

Insights into *Opisthorchis felineus* genome organization

Maslov D.E.^{1,2*}, Ershov N.I.¹, Pakharukova M.Y.^{1,2}, Mordvinov V.A.¹

¹ *Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

² *Novosibirsk State University, Novosibirsk, Russia*

* *bochlit2@gmail.com*

Key words: genome assembly, Hi-C, Opisthorchiidae, Rabl configuration

Motivation and Aim: *Opisthorchis felineus* (cat liver fluke) is a member of epidemiologically important liver trematodes, is one of the causative agents of human opisthorchiasis. An estimated 1.2 million people are infected with *O. felineus* and 12.5 million are at risk of infection [1, 2]. Liver fluke infection is known to adversely affect bile ducts and gall bladder and is recognized as one of the major factors of risk of cholangiocarcinoma [3, 4]. The vast majority of genome assemblies of flatworms, as well as non-model organisms in general, are built based on short-read sequencing and often fragmented. The only available draft assembly of *O. felineus* is no exception. Genome assembly fragmentation hinders the study of the genome functional organization and excludes any possibilities of analyzing spatial organization. The latter, although being thoroughly studied in vertebrate species for a decade now, is still poorly investigated in flatworms.

Results: We obtained a highly-continuous genome assembly of *O. felineus* utilizing an approach integrating long-read sequencing data (PacBio Sequel) and information on the physical proximity of genomic loci generated by Hi-C method. The assembly consists of 7 separate scaffolds reproducing haploid karyotype of the parasite represented by two larger and 5 lesser submetacentric chromosomes. The assembly completeness is further supported by a comprehensive gene annotation. We were able to identify Rabl-like chromosome configuration which contrasts *O. felineus* to vertebrates, which are predominantly characterized by more prominent chromosome territories, at the same time this feature is not unique to *O. felineus* and similar pattern had been previously described for another Opisthorchiidae species *Clonorchis sinensis*. Additionally, low instructiveness of eigenvector-based compartmentalization for chromatin transcriptional activity and inconsistency with observable spatial features indicates a need for more informative compartmentalization metric for species exhibiting similar patterns of chromatin organization.

Conclusion: A highly continuous and complete *O. felineus* genome provides a basis for delineating general peculiarities of its spatial-functional organization using Hi-C. Rabl-like chromosome configuration is a predominant characteristic of *O. felineus* chromatin organization, similar to several other non-vertebrate species.

Acknowledgements: The study was supported by the State Budget Project FWNR-2022-0016.

References

1. Keiser J., Utzinger J. Emerging foodborne trematodiasis. *Emerg Infect Dis.* 2005;11(10):1507-1514.
2. Fedorova O.S., Fedotova M.M., Zvonareva O.I., Mazeina S.V., Kovshirina Y.V., Sokolova T.S. et al. Opisthorchis felineus infection, risks, and morbidity in rural Western Siberia, Russian Federation. *PLoS Negl Trop Dis.* 2020;14:e0008421.
3. Pakharukova M.Y., Mordvinov V.A. The liver fluke Opisthorchis felineus: Biology, epidemiology and carcinogenic potential. *Trans R Soc Trop Med Hyg.* 2015;110:28-36.
4. Schistosomes, liver flukes and Helicobacter pylori. IARC Working Group on the Evaluation of Carcinogenic Risks to Humans. Lyon, 7-14 June 1994. IARC, 1994;61:1-241.