

The complete mitogenome of *Haliotis asinina* (Gastropoda, Haliotidae) from Malaysian waters provides further insights into the phylogeny of the abalone

ABSTRACT

Due to its high economic importance, the aquaculture of abalone has developed significantly as a global industry. However, there is still limited studies of abalone in Malaysia. Therefore, the complete mitochondrial genome of the tropical abalone, *Haliotis asinina* (Linnaeus 1758) sampled in the Malaysian waters is sequenced and analysed for the first time. The mitogenome is 16399 base pairs (bp) in length and contains 13 protein coding genes (PCGs), 2 ribosomal RNA (rRNA) genes and 22 transfer RNA (tRNA) genes. The arrangement and orientation of genes compared with 10 available *Haliotis* mitogenomes were found to be identical. Phylogenetic analysis was conducted to assess their evolutionary relationships. The phylogenetic tree shows that *H. asinina* is closely related to *H. ovina*, *H. diversicolor*, *H. varia*, *H. rubra* and *H. tuberculata*. The genetic information gleaned from this study will be invaluable for the further studies of *H. asinina* especially on population genetics and improvement of aquaculture in the face of climate change effects.