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MITOGENOME ANNOUNCEMENT

 OPEN ACCESS

Complete mitochondrial genome of the geniculate calcified red alga, *Corallina officinalis* (Corallinales, Rhodophyta)

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ABSTRACT

We present the first mitochondrial genome of the calcified, geniculate coralline red alga *Corallina officinalis* (Corallinales). The circular genome consists of 26,504 bp and has a gene content consisting of 23 protein-coding genes, 26 transfer RNA genes and two ribosomal RNA genes, with an overall GC content of 30.1%.

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Calcified macroalgae;
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Corallina officinalis Linnaeus (Corallinales, Rhodophyta) is a geniculate (articulated) coralline macroalga ubiquitous in the intertidal zone of temperate coastal regions across the NE Atlantic (Brodie et al. 2013; Williamson et al. 2015). Turfing assemblages of *C. officinalis* provide habitat for numerous small invertebrates, shelter via their physical structure from environmental stresses associated with intertidal habitats and a substratum for the settlement of macro- and microalgae (Nelson 2009). Given these attributes, *C. officinalis* is considered an important autogenic ecosystem engineer (Nelson 2009). Despite this, very limited genomic data are available for this species or coralline algae in general (Kim et al. 2013). To date, a partial genome has been reported for the geniculate coralline *Calliarthron tuberculosum* (Chan et al. 2011), and the complete mitochondrial genome of the non-geniculate, rhodolith-forming *Sporolithon durum* (Sporolithales) is available (Kim et al. 2013). Further sequencing of calcified macroalgal genomes is therefore a priority in order to advance this field of research.

Total genomic DNA was extracted from 0.5 cm² of a discrete *C. officinalis* frond (accession no. BM001215284, The Natural History Museum, London) collected from Heybrook Bay, southwest Britain (50°31'68"N, 4°11'92"W) using a modified CTAB extraction (Williamson et al. 2015). Following quantification of double-stranded DNA with a Qubit fluorometer 2.0 (Invitrogen, Waltham, MA), an indexed library was constructed using a TruSeq Nano DNA sample preparation kit (Illumina Inc., San Diego, CA) and sequenced on an Illumina MiSeq flowcell; version 3 chemistry, 2 × 300 paired end. Reads were trimmed using default settings in Geneious v.8.1.7 (<http://www.geneious.com>, Kearsse et al. 2012) and subsequently assembled to the previously reported *C. officinalis* epitype *cox1* sequence (Brodie et al. 2013), GenBank accession no. FM180073. Unassembled reads were iteratively mapped and reassembled

to the putative *cox1* sequence until the resulting contig could be circularized. Gene boundaries were annotated using MITOS (Bernt et al. 2013) and verified by visualization of open reading frames and comparison with alignments of Florideophycean mitochondrial genes. Amino acid sequences for each of 24 protein-coding genes (Yang et al. 2015) were aligned with 10 reference mt genomes (Figure 1) using Geneious. Aligned sequences were concatenated, verified by eye and subjected to phylogenetic analysis using Mr Bayes (Ronquist & Huelsenbeck 2003) using the JONES + G amino acid substitution model after Yang et al. (2015).

We determined the mitochondrial genome of *C. officinalis* to be 26,504 bp in length. The sequence is deposited in GenBank under accession no. KU641510. The mitochondrial genome codes for 51 genes: 23 protein-coding genes, 26 tRNA genes and the large and small rRNA genes. Gene order follows a similar pattern to those of other Florideophycean red macroalgae. The ATG start codon is used in all protein-coding genes except *nad2* (GTG) and *sdh3* (ATT). The TAA stop codon is used in all protein-coding genes except *cox2*, *nad6* and *rps12* (TAG). The overall GC content is 30.1% with a GC skew of 0.03 and AT skew of 0.06. Nucleotide composition of the entire mt genome is A = 9823 (37.1%), T = 8706 (32.8%), G = 4099 (15.5%) and C = 3876 (14.6%).

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Disclosure statement

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

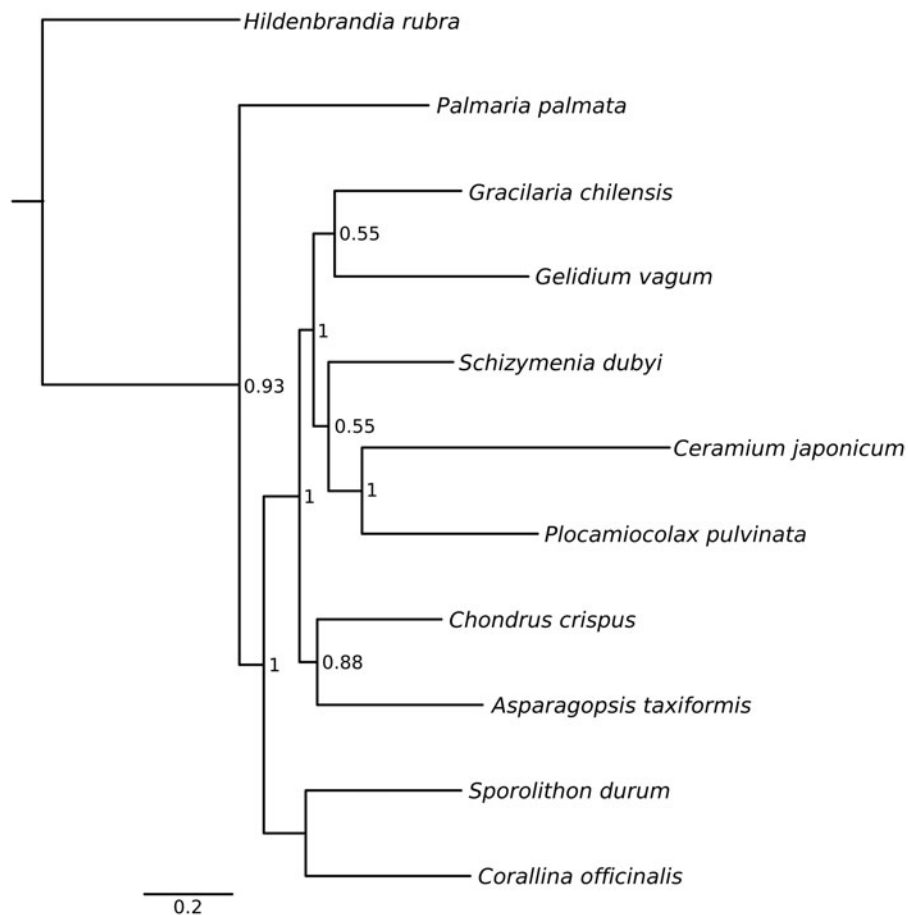


Figure 1. Bayesian inference tree from analysis of concatenated protein-coding genes. Only nodes supported by $pp > 0.50$ are annotated. GenBank accession numbers for each species: *Hildenbrandia rubra* NC026055, *Palmaria palmata* NC026056, *Gracilaria chilensis* NC026831, *Gelidium vagum* NC023077, *Schizymenia dubyi* KJ398163, *Ceramium japonicum* KJ398159, *Plocamioncolax pulvinata* NC014773, *Chondrus crispus* NC001677, *Asparagopsis taxiformis* NC026843, *Sporolithon durum* KF186230 and *Corallina officinalis* KU641510.

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