

Supplementary Caption

Original Data and files for calculation and simulation in paper by Redin, Kartavtsev “The Mitogenome Structure of Righteye Flounders (Pleuronectidae): Molecular Phylogeny and Systematics of the Family in East Asia”.

Figure 1S. BEAST-2 and FigTree topology reconstruction based on 13 PCG-sequences of 26 analyzed flounder representatives of the family Pleuronectidae with posterior probabilities implemented.

Details for the simulation of CA-based tree at current image given in the text, and basically, same as in Fig. 4. For the tree simulation $n=5 \cdot 10^7$ generation are used. Scale (bottom) shows branch length for the tree rooted at the out-group taxon *Paralichthys olivaceus*.

Figure 2S. The phylogram built by PhyloSiut software and its IQ-TREE utility for gene tree reconstruction based on 13 PCG-sequences of 26 analyzed flounder representatives of the family Pleuronectidae with the out-group taxon *Paralichthys olivaceus*.

Bootstrap support scores in $n=5000$ replications for IQ-TREE performed in the two modes, the Ultrafast Bootstrap (Hoang et al., 2018) and the SH-aLRT branch test (Guindon et al., 2010). They are implemented besides nodes with slash. The scale below phylogram shows the branch length.

Figure 3S. График распределения нуклеотидного разнообразия (P_i) на сайт по всей длине последовательностей 13 PCGs митогенома камбал семейства Pleuronectidae.

По оси Y дано распределение значений полиморфизма (diversity), P_i . Красным цветом показано распределение по нуклеотидным позициям (ось X) для значений P_i .

Figure 4S. График распределения попарных различий для 13 PCGs митогенома камбал семейства Pleuronectidae.

По оси Y дано распределение значений частот попарных различий, для 12 выделенных скользящих окон оценки дивергенции. Красным цветом показан диапазон значений k (ось X), зеленым цветом дано ожидаемое распределение для

значений k. Среднее число попарных различий (Average Number of Pairwise Difference) составило, k=1440.113.

Figure 5S. The phylogram built by MEGA-X software and its utility for ML-gene tree reconstruction based on 13 PCG-sequences of 26 analyzed flounder representatives of the family Pleuronectidae with the out-group taxon *Paralichthys olivaceus*.

The ML tree and topology support scores obtained through n=1000 replications throughout the tradition mode of the bootstrap test; the scores given besides the nodes. Numerals below the branches indicate the composition distance, CD (bias) calculated for 26 sequences in the analysis. CD is a measure of the difference in nucleotide composition for a given pair of sequences. It is one half the sum of squared difference in counts of bp or residues. MEGA computes and presents the CD per site, which is given by the total CD between two sequences divided by the number of positions compared, excluding gaps and missing data (MEGA-X help).

Table 1S, Supplement

File: Fl26seq-pt8-11401-123ps4.nex

Table 2S, Supplement

File: Fl26seq-pt8-123ps4-tip-r24b1-n=5E7-fix-pop-hm.xml

Table 3S, Supplement

File: Fl26seq-pt8-11401-123ps4.trees

Table 4S. Nucleotide content of 25 mitogenome sequences of PCGs among Pleuronectidae

Table 5S. Perdomain diversity and DNA varion data for 13 PCGs of 25 selected mitogenome sequences among representatives of Pleuronectidae family

Table 6S. TrN-distance-mtx-13PCRs-Pleuronectidae-taxa-ranked

Table 7S. TrN-distance-mtx-13PCGs-suborder-Pleuronectoidei-taxa-ranked

Table 8S. Test of substitution saturation for Pleuronectoidei PCGs mitogenome sequences

