

Mitochondrial DNA

The Journal of DNA Mapping, Sequencing, and Analysis

ISSN: 1940-1736 (Print) 1940-1744 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn20>

Complete mitochondrial genome and phylogenetic relationship analyses of *Amphioctopus aegina* (Gray, 1849) (Cephalopoda: Octopodidae)

Xiaoying Zhang, Xiaodong Zheng, Yuanyuan Ma & Qi Li

To cite this article: Xiaoying Zhang, Xiaodong Zheng, Yuanyuan Ma & Qi Li (2015): Complete mitochondrial genome and phylogenetic relationship analyses of *Amphioctopus aegina* (Gray, 1849) (Cephalopoda: Octopodidae), *Mitochondrial DNA*, DOI: [10.3109/19401736.2015.1106522](https://doi.org/10.3109/19401736.2015.1106522)

To link to this article: <http://dx.doi.org/10.3109/19401736.2015.1106522>



Published online: 18 Dec 2015.



Submit your article to this journal [↗](#)



View related articles [↗](#)



View Crossmark data [↗](#)

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome and phylogenetic relationship analyses of *Amphioctopus aegina* (Gray, 1849) (Cephalopoda: Octopodidae)Xiaoying Zhang^{1,2}, Xiaodong Zheng^{1,2}, Yuanyuan Ma¹, and Qi Li¹¹Laboratory of Shellfish Genetics and Breeding, Fisheries College, Ocean University of China, Qingdao, China and ²Institute of Evolution & Marine Biodiversity, Ocean University of China, Qingdao, China**Abstract**

In this paper, the circular mitochondrial genome of *Amphioctopus aegina* (Cephalopoda: Octopodidae) was sequenced. The whole mitogenome of *A. aegina* was 15 545 base pairs (bp) in length with a base composition of 42.53% A, 33.26% T, 16.70% C, and 7.51% G. The complete mitogenome contained 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, 22 transfer RNA genes, and a major non-coding region. The gene arrangements of *A. aegina* showed remarkable similarity to other Octopodidae species reported. The phylogenetic relationships were reconstructed with the concatenated sequences of the 13 PCGs of the mitochondrial genome, and illustrated that *A. aegina* had the closest genetic relatives to *A. fangsiao*.

Keywords

Amphioctopus aegina, mitochondrial genome, Octopodidae, phylogenetic relationship

History

Received 1 September 2015

Accepted 7 October 2015

Published online 9 December 2015

Amphioctopus aegina (Gray, 1849) is a moderate-sized species, once called *Octopus aegina* Gray, 1849. It lives on soft substrates of the subtidal zone ranging to at least 40 m depth and muddy coastal waters of continental Asia, from China, south to Malaysia and Indonesia, west to at least Chennai, India (Norman et al., 2013). Compared with molecular studies, there have been more documents concentrating on the farming techniques and life cycle (Ignatius et al., 2011; Osman et al., 2014; Promboon et al., 2011) in recent years. In this paper, we sequenced the mitochondrial (mt) genome of *A. aegina* and analyzed its phylogenetic relationship with other 27 cephalopods.

The sample was collected from Haikou Fishery Market, Hainan Province, China. Total genomic DNA of *A. aegina* was extracted from muscle by the E.Z.N.A.TM Mollusk DNA Kit (OMEGA Bio-Tek Company, Norcross, GA). Primers of 13 protein-coding genes (PCGs) and two ribosomal RNA (rRNA) genes were the same as *Octopus conispadiceus* (Ma et al., 2014). The gene annotation was performed referring to the methods used by Yuan et al. (2012). The complete mtDNA of *A. aegina* was 15 545 bp (GenBank accession no. KT428877) containing 13 PCGs, two rRNA genes, 22 transfer RNA (tRNA) genes, and a major

non-coding region (600 bp in length). The mitogenome of *A. aegina* shared the similar gene length and gene arrangement with other reported octopods (Cheng et al., 2012, 2013). Seven out of 13 proteins were encoded in the plus strand, while the other six proteins, as well as the two rRNAs were encoded in minus strand. The overall A + T content of the plus strand was 74.79%. 10 PCGs in the *A. aegina* mt genome initiated with initiation codon ATA (*cox2*, *cox3*, *atp6*, *atp8*, *cob*, and *nad1-4*, *nad4l*), while *cox1*, *nad5*, and *nad6* started with ATG. 10 PCGs (*cox1-3*, *nad2-5*, *nad4l*, *atp8*, and *cob*) ended their open-reading frames (ORF) with TAA, while *atp6*, *nad1*, and *nad6* ended with TAG. Twenty-two tRNA genes can fold typical cloverleaf structure, ranging from 57 to 74 bp. Two tRNA genes (*trnN(att)* and *trnL3(caa)*) existed D-loop replacement. The A + T content of the tRNA genes was 77.76%. The length of *rrnS* and *rrnL* was 1303 bp and 961 bp, respectively.

Besides *A. aegina*, we also covered the complete mitochondrial sequences of other 27 cephalopods in GenBank for phylogenetic analysis, which was based on the concatenated nucleotide sequences of the 13 PCGs and performed using maximum likelihood (ML) method with MEGA5 (Tamura et al., 2011) under the model of general time reversible. The number of Bootstrap Replications was 1000. The result (Figure 1) showed that *A. aegina* was the closest relative of *A. fangsiao*, both of which were sisters to *O. vulgaris* and two *Cistopus* species. In Octopodidae, *O. minor* was farthest to *A. aegina*. Meanwhile, it exhibited relatively distant genetic relationships with the other octopods, similar to Cheng et al. (2013), which provided more evidences for the mistaken taxonomic status of *O. minor*.

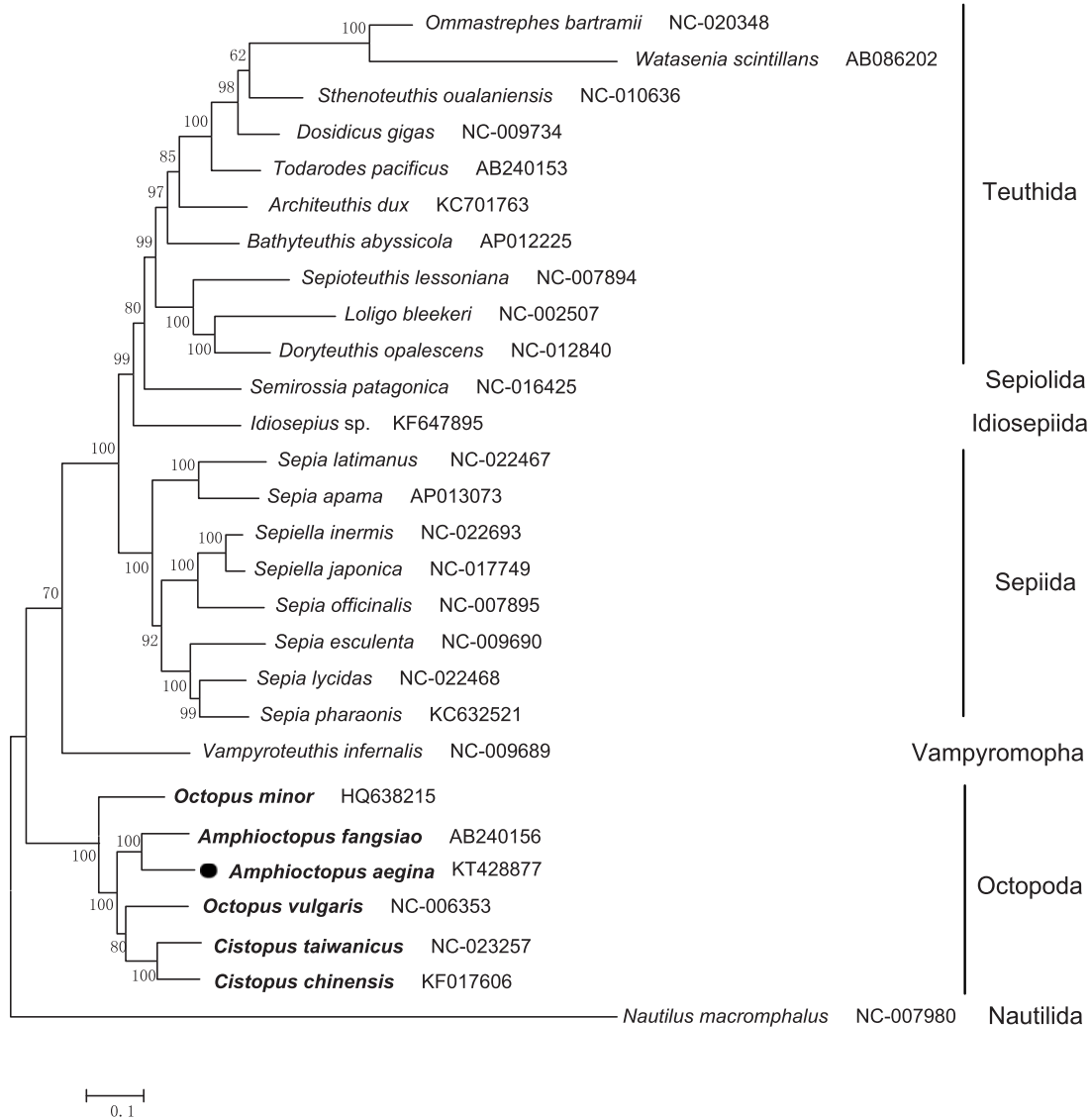


Figure 1. ML analysis of 28 cephalopods based on 13 PCGs.

Acknowledgements

The authors thank Ms. Shao-E Sun, from Laboratory of Shellfish Genetics and Breeding, Ocean University of China, for her constructive suggestions.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This study was supported by research grants from National Natural Science Foundation of China (31172058).

References

- Cheng RB, Zheng XD, Lin XZ, Yang JM, Li Q. (2012). Determination of the complete mitochondrial DNA sequence of *Octopus minor*. *Mol Biol Rep* 39:3461–70.
- Cheng RB, Zheng XD, Ma YY, Li Q. (2013). The complete mitochondrial genomes of two Octopods *Cistopus chinensis* and *Cistopus taiwanicus*: Revealing the phylogenetic position of Genus *Cistopus* within the order Octopoda. *PLoS One* 8:e84216.
- Ignatius B, Srinivasan M, Balakrishnan S. (2011). Reproductive traits of sandbird octopus, *Amphioctopus aegina* (Gray, 1849) from Mandapam coastal waters (Palk Bay), southeast coast of India. *Ocean Sci J* 46: 145–54.
- Jereb P, Roper CFE, Norman MD, Finn JK. (2013). Cephalopods of the world. An annotated and illustrated catalogue of cephalopod species

- known to date, volume 3. Octopods and Vampire Squids. *FAO Species Catalogue for Fishery Purposes*. No. 4, Vol. 3. FAO. Rome, 2013. p68–69.
- Ma YY, Zheng XD, Cheng RB, Li Q. (2014). The complete mitochondrial genome of *Octopus conispadiceus* (Sasaki, 1917) (Cephalopoda: Octopodidae). *Mitochondrial DNA*. *Mitochondrial DNA*, early online, doi: 10.3109/19401736.2014.928866.
- Norman MD, Finn JK, Hochberg FG. (2013). Family Octopodidae. In: Jereb P, Roper CFE, Norman MD, Finn JK, eds. *Cephalopods of the world. An annotated and illustrated catalogue of cephalopod species know to date: Octopods and Vampire Squids*. FAO species catalogue for fishery purposes. Rome: FAO. p 68–69.
- Osman IH, Gabr HR, El-Etreby SG, Mohammed SZ. (2014). Feeding biology and biochemical composition of the Lessepsian migrant *Octopus aegina* (Cephalopoda: Octopodidae). *Egypt J Aquat Biol Fish* 18:15–27.
- Promboon P, Nabhitabhata J, Duengdee T. (2011). Life cycle of the marbled octopus, *Amphioctopus aegina* (Gray) (Cephalopoda: Octopodidae) reared in the laboratory. *Sci Mar* 75:811–21.
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. (2011). MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol* 28:2731–9.
- Yuan Y, Li Q, Kong LF, Yu H. (2012). The complete mitochondrial genome of the grand jackknife clam, *Solen grandis* (Bivalvia: Solenidae): A novel gene order and unusual non-coding region. *Mol Biol Rep* 39:1287–92.