METAGENOMICS OF BACTERIOPHAGES ISOLATED FROM MARINE SEDIMENTS

M. Jakubowska¹, A. Jurczak², M. Łoś², B. Wróbel¹

¹Genetics and Marine Biotechnology Department, Institute of Oceanology Polish Academy of Sciences, Sopot, ²Department of Molecular Biology, Faculty of Biology, University of Gdansk, Gdansk, Poland

Background: In the marine environment, it is estimated that there are about $10^9$-$10^{13}$ bacteriophage particles and $10^5$ viral strains per kg of sediment. We use a metagenomic approach to investigate the diversity of phages in the marine sediments. The metagenomic libraries are searched for genes coding for antibacterial and antibiofilm activities.

Objectives:

1. Bacteriophage isolation from marine sediments.
2. Viral particle analysis using electron and fluorescent microscopy.
3. Construction of metagenomic libraries.

Methods:

1. Phage particle isolation and purification (extraction, filtration, precipitation).
2. Electron microscopy.
3. Fluorescent microscopy.
5. Construction of DNA and cDNA libraries.

Results: The modified method for bacteriophages isolation and purification developed in this work resulted in high concentration of viral particles, which was confirmed by electron and fluorescent microscopy. Some phages were observed to have unusually long tails, up to 1 μm in length. It is possible that this is the result of high concentrations of EPS (the main component of bacterial biofilm) in the marine sediments. The method for the construction of phage metagenomic library developed in this work proved to be very efficient. It allows to obtain about 1500-2000 clones with inserts about 500-1500 bp in length. Preliminary sequencing shows that a high percentage of inserts is similar to known phage sequences.

Conclusions: We have optimized the procedure of isolation and purification of bacteriophages from marine sediments and a method of construction of phage metagenomic libraries. Our preliminary analysis indicates high diversity of phages in the marine environment.