The complete mitochondrial genome of *Saccostrea Kegaki* (Pterioida, Ostreidae)

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**ABSTRACT**

*Saccostrea* are common oysters of Indo-Pacific rocky shores. However, the taxonomy of this genus is confused. In this study, we report the complete sequence of the mitochondrial genome of *S. kegaki*. The complete *S. kegaki* mitogenome is 16,260bp in size. The 16S rRNA gene is split into two parts by a large fragment of genes. Neighbour-joining molecular phylogenetic analysis appears to support the current taxonomic framework of Ostreidae. We expect that the complete mitogenome of *S. kegaki* will provide a useful resource for studies on the molecular phylogeny and conservation genetics of Bivalvia.

Oysters are playing many important roles in coastal ecological processes (Lohan et al. 2015). *Saccostrea* are common oysters of Indo-Pacific rocky shores. Due to the morphological plasticity among the species of genus *Saccostrea*, the taxonomy of this genus is confused (Lam and Morton 2006; Sekino and Yamashita 2016). Although *Saccostrea* is one of the main framework engineers in marine ecosystems, only two mitochondrial genomes have been sequenced.

In this study, we report the complete sequence of the mitochondrial genome of *S. kegaki* (GeneBank accession number NC_030533). The sample was collected from intertidal coasts of Matsu, Taiwan and was deposited in the Fisheries Research Institute (No. TFRIP380). Total genomic DNA was extracted from adductor muscle tissue (Hsiao et al. 2016). The complete mitogenome of *S. kegaki* was amplified by 17 primer pairs.

The complete *S. kegaki* mitogenome is 16,260 bp in size, comprising 12 protein-coding genes, 2 rRNA genes, 23 tRNA gene, and a total of 1408 bp of noncoding nucleotides spread over 22 intergenic regions (each over 5 bp), including a major noncoding region of 365 bp. The 16S rRNA gene is split into two parts by a large fragment of genes, which is commonly presented in Ostreidae species (Danic-Tchaleu et al. 2011), but not otherwise observed in metazoan mitochondrial DNA (Milbury and Gaffney 2005). All genes are encoded on the H-strand.

The overall base composition is 35.8% T, 15.5% C, 26.2% A, and 22.5% G. Most start codons are ATG and GTG, except for Cytb and ND4L, which begin with an ATA codon. All 12 genes had complete termination codons; both TAA and TAG are used as stop codons. The small and large mitochondrial ribosomal RNA genes of *S. kegaki* were located opposite each other on the circular genome, as in other *Saccostrea* (Volatiana et al. 2015) and corals (Wu et al. 2014; Ju et al. 2017), unlike most other metazoans, in which mitochondrial rRNA genes are usually clustered (Boore 1999). Furthermore, the tRNA\textsubscript{Met}, tRNA\textsubscript{Ser}, and tRNA\textsubscript{Leu} genes occur as duplications on the genome of *S. kegaki*, a phenomenon that is also observed in other species of Ostreidae (Ren et al. 2010).

To determine the phylogenetic position of *S. kegaki*, a neighbour-joining molecular phylogenetic tree was constructed based on the 12 protein-coding genes of 23 other Bivalvia species from GenBank with the program MEGA 7 (Kumar et al. 2016) using 1000 bootstrap replicates (Figure 1). The phylogenetic tree resolved a monophyletic clade for the Ostreidae family, which could be divided into three subclades (clades A, B, and C). The results showed that *S. kegaki*, *S. mordax*, and *S. cucullata* clustered into clade C. Our phylogenetic analysis appears to support the current taxonomic framework for Ostreidae, and this relationship has also been verified by molecular phylogenies (Danic-Tchaleu et al. 2011, Volatiana et al. 2015). In conclusion, we expect that the complete mitogenome of *S. kegaki* will provide a useful resource for studies on the molecular phylogeny and conservation genetics of Bivalvia.

**Disclosure statement**

The authors declare that they have no competing interests in the preparation or execution of this study.

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Figure 1. Antioxidant activity of the methanolic extract of the isolated halophilic bacterial strains. The anti-oxidant potential is given in terms of ascorbic acid equivalence (AE) and EDTA equivalence (EE).

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