

Viromic studies of aquatic invertebrates

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In recent decades, research in the field of aquatic virology has reached a new level due to the development of new molecular genetic approaches (high-throughput sequencing, metagenomic analysis, etc.). Despite this fact, the study of viruses of aquatic organisms is one of the little-studied areas. Until recently, researchers paid the main attention to the study of viral diseases of commercial and artificially grown (aquaculture) animals (fish, mollusks and crustaceans). Therefore, in general, the diversity of viruses of aquatic invertebrates (especially freshwater ones) remains practically unknown.

This paper presents a review of new data (both published and personal) on the diversity of viruses circulating in the organisms of marine and freshwater (including Lake Baikal) invertebrates (mollusks, etc.), which was obtained using metagenomic and/or transcriptome analysis. We discuss on various methodological approaches to the study of viromes of aquatic organisms (including those used in our studies), including methods for sampling and primary sample preparation, isolation and purification of viral particles and nucleic acids, preparation of libraries of total viral DNA/RNA and their sequencing as well as methods for bioinformatics processing of metagenomic datasets.

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