

INTERNATIONAL SYMPOSIUM

MAPEEG-2015

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**MODERN ACHIEVEMENTS IN
POPULATION, EVOLUTIONARY AND
ECOLOGICAL GENETICS**

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STRUCTURAL FEATURES AND VARIATION OF MITOCHONDRIAL CONTROL REGION AMONG EELPOUTS (COTTOIDEI: ZOARCALES)

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The control region (CR) is a major non-protein-coding domain of mitochondrial DNA, which contains transcription promoters for both strands of mitochondrial genome as well as binding sites for transcription-replication machinery whereby the *D*-loop is formed, a vital structure for the existence of mitochondrial genome as a replicator. The origin and diversity of structure-functional elements of CR have been intensively investigated with massive recent involvement of new diverse taxa. In this study, we report the preliminary results on the analysis of eelpouts (the fishes of infraorder Zoarcales) CR structure and variation as well as apparent trends of their evolution.

Both intraspecific (28 sequences from *Stichaeus grigorjewi* Herzenstein, 1890) and infraorder (4 families from Zoarcales) levels have been covered in the analysis. CR sequences in *S. grigorjewi* as well as in other eelpouts are restricted by tRNAs *Pro* and *Phe*, which is consistent with the classic scheme among other vertebrates. The mean intraspecies genetic distance is 0.26 ± 0.25 . The nucleotide diversity landscape is not uniform with complete absence of variation in the central part. CR length is 862 bp. No length variation was observed. Three classic domains have been found in the CR structure of *S. grigorjewi*. In total 4 non-tandem putative termination associated sequences (TAS) are present at the 5' end of the CR. Central conservative domain contains full set of sequences previously observed in other vertebrates (represented in classic order CSB-A, CSB-B, CSB-C, CSB-D, CSB-E and CSB-F, in 3'-5' direction). Conservative sequences domain includes 3 common sequences (CSB-I, CSB-II and CSB-III, in 5'-3' direction).

At the infraorder level, the parallel decrease of CR length is observed from the basal to terminal branches, based on following scheme: *Stichaeus grigorjewi* (862 bp) → *Pholis fungi* (853 bp) + *Pholis crassispina* (853 bp) and *Lycodes toyamensis* (863 bp) → *Anarhichas denticulatus* (838 bp) → *Anarhichas minor* (837 bp) → *Anarhichas lupus* (835 bp). Therefore, the apparent trend among eelpouts CR structural evolution, taking into account the taxonomic representation, is the change of length, which is caused by the loss of the first (5' end) TAS sequence.