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The complete mitochondrial and plastid genomes of *Corallina chilensis* (Corallinaceae, Rhodophyta) from Tomales Bay, California, USA

Ivan A. Alejo^a, Teresa E. Aleman^a, Karina Almanza^a, William Alonso^a, Maria Guadalupe Altamirano Manriquez^a, Tyler Armbrister^a, Yoshio Astudillo^a, Lyric Batistiana^a, Jonathan S. Blas Guido^a, Danilo E. Bustamante^b , Martha S. Calderon^{b,c} , Jovany D. Camacho Gonzalez^a, Suiry Cardoso^a, Jose Castro^a, Maria N. Chombo Garcia^a, Lissa P. Colin^a, Karina G. Cortina^a, Andrea Delgado^a, Daniel Espinoza Castro^a, Isabel Estrada^a, Eduardo Felix^a, Stephanie Felix^a, Martin Flores^a, Suzanne Frausto^a, Eli D. Garcia^a, Malia Garcia^a, Gabriela Gasca^a, Daniela Gomez^a, Christian Gonzalez Balcazar^a, Bianca G. Miramontes^a, Victor Gonzalez^a, Clarissa D. Guzman^a, Edgard C. Guzman^a, Timothy B. Hanneman^a, Julissa Hernandez^a, Jeffery R. Hughey^a , Victoria N. Hutchins^a, Eli R. Kallison^a, Sebastian Lepe^a, Serena M. Lopez^a, Feifei Zhai Lorenzo^a, Evelyn Macias Reyes^a, Fernando Madrigal^a, Nayeli G. Madrigal-Gonzalez^a, Rodolfo Mandujano^a, Ricardo Manzo^a, Paloma L. Martinez^a, Sergio Martinez^a, Bianey A. Medina^a, Mario Mendez^a, Jose J. Mendoza Contreras^a, Ana I. Meza^a, Kevin Miller^a, Anna Morales^a, Eduardo Munoz^a, Johnna M. Myers^a, Priya-Anjali Patel^a, Dominic Pina Montes^a, Alejandra N. Ponce^a, Alicia E. Ramirez^a, Elias Rico^a, Aide Rodriguez^a, Jasmine Rodriguez^a, Angel Ruiz^a, Andrea Saldana^a, Rosa A. Sanchez^a, Jessica D. Santana^a, Francisco D. Solano^a, Alejandra Soto Trujillo^a, Sarai J. Soto^a, Alicia Steinhardt^a, Melisa Talavera^a, Monik M. Tapia^a, Odalis Tapia^a, Maria O. Taveras Dina^a, Brenda J. Torresillas^a, Clarissa Vazquez-Ramos^a, Frances L. Wong^a and Hartnell College Genomics Group*

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ABSTRACT

Genomic analysis of the marine alga *Corallina chilensis* from Tomales Bay, California, USA, resulted in the assembly of its complete mitogenome (GenBank accession number MK598844) and plastid genome (GenBank MK598845). The mitogenome is 25,895 bp in length and contains 50 genes. The plastid genome is 178,350 bp and contains 233 genes. The organellar genomes share a high-level of gene synteny to other Corallinales. Comparison of *rbcL* and *cox1* gene sequences of *C. chilensis* from Tomales Bay reveals it is identical to three specimens from British Columbia, Canada and very similar to a specimen of *C. chilensis* from southern California. These genetic data confirm that *C. chilensis* is distributed in Pacific North America.

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Corallina; *Corallina chilensis*; Corallinaceae; mitogenome; plastid genome

Corallina chilensis Decaisne (Harvey 1849) is a calcified, intertidal marine red alga originally collected by Charles Darwin from Valparaíso, Chile. Harvey's species diagnosis described it as being 2.5–5 cm in height with slender stems below and broader and bipinnate stems above (Harvey 1849). The binomial was long regarded as *C. officinalis* var. *chilensis* (Decaisne) Kützinger (1858), but was recently elevated to specific status by Williamson et al. (2016). We performed high-throughput sequencing on a specimen of *C. chilensis* from Tomales Bay, California, to determine its genomic structure and genetic relationship to other species of *Corallina*.

DNA was extracted from *C. chilensis* (Specimen Voucher – UC2050474) following the protocol of Lindstrom et al. (2011). The 150 bp PE Illumina library construction and sequencing was performed using myGenomics, LLC (Alpharetta, Georgia,

USA). The genomes were assembled using default *de novo* settings in Geneious Prime (Biomatters Limited, Auckland, New Zealand) and annotated using Geneious Prime and blastx, NCBI ORFfinder, and tRNAscan-SE 1.21 (Schattner et al. 2005). The *C. chilensis* mitogenome was aligned to other mitogenomes with MAFFT (Katoh and Standley 2013). The phylogenetic analysis was executed using RAXML-NG (Kozlov et al. 2018) with the GTR + gamma model and 100 bootstraps. The tree was visualized with TreeDyn 198.3 at Phylogeny.fr (Dereeper et al. 2008) and pairwise distances were calculated using default parameters in DIVEIN with the GTR model (Deng et al. 2010).

The mitogenome of *C. chilensis* is 25,895 bp in length and contains 50 genes. It is A + T rich (70.5%) and contains 23 tRNA (trnG, trnL, trnM, trnR, trnS are duplicated), 5 ribosomal proteins (rpl16, rpl20, rps3, rps11, rps12), 2 rRNA (rrl, rrs),

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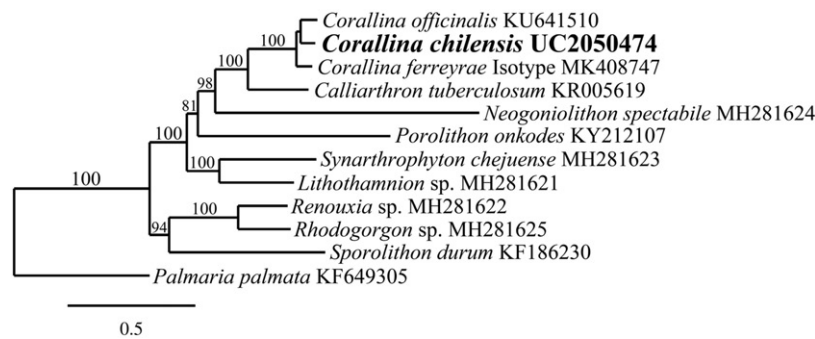


Figure 1. Maximum likelihood phylogram of the mitogenome of *C. chilensis* and related calcified red algae. Numbers along branches are RaxML bootstrap supports based on 100 replicates. The legend below represents the scale for nucleotide substitutions.

orf158, TatC, ymf39, and 17 other genes involved in electron transport and oxidative phosphorylation. The plastid genome of *C. chilensis* is 178,350 bp and contains 233 genes. The genome is also A+T biased (70.0%) and contains 47 ribosomal proteins, 31 tRNA, 30 photosystem I and II, 28 ycf, 10 phycobiliprotein, 8 cytochrome b/f complex, 8 ATP synthase, 4 RNA polymerase, 4 orfs, 3 rRNA, and 60 other genes. The mitogenome and plastid genome of *C. chilensis* are similar in length, content, and organization to other coralline red algae (Janouškovec et al. 2013; Bi et al. 2016; Williamson et al. 2016; Lee et al. 2018; Gabrielson et al. 2018; Bustamante et al. 2019).

Phylogenetic analysis of the *C. chilensis* mitogenome resolved it in a fully supported clade with *C. officinalis* L. and *C. ferreyrae* E.Y. Dawson, Acleto & Foldvik (Figure 1). The mitogenome of *C. chilensis* differed in pairwise distance from *C. officinalis* by 9.8% and *C. ferreyrae* by 10.8%. The plastid genome of *C. chilensis* differed from *C. ferreyrae* by 2.9%. A BLAST analysis of *cox1* and *rbcl* sequences of *C. chilensis* from Tomales Bay identified three identical sequences from British Columbia, Canada (as *C. frondescens*) (Hind and Saunders 2013) and a nearly identical sequence from a specimen of *C. chilensis* from Monarch Bay, Orange County, California (Williamson et al. 2015).

Disclosure statement

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