



Mitochondrial DNA Part B Resources

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Complete mitochondrial genome of six *Cheilinus undulatus* (Napoleon Wrasse): an endangered marine fish species from Sabah, Malaysia

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ABSTRACT

We report here the complete mitochondrial (mt) genomes of six individuals of *Cheilinus undulatus* (Napoleon Wrasse), an endangered marine fish species. The six mt DNA sequences had an average size of 17,000 kb and encoded 22 tRNA, two sRNA, 13 highly conserved protein coding genes and a control region. The polymorphic variation (control region) in these six individuals suggests their potential use as a specific marker for phylogeographic conservation. Moreover, the sequence polymorphism within the control region (D-loop) suggests that this locus can be applied for phylogenetic studies.

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Mitochondrial genome;
Cheilinus undulatus;
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This is the first study of mitochondrial (mt) genome for endangered marine fish species *Cheilinus undulatus* from Sabah, Malaysia waters. *Cheilinus undulatus* is listed on the International Union for Conservation of Nature (IUCN) Red List of Threatened Species, and is protected by the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) Appendix 2. In the last few decades, the worldwide population of *C. undulatus* has declined. In Sabah State, targeted and overfishing activities to fulfil the local seafood demand (Scales et al. 2007) and international market (Sadovy et al. 2003) have contributed to this decline. The realization of the imminent loss of this fisheries resource has prompted the Malaysian government to regulate its international trade by listing the species on CITES Appendix 2 in 2014 (Fabinyi et al. 2014). Such listing effectively bans the international export of *C. undulatus*.

Here, as a part our efforts to establish specific fish phyto-geography markers, we sequenced the full length mitochondrial DNA (mtDNA) of *Cheilinus undulatus*, collected from two geographic points: M3ss and M8ss (obtained from Sandakan (5.839°N, 118.117°E), Sabah, Malaysia) and M11kk, M12kk, M15kk, and M17kk (obtained from Kota Kinabalu (5.980°N, 116.073°E), Sabah, Malaysia). The assembly reads generated by MiSeq Illumina pair-end fastq were trimmed, automated error correction and assembled using the SPAdes De Novo Assembler (Bankevich et al. 2012). Mis-assemblies were corrected using Geneious version 11.0.5 (Kearse et al. 2012). The mtDNA genome was annotated using MITOFish online annotation pipeline (Iwasaki et al. 2013). All six mtDNA were aligned using clustalW in MEGA 6 (Tamura et al. 2013)

software with the two references of mtDNA of *C. undulatus* (accession number GU296101.1 and KM17184.1) which was previously published (Qi et al. 2013; Han et al. 2016).

The MiSeq Illumina platform yielded an average 85,000 paired reads for all six individuals. The length of the mtDNA of M3ss (MH675879), M8ss (MH675880), M11kk (MH688049), and M15kk (MH688051) were 17,185 bp whereas, M12kk (MH688050) and M17kk (MH688052) were found to be 17,184 bp. The G + C content was 47.5% and 47.6%, respectively. A total of 38 genes were identified which consisted of two rRNAs (12sRNA and 16sRNA), 22 tRNA, 13 highly conserved respiratory genes, and a control region (D-loop). The gene arrangement was found to be similar with the gene arrangement for animal mt (Lee et al. 1995; Boore 1999). Notably, sequence polymorphisms were observed in all six individuals when aligned with the reference genome (accession number GU296101.1 and KM17184.1) especially in the control region which spans a region of 903 basepairs. This region can be applied to detect polymorphisms within individuals for the subsequent development of molecular markers. The evolutionary phylogenetic tree history of *Cheilinus undulatus* was inferred using the neighbour-joining method (Saitou and Nei 1987) using MEGA6 software (Tamura et al. 2013) (Figure 1).

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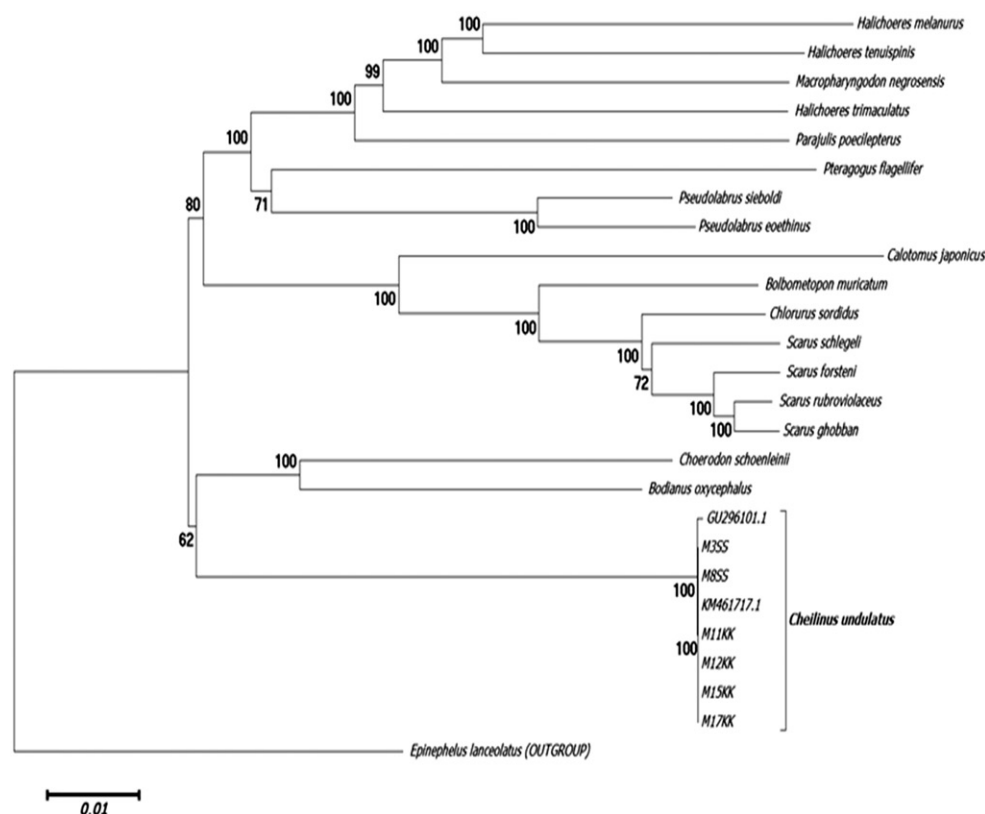


Figure 1. Molecular phylogeny of *Cheilinus undulatus* and 17 other Labridae species based on complete mitochondrial genome using neighbour-joining method (1000 bootstrap). The complete mitochondrial genome is downloaded from NCBI database and the phylogeny tree is constructed by MEGA6 software. The accession number for each gene used in the tree construction is listed as follows: *Halichoeres melanurus* (AP006018.1), *H. tenuispinis* (EU082205.1), *H. trimaculatus* (EU087704.1), *Macropharyngodon negrosensis* (KP013102.1), *Parajulis poecilepterus* (EF192032.2), *Pteragogus flagellifer* (EF409976.2), *Pseudolabrus sieboldi* (AP006019.1), *P. eoethinus* (EU560728.1), *Calotomus japonicus* (AP017568.1), *Bolbometopon muricatum* (KY235362.1), *Chlorurus sordidus* (AP006567.1), *Scarus schlegelii* (FJ595020.1), *S. forsteni* (FJ619271.1), *S. rubroviolaceus* (FJ227899.1), *S. ghobban* (FJ449707.1), *Choerodon schoenleinii* (KM487697.1), *Bodianus oxycephalus* (KT591189.1), *Cheilinus undulatus* (GU296101.1, KM461717.1). *Epinephelus lanceolatus* (FJ472837.1) was used as the outgroup.

Disclosure statement

No potential conflict of interest was reported by the authors.

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