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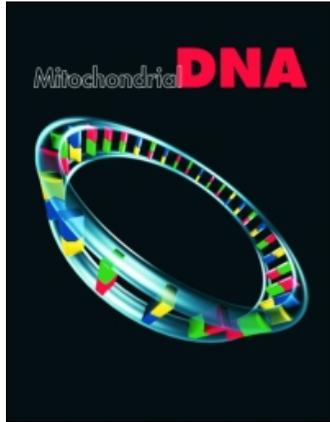
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The complete mitochondrial genome of the rocky reef fish *Cheilodactylus variegatus* Valenciennes, 1833 (Teleostei: Cheilodactylidae)

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MITOGENOME ANNOUNCEMENT

**The complete mitochondrial genome of the rocky reef fish
Cheilodactylus variegatus Valenciennes, 1833 (Teleostei:
Cheilodactylidae)**Claudio Quezada-Romegialli¹, David Véliz², Felipe Docmac¹, and Chris Harrod¹¹*Fish and Isotope Ecology Laboratory, Facultad de Ciencias del Mar y Recursos Biológicos, Instituto de Ciencias Naturales Alexander von Humboldt, Universidad de Antofagasta, Antofagasta, Chile and* ²*Departamento de Ciencias Ecológicas, Instituto de Ecología y Biodiversidad, Núcleo Milenio de Ecología y Manejo Sustentable de Islas Oceánicas, Universidad de Chile, Santiago, Chile***Abstract**

Cheilodactylus variegatus is a common benthivorous marine fish inhabiting in rocky subtidal habitats in the eastern south Pacific coast of Chile and Peru. However, its biology and ecology are relatively understudied and its taxonomic assignment has been debated recently. The complete mitochondrial genome was assembled *de novo* and mapped to a reference using 5.97 million of reads obtained through Ion Torrent next generation sequencing, resulting in a circular sequence of 16,652 bp in length. Gene composition and arrangement comprised to that reported for most fishes and contained the typical structure of 2 rRNAs, 13 protein-coding genes, 22 tRNAs and 1 non-coding region. This mitogenome provides a valuable resource for studies of fish molecular systematics, phylogeography and population genetics.

Keywords

Bilagay, marine fish, NGS

History

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Cheilodactylus variegatus Valenciennes, 1833 (Common name in Spanish: *Bilagay*, *Pintacha*; in English: *Peruvian morwong*) is a marine fish species of the southeast Pacific distributed between 5° S (Paita, Peru) to 40° S (Metri, Chile) (Vargas & Pequeño, 2001). This species inhabits in subtidal macroalgal-dominated coastal rocky reefs (Samamé et al., 1995), where it typically feeds on benthic invertebrates (Angel & Ojeda, 2001). Although common, little quantitative information has been gathered on basic aspects of its biology and ecology (Palma & Ojeda, 2002), and its taxonomic assignment has been discussed using only two mitochondrial genes (Burridge & Smolenski, 2004). In this study we described the complete mitochondrial genome of *C. variegatus* in order to provide an important reference for scientists working on fish molecular systematics, phylogeography and population genetics.

The entire mitochondrial genome of *C. variegatus* was assembled with 5,976,658 sequences (270.1 bp mean length; min 8 bp; max 633 bp) obtained through one run on a Ion Torrent PGM Sequencer (Life Technologies, Carlsbad, CA) using a 318v2 chip (Omics Solutions, Santiago, Chile; <http://www.omics-solutions.cl>). A specimen of *C. variegatus* was collected in Guala Guala, Chile (22°46'24"S; 70°18'39"W) in May 2014, and identified following Chirichingo (1974). Stock tissue (no. ST2014-CVGUA12) and source DNA sample (no. DS2014-CVGUA12) are kept from voucher specimen in our laboratory. Total genomic DNA was extracted from a sample of fish dorsal

muscle using the Wizard Genomic DNA Purification Kit (Promega, Madison, WI). Reads were mapped (mean coverage 50×) against the sequence of *Cheilodactylus zonatus* (Lavoué et al., 2014; GenBank accession no. AP006013) using Geneious v8.0.5 (Biomatters Ltd., Auckland, New Zealand) after trimming low quality bases at 5' and 3' ends. A total of 3358 reads with a 100% coverage were assembled *de novo* producing a circular sequence of 16,656 bp (GenBank accession no. KP704218), similar in length to *C. zonatus* (16,690 bp). Potential indels and ambiguities were checked against the depth and quality of NGS reads.

Annotations were confirmed by comparing MitoFish (Iwasaki et al., 2013) with MITOS-generated annotations (Bernt et al., 2013). The genome structure consisted of 13 protein-coding genes, 12s and 16s rRNA, 22 tRNA genes and a non-coding region. The overall nucleotide composition was A, 27.5%, C, 29.2%, G, 16.9%, and T, 26.3%, and a comparison with *C. zonatus* shows 15,134 identical sites (90.7%), suggesting important mitochondrial divergence within the Cheilodactylidae family.

Finally, a search was conducted in GenBank and the 12 more closely related mitogenomes (min 84%, max 91% of identical bases) were downloaded and aligned with MUSCLE 3.5 (Edgar, 2004). A maximum likelihood phylogenetic search (15,720 concatenated positions, not considering the control region) was conducted with RAxML 7.2.8 (Stamatakis et al., 2008) under a GTR+G model, with 1000 rapid bootstrap replicates. The phylogenetic analysis (Figure 1) resolved a well-supported clade of Cheilodactylidae in which this family appears to be sister group of Siniperca. The newly described mitogenome can be used in the future to disentangle the taxonomy within Cheilodactylidae and the systematic position of *Cheilodactylus variegatus* in an integrative approach.

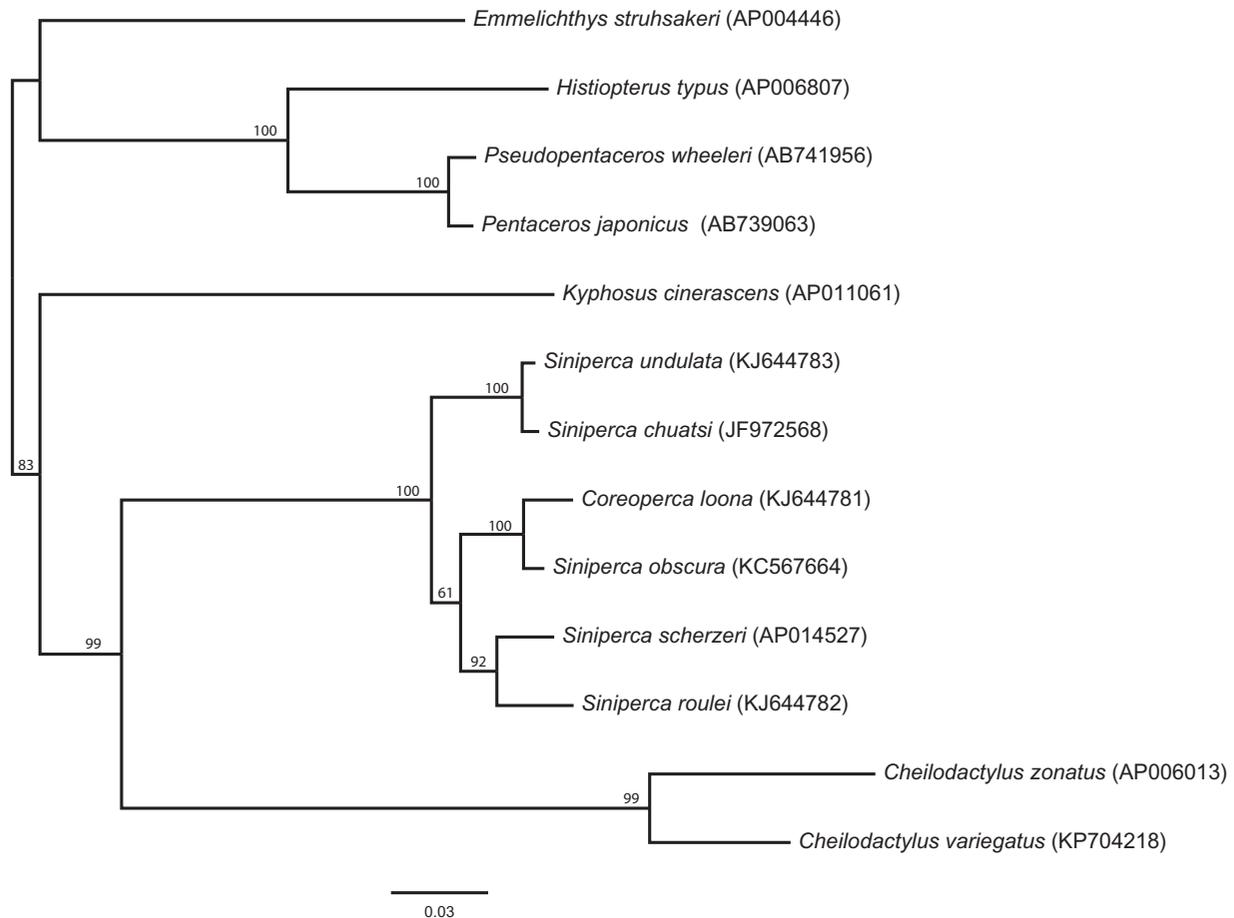


Figure 1. Unrooted tree of a maximum likelihood phylogenetic analysis of *Cheilodactylus variegatus* and closely related mitochondrial sequences. Above each branch is denoted maximum likelihood bootstrap support. Genbank accession numbers of species are shown in parentheses.

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Declaration of interest

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

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