Are Aquatic Viruses a Biological Archive of Genetic Information from Universe?

F. Toparceanu (1), Gh. T. Negoita (2), I. I. Nita (2), and D. Sava (3)

(1) Institute of Virology, Antiviral Therapy, Bucharest, Romania (florisci@hotmail.com), (2) Romanian Polar Research Institute, Bucharest, Romania, (3) Faculty of Natural and Agricultural Sciences, Constanza, Romania

After 1990, when the viruses were admitted as the most abundant lifeforms from aquatic environments, it became obvious that viral lysis had an essential role on release and recycling of nutrients. Studies on cellular cultures and modeling suggest that this is an important quantitative process.

The viruses from oceans represent the widest source of genetic diversity on the Earth, uncharacterized yet. The ancient lifeforms records stretching back a million years are locked in ice caps. The trend of glaciers melting as effect of actual climate change will promote the release of ancient viruses from ice caps. The increasing of the freshwater layer led to the replace of some algae species by others.

Law-Racovitza Station (69°23’S 76°23’E) from East Antarctica (Larsemann Hills Oasis) offers opportunities to study the Antarctic marine ecosystem, as well as archaic aquatic ecosystems from this area (150 lakes and waterways resulted from ice and snow melting during the austral summer). According to Law-Racovitza Station Scientific Program, we are performing studies regarding the effect of climate changes on virus-algae host relationship in these aquatic ecosystems. Phycodnaviruses, that infect the eukaryote algae, are comprised of ancient genes and they are considered a “peek” of genetic diversity useful in biological studies and exobiology regarding the evolution of genetic sequencing.

The latest discoveries of the giant aquatic viruses open the unexpected perspectives for understanding the role of viral infection in global ecosystem; beyond the old concept which considered that the viruses were only etiological agents of human, animals and plants illnesses. The aquatic viruses which infect microalgae contain similar genes of other viruses, bacteria, arhebacteria and eukaryotes, all of them being on the same genome.

Which is the signification of enormous abundance of viruses and excessive diversity of genetic information encoded by viruses? There is the possibility that the viruses to be a biological archive which contains all genetic information of the whole Earth? So, there are a lot of questions and we are attempting to find answers in the present work which will be examined in the framework of the project entitled “The structure and dynamics of polar ecosystems: interhemispheric comparisons of micro, macroflora and biogeochemical processes in relation to climate change” (PolarCLIMATE programme of ESF PP-039/24.11.2008) coordinated by Romania.