Half-fin anchovy (Setipinna tenuifilis), one of the most important economic fishes, is a highly migratory species. The complete mitochondrial genome of S. tenuifilis was determined by polymerase chain reaction amplification and sequencing, using 13 pairs of primers which were designed based on the mitogenome sequence of S. tenuifilis (GenBank number AP011565.1), a closely related species of Setipinna melanochir (WANCY region, Table 1). The complete mitogenome of S. tenuifilis was deposited in GenBank database with accession number MH037012. Muscle tissues were persevered in 95% ethanol for DNA extraction. Total genomic DNA was extracted from muscle tissue by standard phenol–chloroform procedure (Sambrook et al. 1989).

The complete mitogenome of S. tenuifilis was determined to be 16,215 bp, comprising 37 coding and two non-coding regions. The 37 coding regions include 13 protein-coding genes (ATP6 and 8, COI–III, Cytb, ND1-6, and 4L), 22 transfer RNA genes (tRNAs), and two ribosomal RNA genes (12S and 16S rRNAs), with gene arrangement and content basically identical to those of other species of Engraulidae. The result of phylogenetic analysis strongly supported that S. tenuifilis was first clustered together with Setipinna melanochir and formed a monophyly in the genus Coilia, and then they constituted a sister-group relationship with two genus Engraulis, and Stolephorus. It concluded that the S. tenuifilis should be classified into the genus Setipinna. The present study also revealed the phylogenetic relationship of this genus at molecular levels. The complete mitochondrial genome sequence of S. tenuifilis can provide basic information for the studies on molecular taxonomy and phylogeny of teleost fishes.
Phylogenetic analysis was performed by MEGA 6.06 (Tamura et al. 2013) based on complete mitogenome sequence of *S. tenuifilis* and those of 13 closely related species belonging to four genus *Engraulis*, *Stolephorus*, *Setipinna*, and *Coilia*. The neighbour-joining tree (Figure 1) showed that *S. tenuifilis* first clustered together with *Setipinna melanochir* and formed a monophyly in the genus *Coilia*, and then they constituted a sister-group relationship with other two genus.

### Table 1. Characteristics of the mitochondrial genome of *Setipinna tenuifilis*.

| Locus   | Abbreviation | From | To  | Size nucleotide (bp) | Codon | Amino acid (AA) | Anti-codon | Intergenic nucleotide | Strand |
|---------|--------------|------|-----|-----------------------|-------|-----------------|------------|------------------------|--------|
| tRNA<sup>F</sup> | F            | 1    | 69  | 69                    | GAA   | 0               | H          |                        |        |
| 12S rRNA | 12S          | 70   | 1020| 951                   | TAC   | 0               | H          |                        |        |
| tRNA<sup>Val</sup> | I           | 3850 | 3921| 72                    | CAT   | -1              | H          |                        |        |
| 16S rRNA | 16S          | 1093 | 2779| 1687                  | TTA   | 0               | H          |                        |        |
| tRNA<sup>Met</sup> | M           | 3991 | 4059| 69                    | CAT   | 0               | H          |                        |        |
| ND 1    | nd1          | 2869 | 3807| 939                   | ATG   | 313             | H          |                        |        |
| tRNA<sup>Phe</sup> | W           | 5075 | 5146| 72                    | TCA   | 2               | H          |                        |        |
| tRNA<sup>Leu</sup> | A           | 5149 | 5217| 69                    | TGC   | 1               | L          |                        |        |
| tRNA<sup>Leu</sup> | N           | 5219 | 5291| 73                    | GTT   | 0               | L          |                        |        |
| Rep origin |             | 5292 | 5320| 29                    |       |                 |            |                        |        |
| tRNA<sup>Cys</sup> | C           | 5321 | 5387| 67                    | GCA   | 0               | L          |                        |        |
| tRNA<sup>Met</sup> | Y           | 5388 | 5458| 71                    | GCA   | 0               | L          |                        |        |
| COX I    | cox1         | 5466 | 6989| 1524                  | ATC   | 508             | H          |                        |        |
| tRNA<sup>Trp</sup> |             | 6095 | 7065| 71                    | TGA   | 5               | L          |                        |        |
| tRNA<sup>Y</sup> | D            | 7071 | 7139| 69                    | GTC   | 11              | H          |                        |        |
| COX II   | cox2         | 7151 | 7813| 663                   | ATG   | 221             | H          |                        |        |
| tRNA<sup>Ser</sup> |             | 7844 | 7916| 73                    | TTT   | 1               | H          |                        |        |
| ATP 8    | atp8         | 7918 | 8082| 165                   | ATG   | 55              | H          |                        |        |
| ATP 6    | atp6         | 8076 | 8756| 681                   | ATG   | 227             | H          |                        |        |
| COX III  | cox3         | 8739 | 9541| 783                   | ATG   | 261             | H          |                        |        |
| tRNA<sup>Ser</sup> |             | 9544 | 9615| 72                    | TCC   | 0               | H          |                        |        |
| ND 3     | nd3          | 9616 | 9963| 348                   | ATG   | 116             | H          |                        |        |
| tRNA<sup>Arg</sup> |             | 9965 | 10,033| 69                   | TCG   | 0               | H          |                        |        |
| ND4L     | nd4L         | 10,034| 10,327| 294                 | ATG   | 98              | H          |                        |        |
| ND 4     | nd4          | 10,324| 11,694| 1371               | ATG   | 457             | H          |                        |        |
| tRNA<sup>Glu</sup> |             | 11,705| 11,772| 68                  | GTG   | 1               | H          |                        |        |
| tRNA<sup>Trp</sup> |             | 11,774| 11,840| 67                 | GCT   | 0               | H          |                        |        |
| tRNA<sup>A</sup> |             | 11,841| 11,912| 72                 | TAG   | 0               | H          |                        |        |
| ND 5     | nd5          | 11,913| 13,039| 1127               | ATG   | 375             | H          |                        |        |
| ND 6     | nd6          | 13,045| 13,563| 519               | AAC   | 173             | L          |                        |        |
| tRNA<sup>Cyt</sup> |             | 13,564| 13,632| 69                 | TCC   | 0               | L          |                        |        |
| Cyt b    |              | 13,637| 14,767| 1131              | ATG   | 377             | H          |                        |        |
| tRNA<sup>Thr</sup> |             | 14,823| 14,891| 69                 | TGT   | -1              | H          |                        |        |
| tRNA<sup>Pro</sup> |             | 14,891| 14,961| 71                 | TGG   | 0               | L          |                        |        |
| Control region | CR        | 14,962| 16,215| 1254             |       |                 |            |                        |        |

**Figure 1.** Phylogenetic position of the half-fin anchovy.

Phylogenetic analysis was performed by MEGA 6.06 (Tamura et al. 2013) based on complete mitogenome sequence of *S. tenuifilis* and those of 13 closely related species belonging to four genus *Engraulis*, *Stolephorus*, *Setipinna*, and *Coilia*. The neighbour-joining tree (Figure 1) showed that *S. tenuifilis* first clustered together with *Setipinna melanochir* and formed a monophyly in the genus *Coilia*, and then they constituted a sister-group relationship with other two genus.
This result strongly supported that *S. tenuifilis* should be classified into the genus *Setipinna*. This study also revealed the phylogenetic relationship of the genus *Coilia* at molecular levels.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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