

Text S1. Alignment of variable nucleotide sites of the *Protosalanx chinensis* (KJ499917, MW291629) and *Neosalanx tangkahkeii* (KP170510) full mitochondrial genomes, showing evidence of recombination at the *COI* and *ND4* genes, and also at the control region

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#KP170510_Neosalanx_tangkahkeii	ATCATTTCCGC	CAGGTCTTAT	ACCGCCCAAC	GGCCCATGAA	TAAAGTTTACA	GAAACCGCGA	GTTTCTCTGC	ATAGCAACAG	ACCTA
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#KP170510_Neosalanx_tangkahkeii	CACTGTCTGG	TATGATCCCT	CCAATCGCTG	GTTCCCTTACG	GTTCAACCGA	TTTCGGCCGC	GCCCCGCACG	CGGACCCGCT	CTTTT	
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#KP170510_Neosalanx_tangkahkeii	TAGGCACAGA	CCGAGGACTT	TGTCAAGGCC	CCCAGAACTC	TATCATATTT	TAACATAGCA	CGACAGTATT	GCGCCACCTA	GCCTT	
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#KJ499917_Protosalanx_chinensis	AGCTCGTAAT	CCTATTTATA	ATCTTATAAT	CTAACCCCTT	GCGTTGGGAC	GGCGCGGTTA	CTCAGTTTTT	CGTACACCTT	GCATA	
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#MW291629_Protosalanx_chinensis	ATCTTCACAT	TAATTATGTC	TTGTTTCAGC	GTACTTAAGT	ATATATGAAG	TCTGCCATT	TTGTTCGATT	AACGATTC..	
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The species name *Protosalanx hyalocranius* was used for the originally published mt genome KJ499917 [1]. However, *P. hyalocranius* is a synonym of *P. chinensis* [2]. Consequently, we use the species name *P. chinensis* for the mt genome KJ499917 to avoid any confusion. The *COI* (5585-5699), *ND4* (10173-11826), and *CR* (15622-16163) recombinant regions are highlighted in red bold. The recombinant regions are limited by flanking polymorphic sites and do not exactly correspond to the beginning and ending breakpoints detected by the program RDP4 [3]. Dots indicate nucleotide identity with the recombinant sequence (KJ499917). The hyphens represent deleted nucleotides. The numbers above the top sequence represent the position of segregating sites. Nucleotides are numbered from the beginning of the GenBank sequences (accession numbers see above).

References

1. Lu, C.; Gu, Y.; Li, C.; Cheng, L.; Sun, X.; Tang, F. Complete mitochondrial genome of clearhead icefish *Protosalanx hyalocranius* (Salmoniformes: Salangidae). *Mitochondrial DNA* **2016**, *27*, 514–515, doi:10.3109/19401736.2014.905834.

2. Zhang, J.; Li, M.; Xu, M.; Takita, T.; Wei, F. Molecular phylogeny of icefish Salangidae based on complete mtDNA cytochrome b sequences, with comments on estuarine fish evolution. *Biol. J. Linn. Soc.* **2007**, *91*, 325–340.
3. Martin, D.P.; Murrell, B.; Golden, M.; Khoosal, A.; Muhire, B. RDP4: Detection and analysis of recombination patterns in virus genomes. *Virus Evol.* **2015**, *1*, vev003, doi: 10.1093/ve/vev003.