Next-generation sequencing yields the complete mitogenome of *Favia favus*

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**ABSTRACT**

In the present study, we determined the complete mitogenome sequence of scleractinia, *Favia favus* using the Illumina HiSeq platform. The assembled mitogenome was 17,054 bp in length, comprising unique 13 protein-coding genes (PCGs), 2 ribosomal RNAs, and 2 transfer RNAs genes of each, showing a typical scleractinarian pattern. New phylogenetic analysis upon complete mitogenomics revealed that *F. favus* is most closely related to *Favites abdita*, with high bootstrap values.

**KEYWORDS**

Scleractinia; complete mitogenome genome; *Favia favus*

In recent years, mass global bleaching event devastated the relatively healthy coral reefs (Roelfsema et al. 2018). Coral reefs, for instance, are increasingly under pressure due to coastal development and resource use (Shidqi et al. 2018). Mitochondria genome structure is important to the growth and developmental Progression in the Coral (Reyes-Bermudez et al. 2016). *Favia favus*, which belongs to the Faviinae family, is widely distributed throughout the Indo-Pacific. And it is most massive and spherical. The first establishment of mitogenome is important for further evolutionary and phylogenetic analyses for stony coral (Wang et al. 2018).

Samples (voucher no. YM03) of *F. favus* were collected from Yangmeiken in Guangdong, China (114°34′40.30″E, 22°32′47.63″N) on July 2018 and deposited at South China Sea Fisheries Research Institute Shenzhen test base Herbarium. We used the next-generation high-throughput sequencing method to acquire the *F. favus* complete mitochondrial genome sequences. The raw next-generation sequencing reads generated from HiSeq X-ten (Illumina, San Diego, CA). The reads were de novo assembly by using commercial software (SOAPdenovo V2.04, BGI, CHN) to produce a single, circular form of complete mitogenome with about an average 294 coverage. The complete mitogenome of *F. favus* was 17,054 bp in size (GenBank MKS16277) and its overall base composition is 25.0% for A, 13.1% for C, 20.4% for G, and 41.5% for T, and have GC content of 33.5%, showing 100% identities to *Favites abdita* (GenBank KY094479.1). The protein coding, rRNA and tRNA genes of *F. favus* mitogenome were predicted by using DOGMA (DOGMA, the University of Texas at Austin, USA) (Wyman et al. 2004) server tools, and manually inspected. The complete mitogenome of *F. favus* includes unique 13 protein-coding genes (PCGs), 2 transfer RNA genes (tRNAMet, tRNA-Trp), and 2 ribosomal RNA genes. Among the 13 PCGs, the longest one is the *ND5* gene (1815 bp), whereas the shortest is *ATP8* gene (198 bp). The *ND5* gene is split into two parts by a large fragment of genes, which commonly presented in scleractinian coral, and the size of the inserted fragment was usually over 10 Kb.

All PCGs, tRNA, and rRNA genes were encoded on H-strand. The most start codon is ATG. There are 10 PCGs started with ATG codon (*ND1, ND3, ATP6, COX3, COX2, ND4, ND4L, ND5, ND6*, and *ATP8*), two ATT codon (*ND2 and COX1*), and one with TAA codon (*Cyt b*). Nine of the 13 PCGs are inferred to terminate with TAA (*ATP6, Cytb, ND3, ND2, ND6, ATP8, ND4L, COX2, and COX3*), 4 with ATG (*ND1, ND4, ND5, and COX1*). The small and large mitochondrial ribosomal RNA genes of *F. favus* were located opposite each other on the circular genome as in other corals (Ju et al. 2017).

To determine the phylogenetic position of *F. favus*, we used MEGA Version10.0.4 (Knyaz et al. 2018) software to construct a Maximum likelihood tree using 500 bootstrap replicates and Kimura 2-parameter model (Tian and Niu 2017). The phylogenetic tree was reconstructed with 13 coral species complete mitogenomes derived from GenBank (Figure 1).

The result showed *F. favus* was grouped into a single clade of with *Favites abdita*. This relationship has been verified by molecular phylogenies. Which were with 100% bootstrap value supported. In conclusion, the complete mitogenome of the *F. favus* determined is expected to provide essential phylogenetic and evolutionary information of corals in this study.

The genus Favia, common across the Indo-Pacific, is characterized by a genus-specific septal formula. It is similar to genus Favites in appearance. Species identification to date has been conducted most using traditional macromorphologies, such as...
colony growth form, corallite dimensions, and number and fusion pattern of septa (Edinger and Risk 2000; Terraneo et al. 2016; Gonzálezespinoza et al. 2018). However, it is taxonomic uncertainty due to confusing patterns of morphological variation, with surprising examples of convergent evolution, rapid evolution, and phenotypic plasticity (Tisthammer and Richmond 2018).

Disclosure statement
No potential conflict of interest was reported by the authors.

Funding
This work was supported by the Shenzhen science and technology innovation project under Grant NO. [CYJ20160331141759795]; Excellent youth talent program from Shanghai Municipal Commission of Health and Family Planning [2017YQ007], the general program from the National Natural Science Foundation of China [81770329], and Guangdong Natural Science Foundation - Doctoral program under Grant NO. [2017A030310631].

References
Edinger EN, Risk MJ. 2000. Reef classification by coral morphology predicts coral reef conservation value. Biol Conserv. 92:1–13.
Gonzálezespinoza PC, Pazgarcía DA, Reyesbonilla H, Cabraltena RA, Balart EF. 2018. Evidence of sexual dimorphism in skeletal morphology of a gonochoric reef coral. Royal Soc Op Sci. 5:1–7.
Ju YM, Hsiao ST, Kuo FW, Wu JH. 2017. The complete mitochondrial genome of Montipora aequituberculata (Scleractinia, Acroporidae). Mitochondrial DNA Part B. 2:62–63.
Knyaz C, Stecher G, Li M, Kumar S, Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Mol Biol Evol. 35:1547–1549.
Reyes-Bermudez A, Villar-Briones A, Ramirez-Portilla C, Hidaka M, Mikheyev AS. 2016. Developmental progression in the coral Acropora digitifera is controlled by differential expression of distinct regulatory gene networks. Genome Biol Evol. 8:851–870.
Roelfsema C, Kovacs E, Ortiz JC, Wolff NH, Callaghan D, Wettle M, Ronan M, Hamylton SM, Mumby PJ, Phinn S. 2018. Coral reef habitat mapping: a combination of object-based image analysis and ecological modelling. Remote Sens Environ. 208:27–41.
Shidqi RA, Pamuji B, Sulistiantoro T, Risza M, Faozi AN, Muhammad AN, Muhamr MR, Putri ED, Hartini R, Valentina B, et al. 2018. Coral health monitoring at Melinjo Island and Saktu Island: influence from Jakarta Bay. Region Stud Mar Sci. 18:237–242.
Terraneo TI, Benzoni F, Arrigoni R, Berumen ML. 2016. Species delimitation in the coral genus Goniopora (Scleractinia, Poritidae) from the Saudi Arabian Red Sea. Mol Phylogenet Evol. 102:278–294.
Tian P, Niu W. 2017. The complete mitochondrial genome of Acropora pruinosa. Mitochondrial DNA Part B. 2:652–653.
Tisthammer KH, Richmond RH. 2018. Corallite skeletal morphological variation in Hawaiian Porites lobata. Coral Reefs. 37:1–12.
Wang X, Tian P, Niu W, Yu S. 2018. The complete mitochondrial genome of the Montipora peltiformis (Scleractinia: Acroporidae). Mitochondrial DNA Part B. 3:99–100.
Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organelar genomes with DOGMA. Bioinformatics. 20:3252–3255.