Mitochondrial genome of Japanese amberjack, *Seriola quinqueradiata*, and yellowtail amberjack, *Seriola lalandi*

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**ABSTRACT**

The mitochondrial genomes of *Seriola quinqueradiata* and *S. lalandi* were 16,539 and 16,535 base pairs long, respectively, whose organizations were similar to those of other bony fishes. The sequence similarity of two species was 93% in the mitochondrial whole genome. Between each coding gene, rRNA, and control region, the highest similarity was 98% in ATP8 and lowest similarity was 87% in the control region. Phylogenetic analysis of Carangidae mt 12 protein-coding genes showed that *Seriola* and *Carangoides* do not form a monophyletic genus.

*Seriola* is a genus of Carangidae in Perciforms, known as amberjacks. Japanese and Yellowtail amberjack, *Seriola quinqueradiata* and *Seriola lalandi*, respectively, are morphologically very similar, produced through aquaculture, and valuable foods in Korea and Japan.

For complete mitochondrial (mt) genome analysis, we extracted genomic DNA from blood samples of *S. quinqueradiata* and *S. lalandi* provided by the Jeju Fisheries Research Institute. Genomic DNA was stored at −80°C.

The mt genomes of *S. quinqueradiata* and *S. lalandi* were 16,539 and 16,535 base pairs, respectively. The mt genome sequences were deposited in the GenBank database (Accession No. MK158067 and MK158068, respectively). Like the mt genomes of other bony fishes, both genomes contain 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and a non-coding control region.

The overall base compositions were as follows: *S. quinqueradiata*: A, 26.54%; C, 30.26%; G, 18.08%; T, 25.13%; *S. lalandi*: A, 26.57%; C, 30.22%; G, 17.91%; T, 25.30%. The respective proportions of A and T in the base composition were relatively low. The respective proportions of C and G were slightly higher than in *S. dumerili* (AB517558) and *S. rivoliana* (KP733847).

The PCGs of *S. quinqueradiata* and *S. lalandi* begin with ATG except for cytochrome c oxidase subunit 1, which begins with GTG and ends with TAG, TAA, or incomplete termination codon, T. Incomplete termination codons, which are added through posttranscriptional polyadenylation (Ojala et al. 1981), are common in bony fish mt genomes (Ishiguro et al. 2001; Miya et al. 2003; Oh et al. 2008).

The mt genomes of *S. quinqueradiata* and *S. lalandi* contain 22 tRNA genes. We identified 2 types of trnL(UUR and CUN) and trnS(UJC and AGY) and 3 clusters (IQM, WANCY, and HSL), which are conserved in *Seriola* fishes and bony fish mt genomes (Ishiguro et al. 2001; Miya et al. 2003; Oh and Jung 2008).

Examination of the differences in mt genes and the control region revealed that the 13 PCGs ranged between 87% (control region) and 98% (ATPase subunit 8 and 12S rRNA) identity. Overall, the mt genome of *S. quinqueradiata* and *S. lalandi* showed 93% identity.

To phylogenetically analyze Carangidae fishes, we constructed a maximum likelihood tree using MEGA X software (Kumar et al. 2018) with 12 PCGs excluding NADH dehydrogenase subunit 6 gene because of its heterogeneous base composition and consistently poor phylogenetic performance (Zardoya and Meyer 1996; Miya and Nishida 2000). GTR+G+I mode was selected as the best substitution model based on AIC criterion (Akaike 1973).

Phylogenetic analysis of Carangidae showed that *Seriola* is not a monophyletic group (Figure 1). The black-banded trevally, *Seriolina nigrofasciata*, was between *S. dumerili* + *S. rivoliana* and *S. quinqueradiata* + *S. lalandi*. This result slightly differed from that of a previous study (Santini and Carnevale 2015) showing that *S. nigrofasciata* was the first lineage to branch off and *Seriola* formed a diverse clade with *Naucrates doctor*. *Carangoides* was also a non-monophyletic genus in this study and according to Santini and Carnevale (2015). Our phylogenetic analysis suggested that Carangidae fish phylogeny should be re-examined.

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