edgar 2004) parameters to eight representative species with the octocoral ancestral mitochondrial gene order and complete mitogenomes available in GenBank: all Calcaxonia species, one randomly selected representative from each Alcyonacea subclass, and all Helioporacea and Pennatulacea species. The latter two taxa generally are sister to the clade containing Primnoidae (Brockman and McFadden 2012; Polisenio et al. 2017). A maximum-likelihood, phylogenetic tree was constructed in RAxML 8.2.11 (Stamatakis 2014) (Figure 1). Extended methods and *cox1*+*igr1*+*mtMutS* alignment are available at figshare (DOI: 10.6084/m9.figshare.6998459).

The complete mitogenome is 18,937 bp (27.8% A, 18.3% C, 19.8% G, and 34.1% T), has the ancestral octocoral gene order, and has one tRNA, two rRNA, and 14 protein-coding genes. Despite the utility of gene-sequence data in resolving coral phylogenies (e.g. Soler-Hurtado et al. 2017), this mitogenome report is the first for *Callogorgia* and second for Primnoidae. *C. cf. gracilis* is sister to and ~96.6% similar (uncorrected) to the only other Primnoidae, *N. hawaiiensis*, but the relative position of Primnoidae among octocoral families is not well supported (Figure 1). The *C. cf. gracilis* mitogenome was deposited in GenBank (MH719202) and the specimen in the Smithsonian National Museum of Natural History (USNM1507967).

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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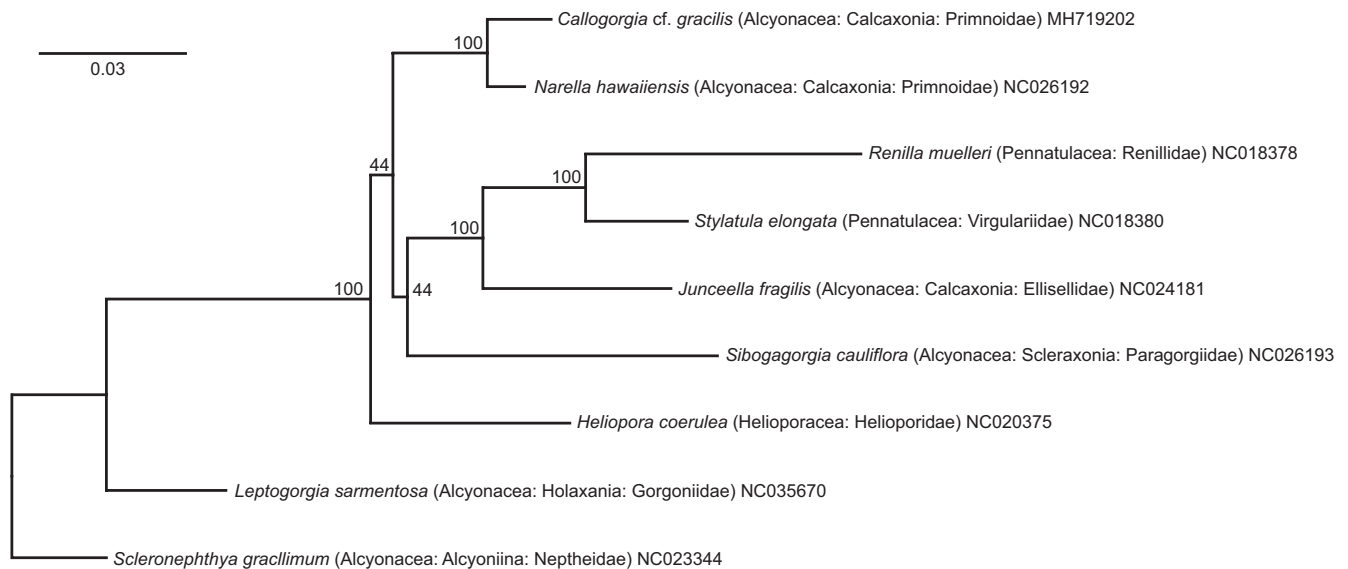


Figure 1. Maximum-likelihood, phylogenetic tree of the complete mitogenomes of *Callogorgia cf. gracilis* (this study) and eight representative octocorals (taxonomic position and GenBank accession numbers in tip labels). In Geneious R10.2.6, complete mitogenomes were aligned with default MUSCLE parameters; the resulting alignment was used to construct the phylogenetic tree in RAXML 8.2.11 with the following changes to the default settings: bootstrap replicates = 1000, algorithm = rapid bootstrapping and search for best-scoring ML tree, outgroup = NC023344, nucleotide model = GTR CAT I. Bootstrap values are reported at the nodes. See figshare (DOI: 10.6084/m9.figshare.6998459) for extended methods.

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