Clarification of taxonomic assignment of smelt complete mitochondrial genome: GenBank accession number KP281293.1 (NC_026566.1)

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ABSTRACT
According to the reference data in GenBank, the complete mitochondrial genome KP281293.1 presumably belongs to Hypomesus o lidsus from China. The phylogenetic analysis based on the Cytb and Col genes of the smelt genus Hypomesus suggests that the Chinese specimen belongs to Hypomesus nipponensis. The difference in the studied region of mitogenome is low, 0.6%, which is in agreement with the values of intraspecific divergence for the smelts. The use of the sequence KP281293.1 as a marker for H. o lidsus will not help in improving the understanding of the taxonomic relationships gained from previous morphological studies and is phylogenetically misleading.

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The geographic distribution pattern of mtDNA sequence polymorphisms of H. o lidsus Pallas 1814, over most of the range in the Northwestern Pacific, was previously examined (Skurikhina et al. 2012). Having studied more samples, we found a mistake in the taxonomic identification of the complete mitochondrial genome of H. o lidsus from Bai et al. (2017). Incomplete phylogeny of the family Osmeridae has been recently published, including the mitogenomes of this smelt (Balakirev et al. 2018). However, taxonomic errors can lead to inaccurate phylogenetic conclusions. In the present study, we would like to warn the investigators against such mistakes.

The specimen KP281293.1 has a taxonomy ID (NCBI: txid240830) and presumably belongs to H. o lidsus from Yuqiao Reservoir, Tianjin, China (40°01’ N/117°54’ E). To explore the phylogenetic position of this specimen, phylogenies involving other smelt species were constructed using public Cytb and Col genes sequences. 119 specimens of H. o lidsus from nine different locations were included to place our findings within a broader phylogenetic group.

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include all specimens of *H. olidus* reported by Skurikhina et al. (2012) and Melnikova et al. (2018). All sequences were obtained from the Genbank/NCBI database (HQ115079-HQ115271, FJ205570-FJ205572, FJ010869-FJ010871, MK038781-MK038784, MK038788-MK038807, MK038813-MK038816, MK038818-MK038837, and KY400645-KY400647). The samples of smelts *H. nipponensis* and *H. japonicus* from the Olga Bay of the Sea of Japan (43°43′ N/135°15′ E) were included for comparison. The fish specimens are stored in the collection of Genetics Laboratory, National Scientific Center of Marine Biology, Vladivostok, Russia (www.imb.dvo.ru). The complete mitochondrial genome of *H. nipponensis* (HM106489.1) from Jingpo Lake, China (43°52′ N/128°56′ E) was added to the analysis. The total length of mtDNA nucleotide sequences was 1668 bp.

As shown in the maximum-likelihood tree (Figure 1), the specimen KP281293.1 was clustered with *H. nipponensis* with a very low level of sequence divergence ($D_{xy} = 0.006 \pm 0.002$), while all sequences of *H. olidus* proper formed a different cluster. The low level of sequence divergence was also detected within the group of *H. olidus* (0.0001 ± 0.0001 – 0.0024 ± 0.0010), significantly lower than that between KP281293.1 and *H. olidus* (0.1296 ± 0.0085).

Our results suggest that the specimen KP281293.1 belongs to *H. nipponensis*. With respect to *Hypomesus* phylogeny, the relationships between *H. olidus* and *H. nipponensis* are not yet clear (Ilves and Taylor 2009; Skurikhina et al. 2013). In this situation, the inclusion of the complete mitogenome KP281293.1 may cause a conflicting phylogenetic signal. The arguments for the erroneous taxonomic assignment by Bai et al. (2017) are the following. Of the three species (*H. japonicus*, *H. nipponensis*, and *H. olidus*) inhabiting the Sea of Japan basin, *H. olidus* is only found in its northern part (Chereshnev et al. 2001). We suppose that the specimen KP281293.1 was caught in China, where *H. olidus* is never found in natural populations.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

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