

## MARKER REGIONS OF THE GENOME FOR MOLECULAR DIAGNOSTICS OF *OPISTHORCHIIDAE* FAMILY

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Infectious diseases caused by representatives of the *Opisthorhidae* family rank 8th in terms of health concern in the world among all food parasites. According to FAO data, studies of representatives of the *Opisthorhidae* family rank first and range from 0.66 to 88.7%.

When performing a PCR analysis, a molecular marker plays an important role. In our studies, ribosomal genome clusters and mitochondrial genes were used as molecular markers.

In eukaryotic organisms, ribosomal genes are presented in the form of clusters located in groups on different chromosomes. Each cluster includes three ribosomal genes (18S, 5.8S and 28S), separated by spacer regions. The ribosomal gene cluster consists of a transcribed region, internal transcribed spacers (*ITS - Internal Transcribed Spacer*) and flanking external transcribed spacers (*ETS - External Transcribed Spacer*)

The ITS noncoding sequence differs greatly among closely related organisms and is therefore

used to classify parasites at the genus, species, and subspecies level. The ribosomal nuclear gene 5.8S forms the complete transcribed internal spacer region together with the molecular markers ITS1 and ITS2. This region of the genome is used in species studies of 19 families of digenetic flukes.

Mitochondrial genes are also one of the most commonly used mtDNA gene fragments in the molecular identification of the family *Opisthorchiidae*. The advantage of using COX in research is the high degree of mutation, which makes it possible to differentiate closely related species

The use of these genome regions makes it possible to quickly and accurately identify pathogens of the family *Opisthorchiidae*, even for such individuals with practically indistinguishable morphological stages of the life cycle, such as parasite eggs and capsules in fish muscles. Therefore, in our studies, primers were used for the nuclear regions of ribosomal DNA ITS1, ITS2 and mitochondrial genes COX1, COX3.