

Mitochondrial DNA



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MITOGENOME ANNOUNCEMENT

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

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In this paper, the circular mitochondrial genome of *Amphioc op a 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. fangaiao*.

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Amphioc op aegina, mitochondrial genome, Octopodidae, phylogenetic relationship

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)S A. aegina (cox2, cox3, atp6, atp8, cob,nad1-4, nad4l), cox1, nad5, nad6st t ε (cox1-3, nad2-5, nad4l, atp8, cob)) t 🌁 atp6, nad1, nad6 s (trnN(att)₽ trnL3(caa)) . st rrnS3 rrnLs A. aegina, 22, t A. aegina s st A. fangsiao, O. vulgaris s t stt A. aegina. 2,2 st t.s O. minor

— Sthen Dosidie