Complete mitochondrial genome of blunt slipper lobsters *Scyllarides squammosus* (H. Milne Edwards, 1837)

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**ABSTRACT**

The complete mitochondrial genome of *Scyllarides squammosus* was first determined and characterized. With a length of 15,644 bp, it consists of 22 tRNA genes, 2 rRNA genes, 13 protein-coding genes (PCGs), and 1 control region. The nucleotide composition is significantly biased with AT contents of 65.6%. Among these PCGs, five of them used an unusual initiation codon, and nine genes ended with an incomplete or abnormal stop codon. Two microsatellites were identified and located in COX3 gene and D-loop region. Phylogenetic analysis demonstrated that *S. squammosus* was first clustered with *Scyllarides latus*, which was consistent with the previous work.

*Scyllarides squammosus*, known as scaly slipper lobster or blunt slipper lobster, is a highly valuable species in the family Scyllaridae, Achelata, the price of which is almost similar to *S. latus*, which was consistent with the previous work.

The samples were collected from Huanqiu wharf of Wenchang, Hainan province, China (19°33′57.91″ N, 110°49′12.10″ E), and stored in Qionghai research base of Hainan Academy of Ocean and Fisheries Sciences for reference and DNA extraction.

The complete mitogenome sequence of *S. squammosus* is 15,644 bp in length (GenBank Accession no. MK783265). The base content was 31.2% A, 13.2% G, 34.3% T, and 21.2% C. The 65.6% of (A + T) showed great preference to AT. The circular mitogenome contained 22 tRNA genes, 2 rRNA genes, 13 protein-coding genes (PCGs), and 1 control region (D-loop). Four PCGs (ND1, ND4, ND4L, and ND5), eight tRNA genes and two rRNA genes were encoded on the light strand, the others were encoded by the heavy strand.

The 22 tRNA genes of the *S. squammosus* mitogenome ranged in length from 63 to 73 bp. The genes tRNA-Leu and tRNA-Ser have two copies each, identified with different codons (tRNA-leu uses TAA and TAG; tRNA-Ser uses TCT and TGA). The 12S rRNA is located between rRNA-Val and D-loop with the length of 863 bp, and the 16S rRNA is 1339 bp, located between rRNA-Val and tRNA-Leu. Except for five PCGs using an abnormal start codon (ND1 and ND4L use TTA; COX1 uses ACC; ND4 uses CAG; ND5 uses AAC), the others use a common initiation codon ATN. We also found that except for 4 PCGs using TAA or TAG, the stop codon of the other nine genes were abnormal: COX2, ND2, ND3, and ND5 use a single base T; ND4 uses AT; COX1 uses TT; CYTB uses TG; ND4L uses CAT; and ND1 uses CAC. With a length of 716 bp, the control region is located between 12S rRNA and tRNA-Ile. Two microsatellites (SSR) were found in the mitogenome of *S. squammosus* using MISA software. The two (T)\textsubscript{10} SSRs were located in the codon region of COX3 gene and the non-codon region of D-loop, respectively.

To investigate the phylogenetic relationship of *S. squammosus* in the Achelata, a phylogenetic tree was constructed based on the 13 PCGs nucleotide sequences of 16 Achelata species mitogenome available in the GenBank using the maximum-likelihood (ML) method with 1000 bootstrap replicates. The result (Figure 1) show that *S. squammosus* was first clus-
tered with *Scyllarides latus*, which was consistent with the previous work (Palero et al. 2016).

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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**References**

Clarke RP, Yoshimoto SS. 1990. Application of the Leslie model to commercial catch and effort of the slipper lobster, *Scyllarides squammosus*, fishery in the northwestern Hawaiian Islands. Mar Fisheries Rev. 52: 1–7.

Coutures E. 2001. On the first phyllosoma stage of *Parribacus caledonicus* Holthuis, 1960, *Scyllarides squammosus* (H. Milne-Edwards, 1837) and *Arctides regalis* Holthuis, 1963 (Crustacea, Decapoda, Scyllaridae) from New Caledonia. J Plankton Res. 23:745–751.

DeMartini EE, McCracken ML, Moffitt RB, Wetherall JA. 2005. Relative pleopod length as an indicator of size at sexual maturity in slipper (*Scyllarides squammosus*) and spiny Hawaiian (*Panulirus marginatus*) lobsters. Fishery Bull. 103:23–33.

DeMartini E, Williams H. 2001. Fecundity and egg size of *Scyllarides squammosus* (Decapoda: Scyllaridae) at Maro Reef, Northwestern Hawaiian Islands. J Crustacean Biol. 21:891–896.

Lau CJ. 1987. Feeding behavior of the Hawaiian slipper lobster, *Scyllarides squammosus*, with a review of decapod crustacean feeding tactics on molluscan prey. Bull Mar Sci. 41:378–391.

Matthews DC. 1954. A comparative study of the spermatophores of three scyllarid lobsters (*Parribacus antarcticus*, *Scyllarides squammosus*, and *Scyllarus martensii*). J Cell Sci. 3:205–215.

O’Malley JM. 2004. Trap-weight influence on catches of Hawaiian spiny lobster (*Panulirus marginatus*) and scaly slipper lobster (*Scyllarides squammosus*) from the northwestern Hawaiian Islands. Honolulu (HI): Joint Institute for Marine and Atmospheric Research. Administrative Report H-04-06.

O’Malley JM. 2011. Spatiotemporal variation in the population ecology of scaly slipper lobsters *Scyllarides squammosus* in the Northwestern Hawaiian Islands. Mar Biol. 158:1887–1901.

O’Malley JM, Walsh WA. 2013. Annual and long-term movement patterns of spiny lobster, *Panulirus marginatus*, and slipper lobster, *Scyllarides squammosus*, in the northwestern Hawaiian Islands. Bull Mar Sci. 89: 529–549.

Palero F, Genis-Armero R, Hall MR, Clark PF. 2016. DNA barcoding the phyllosoma of *Scyllarides squammosus* (H. Milne Edwards, 1837)(Decapoda: Achelata: Scyllaridae). Zootaxa. 4139:481–498.