



## Review

## Viruses in Antarctic Habitats: Occurrence and Ecological Importance

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### Abstract

The review describes the spreading of viruses in Antarctic ecosystems including terrestrial, marine, and freshwater habitats. The great attention is paid to virus infections in Antarctic animal and plant populations. Observation on viruses in Antarctic ecosystems might contribute for their diversity and systematics, as well as for viral ecology. Comparison of the detected viruses with the well-known viruses, using modern methods, reveals some structural differences in their nucleic acids and proteins. Several new virus species unknown in temperate geographic regions were described. Distribution of viruses in Antarctica may elucidate their migration, potential reservoirs, and hosts. Observations on viruses would explain the processes of virus infections, survival, pathogenicity, and medicine.

**Key words:** viruses, Antarctica, terrestrial and aquatic ecosystems, animal and plant hosts, bacteriophages

### Резюме

Обзорът описва разпространението на вируси в екосистемите на Антарктида, включително земните, морските и пресноводните находища. Особено внимание е обърнато на вирусните инфекции в животинските и растителните популации в този континент. Наблюдението на вирусите в антарктическите екосистеми би могло да допринесе за проучване на техното разнообразие и систематика, както и за екологията им. Извършено е сравнение на изолираните в Антарктида вируси с познатите вируси чрез използване на съвременни методи, разкриващи някои структурни разлики в техните нуклеинови киселини и протеини. Описани са няколко нови вида вируси, непознати в географските региони с умерен климат. Разпространението на вирусите в Антарктида би могло да осветли тяхната миграция, потенциални резервоари и гостоприемниците им. Наблюденията върху вирусите в Антарктида би могло също така да обясни някои процеси във вирусните инфекции, техното преживяване, патогенност и медицинско значение.

### Introduction

Viruses occupied an extremely important place in the life of our planet. They were proved as causative agents of more than 93% of infectious diseases. Moreover, they are etiologically connected with a substantial part of the neoplasms. It is noteworthy to stress the increasing role of emerging viral infections in the end of 20<sup>th</sup> and the beginning of the 21<sup>st</sup> century. As principal factors in the appearance of novel virus infections could be considered (i) viral adaptation and evolution: viruses more than all other microorganisms possess the capability to adapt to their hosts, to the environment, and to new ecological niches supplied by the man when he invades their territory; (ii) the increase and the movement of the global population (the substan-

tially increased transport communications); (iii) human activities; and (iv) the ecological factors and changes in the environment. The changes in the environment as a result of the human intervention lead to new ecosystems. During the last years we are witnesses of many examples of a global menace for the human population by diseases with origin in other species of the animal world - the so-called zoonoses. Their emergence is strongly dependent on both the climate changes and the environment changes caused by the human activities.

Tropical and subtropical areas of the Earth are the main objects of the research on the emerging viral infections, predominantly arboviral infections, as well as on another studies connected with the sources of emerging and re-emerging viral in-

fections on a global scale. A great number of investigations are directed to the clearing up of the factors contributing to the spread of viruses and the virus infections in the Earth areas with a temperate climate (mainly Europe and North America). In contrast with the latter, studies on viral progenies in the zones around poles - Arctica and Antarctica - are comparatively scarce. There is a reason to believe that viral progenies from these zones could be involved in the processes of the spreading of the viral infections around the globe.

The genome structure of viruses ensures their replication in different ecosystems, including terrestrial, marine, and freshwater habitats, and live in microbial, plant, and animal hosts. A review has already been published on the role of viruses in microbial communities in the Antarctica (Pearce and Wilson, 2007). However, a systematic view on the viruses in animal hosts in Antarctic area is not done. Besides, little data exist on viruses associated with plants, including mosses (Polischuk *et al.*, 2007), although viruses have been observed in *Stilborcarpa* (Skotnicki *et al.*, 2003).

All this shows a need for profound researches on viruses found in the polar areas, predominantly in Antarctica, their reproductional dynamics, survival, and persistence in different substrates and hosts. This is the main task of the present review.

### Viruses in Animal Hosts

The possibility of the introduction of infectious agents to Antarctica animal life and its spread from Antarctica to other continents is discussed by the Antarctic Treaty. The migratory birds could be a potential vector for infectious agents.

Data on the occurrence of avian pathogen **infectious bursal disease virus** (IBDV) in Antarctic penguins near the centers of human activities indicated a possibility of virus introduction (Gardner *et al.*, 1997). Although IBDV is a pathogen of domestic chicken (*Gallus domesticus*), antibodies have been found in a variety of world bird species (Wilcox *et al.*, 1983). IBDV was detected in emperor (*Aptenodytes forsteri* Gray) and Adélie (*Pigoscelis adeliae*) penguins.

**Influenza A viruses** and **paramyxoviruses** are widely distributed among wild birds in temperate regions which play a role in the spread of pathogenic paramyxoviruses and Newcastle disease virus (NDV). There is evidence that aquatic wild birds are the reservoir of all influenza viruses for avian and mammalian species, including humans (Webster *et al.*, 1992).

**Paramyxoviruses** have been found in Adélie penguins at Cape Bird and Casey, some 4 000 km away, in Antarctica (Morgan and Westbury, 1981, 1988; Austin and Webster, 1993). Viruses isolated from a cloacal swab taken from an adult penguin were classified as paramyxoviruses according to their morphology (Morgan and Westbury, 1981; Alexander *et al.*, 1989). On Macquarie Island - a sub-Antarctic island in the Southern Ocean - six paramyxoviruses, including a low pathogenic strain of NDV, were also isolated from cloacal swabs collected from 831 penguins of four species (Morgan *et al.*, 1981; Morgan, 1988). Samples of 100 penguins from King George Island were tested by real-time polymerase chain reaction (PCR), two of which have been positive for NDV (Thomazelli *et al.*, 2010). Antibodies to a **flavivirus** and an avian paramyxovirus, different from NDV, were detected in three of the four penguin species. The detection of an avian paramyxovirus from an apparently healthy Adélie penguin, and the presence of paramyxovirus and influenza virus antibodies in penguins and skuas, *Stercorarius skua maccormicki* (Saunders), demonstrated that these viruses may infect the avifauna of the Ross Sea Dependency (Austin and Webster, 1993). Sera from 1002 penguins of four species on Macquarie Island, a sub-Antarctic island in the Southern Ocean, were examined for antibody to NDV and other avian paramyxovirus, influenza A virus, alphavirus, and flavivirus. Sera from 6% of royal penguins sampled gave positive reactions to NDV, while to the other three species were negative. Six paramyxoviruses, different from NDV, were obtained from swabs taken from royal and king penguins at two widely separated sites on the island. Miller *et al.* (2010) isolated a paramyxovirus from rockhopper penguins (*Eudyptes chrysocome*) in Falkland Islands and suggested that this virus represented a new avian paramyxovirus (APMV) group - APMV10. Its viral hemagglutination (HA) activity was not inhibited by antisera against any of the nine defined APMV serotypes.

Penguin blood samples collected at Bird Island, a sub-Antarctic South Georgia Island, gave serologic indications that **influenza A virus** is present amongst these penguin species (Wallensten *et al.*, 2006). Baumeister *et al.* (2004) showed an infection of the birds, giant petrels, *Macronectes giganteas*, and penguins in Southern Shetland Islands with influenza A viruses of the subtypes A (H1), A (H3), A (H7), and A (H9). Recently, avian influenza virus A(H11N2) was isolated from Adélie penguins (<http://mbio.asm.org/content/5/3/e01098-14>).

full.pdf+htm). This virus is considered as a representative of evolutionary distinct lineage of avian influenza A virus (Hurt *et al.*, 2014).

Edison Durigon who coordinates a group of hunters of dangerous viruses in Sao Paulo, Brazil, that monitors birds and mammals from the Amazon to the subpolar islands said on August 23, 2009, that they have the first evidence that influenza is circulating among penguins in Antarctica. His new data, not yet submitted to the scientific community, indicate that the presence of influenza in this region is high, between 8-10% in a study population of one hundred animals. In other communities of birds from the icy continent, which have been analyzed, the occurrence of the same virus usually alternates around 1%. None of Antarctic penguins studied had symptoms of the disease.

The human population in Antarctica increases, because of the presence of the scientists and the growth of tourism in the region. Almost 40 000 tourists visited the continent only in the summer of 2008/2009, according to data from IAATO (International Association of Tour Operators in Antarctica). This is coupled with the fact that different **influenza virus** strains like to swap genes between each other, which sometimes leads to occurrence of a more aggressive virus. Thus, a potentially harmful scenario was riding possibly transforming the Antarctic in a nest of influenza virus strains, which could migrate to another regions. Evidently, the polar regions deserve an increased attention on the transmission of viruses (from who and to whom the viruses are passed), or what type of influenza virus is in circulation (seasonal human or avian H5N1). The penguins live along the international monitoring of the influenza viruses. According to Jansen Allen from the Durigon's research group the studies conducted so far do not allow us to say with certainty the side of migratory birds such as skuas and giant petrels - the analysis of their faeces were also positive for influenza - as well as of mammals such as elephant seals and sea lions (<http://www1.folha.uol.com.br/folha/c...6u613636.shtml>). Penguin blood samples collected at Bird Island, a sub-Antarctic South Georgia Island, gave serologic indications that influenza A viruses present amongst these penguin species (Wallensten *et al.*, 2006).

As concerns DNA containing viruses in Antarctica, the group of Alcami isolated in Antarctic lakes numerous unknown DNA viruses varying in size (Lopez-Bueno *et al.*, 2009). Later, a novel adenovirus species was isolated from Chinstrap penguins (*Pygoscelis antarctica*), designated Chinstrap

penguin adenovirus type 1 (CSPAdV-1) (Lee *et al.*, 2014). A novel papillomavirus among the Adélie penguins (*Pygoscelis adeloae*) in Ross Island was also found by an Australian research group (Varsani *et al.*, 2014). Antibodies to **poxvirus** were found in Antarctic Peninsula by Shearn-Boschler *et al.* (2008).

Have *et al.* (1991), and Heidejorgensen *et al.* (1992) detected evidence for prior infection by phocine **distemper virus** in Arctic and Antarctic seal populations, while Harder *et al.* (1991) found the antibodies against phocine **herpesvirus** in sera from Antarctic seals. Stenvers *et al.* (1992) reported that Weddell and crabeater seals in the Antarctica had high neutralizing titres to phocine, canine, and feline herpesviruses. In the same time, antibodies to canine distemper virus were detected in Antarctic seals by Bengtson *et al.* (1991). Harder *et al.* (1991) pointed that spreading of viruses may be done by nomadic movements of crabeater seals in a wide geographical region.

Rockhopper (*Eudyptes chrysocome*), royal (*Eudyptes schlegeli*), and king (*Aptenodytes patagonicus*) penguins living in Macquarie Island, a small sub-Antarctic island, are harbours for ticks (*Ixodes uride*). It was established that associated with penguin ticks carried four genera **arboviruses**: a flavivirus, an orbivirus, a phlebovirus, and a nairovirus (Morgan, 1988; Major *et al.*, 2009). The **flavivirus** was nearly identical to Gadgets Gully isolated 30 years ago, which showed the remarkable genetic stability of this virus. The authors named the detected **orbivirus** as Sandy Bay virus and considered that the nearest relative to the orbivirus is the Scottish Broadhaven virus, and it provided only the second available sequences from the Great Island orbivirus serogroup. For **phlebovirus** they propose the name Catch-me-cave virus and believe that it is distinct, but related to the previously isolated Precarious Point virus showing homology with the Finnish Uukuniemi virus. These viruses, isolated from penguins, provided the second and third available sequences for the Uukuniemi group of phleboviruses. The **nairovirus** named Finch Creek virus was shown to be related to the North American Tillamook virus, the Asian Hazara virus, and Nairobi sheep virus. Authors concluded that Macquarie Island penguins carried arboviruses from at least four of the seven arbovirus-containing genera, with related viruses often found in the Northern Hemisphere

Polar skuas, *Catharacta maccormicki* Saunders, living around Antarctic Davis Station, had no

ticks and the authors were not able to isolate any viruses (Miller *et al.*, 2008). It was established that skuas were seropositive to some avian viruses: 16.9% had antibodies to infectious bursal disease virus and 10.5% were seropositive for Newcastle disease. One percent of skuas had antibodies to avian influenza and there was no evidence of egg drop syndrome, but 27.8% had antibodies to flaviviruses. Perhaps, polar skuas encounter a variety of pathogens either in Antarctica or during their migration in the non-breeding season.

**Viruses in seals.** Tryland *et al.* (2005) isolated from skin lesion on the neck of a Weddell seal (*Leptonychotes weddellii*), in Queen Maud Land, Antarctica, proliferative papilloma-like structures. Electron microscopy revealed typical **parapoxvirus** particles.

New strains of murine cytomegavirus in wild mice were isolated by Booth *et al.* (1993) and arboviruses, including both new flavivirus and bunyavirus from *Ixodes uriae* detected at Macquarie Island (Doherty *et al.*, 1975; St George *et al.*, 1985). Linn *et al.* (2001) isolated a novel **alphavirus** from the louse *Lepidophthirus macrorhini*, collected from southern elephant seals (SES), *Mirounga leonina*, on Macquarie Island, Australia. The virus possessed classic alphavirus ultrastructure and appeared to be serologically different from any known Australasian alphaviruses. All Macquarie Island elephant seals tested had neutralizing antibodies against the virus. Sequence analysis demonstrated that the SES virus segregates with the Semliki Forest group of Australasian alphaviruses. Phylogenetic analysis of the known alphaviruses suggests that they might be grouped according to their enzootic vertebrate host class. The SES virus is an arbovirus of marine mammals and can be transmitted by lice.

Czaker (2002) found an unknown *Aggregata* sp. in the renal organ of an antarctic *Benthocopus* sp., when it was inspected for the presence of dicymid mesozoans. Merozoites invaded the renal epithelium, while sporogony stages resided in the submucosal connective tissue. Individuals of all developmental stages were found to be infected with unknown virus-like particles. They are spherical in shape, non-enveloped, and measuring approximately 30 nm in diameter, and could be observed in the nuclei as well as within the cytoplasm. Virus-like particles had a feature to arrange in paracrystalline arrays. No pathogenic effect on the parasites was detected. Based on the host specificity, size, morphology, and histochemical analysis, which sug-

gested the putative viral genome as RNA, a relationship with *Totoviridae* was assumed.

### Viruses in Plants

Skotnicki *et al.* (2003) described plant *Stilborcarpa* mosaic bacilliform badnavirus (SMBV) from Macquarie Island. Barley yellow draft virus-PAV was isolated in the sub-Antarctic Kerguelen Islands, two new luteovirus species been proved (Svanella-Dumas *et al.*, 2013). Plant samples of four moss genera - *Polytrichum*, *Plagiategium*, *Sanionia*, and *Barbilophozia*, and one plant species, *Deschampsia antarctica* - were collected, and they were subjected to enzyme-linked immunosorbent assay of testing for the presence of common plant viruses (Polischuk *et al.*, 2007). Samples of *Barbilophozia* and *Polytrichum* mosses contained antigens of viruses from the genus *Tobamovirus*, tobacco mosaic virus, and cucumber green mottle mosaic virus, which normally parasitize. Viral agents mainly from order *Caudovirales* were found in soil samples (Polischuk *et al.*, 2007).

### Viruses and Bacteriophages in Polar Aquatic Ecosystems

It was established that viruses are ecologically significant component of water saline and fresh environments (Hennes *et al.*, 1995; Weinbaur and Hofle, 1998; Wilhelm and Smith, 2000). Viruses that infect eukaryotic phytoplankton are an important member of aquatic ecosystems and they control a number of potential host species, however in lakes they remain largely unobserved yet. Although certain virus antibodies have been found, the presence of viruses is difficult to evaluate - only a small number of disease-causing viruses were isolated (Barbosa and Palacios, 2009).

Antarctic lakes are extreme ecosystems in which viruses may be important in controlling microbial community dynamics. Kepner *et al.* (1998) showed that water samples collected from four ice-covered Antarctic lakes contained high densities of extracellular viruses. Majority of these viruses were found to be morphologically similar to double-stranded DNA viruses that are known to infect algae and protozoa. The abundance of planktonic viruses indicates that viral lysis may be a major factor in the regulation of microbial populations in these extreme environments. Water samples from fresh-water Antarctic lakes on Signy Island (in the South Orkney Islands) contained virus-like particles (VLP), ubiquitous, morphologically diverse, and abundant, with high concentrations ranging

from  $4.9 \times 10^6 \text{ ml}^{-1}$  to  $3.1 \times 10^7 \text{ ml}^{-1}$ . The hosts included bacteria, cyanobacteria, and eukaryotic algae. In addition, an unusually large virus morphotype was observed with a head diameter of  $370 \times 330 \text{ nm}$  and a  $1.3 \text{ }\mu\text{m}$  long tail (Wilson *et al.*, 2000). Lisle and Priscu (2004) showed that in McMurdo Dry Valleys of Antarctica lakes total bacterial abundances ranged from  $3.8 \times 10^4$  to  $2.58 \times 10^7 \text{ cells ml}^{-1}$  and VLP abundances ranged from  $2.26 \times 10^5$  to  $5.56 \times 10^7 \text{ VLP ml}^{-1}$ . VLP abundances were significantly correlated ( $p < 0.05$ ) with total bacterial abundances, bacterial productivity, chlorophyll *a*, and soluble reactive phosphorus, while lysogenic bacteria, determined by induction with mitomycin C, made up between 2.0% and 62.5% of the total population of bacteria. The contribution of viruses released from induced lysogens was  $< 0.015\%$  of the total viral production rate. Carbohydrate and protein forming organic aggregates in lake water were abundant and were heavily colonized by bacteria and VLPs. VLP abundances in nine freshwater to saline lakes in the Vestfold Hills, Eastern Antarctica, were determined by Laybourn-Parry *et al.* (2001). In the ultra-oligotrophic to oligotrophic freshwater lakes VLP abundances ranged from  $1.01$  to  $3.28 \times 10^6 \text{ ml}^{-1}$  in the top 6 m of the water column, while in the saline lakes the range was between  $6.76$  and  $36.5 \times 10^6 \text{ ml}^{-1}$ . The lowest value was detected in Ace Lake and the highest value in hypersaline Lake Williams.

Virus-to-bacteria ratios were lowest in the freshwater lakes and highest in the saline lakes. Divergent morphologies among VLP was observed, including phages with short (*Podoviridae*) and long tails, icosahedral viruses of up to  $300 \text{ nm}$  and star-like particles of about  $80 \text{ nm}$  diameter. In these ecosystems dominated by microbes, no correlation between VLP and bacterial numbers was found. There was a significant correlation between VLP abundances and dissolved organic carbon concentration. The data indicated that viruses attack bacteria and protozoan species. VLP numbers in the freshwater lakes were lower than values indicated for lower latitude systems. Those in the saline lakes were comparable with abundances found from other Antarctic lakes, and were higher than most values published for lower latitude lakes and many marine systems. S awstr om *et al.* (2008a, b) studied distribution of VLP in ten lakes in the Vestfold Hill, Antarctica, and detected lysogeny, determined with mitomycin C only in one of the lakes, indicating that viral replication was occurring predominately via the lytic cycle.

Principal component analysis and confirmatory correlation analysis of individual variables confirmed that high abundances of VLP occurred in lakes of high conductivity with high concentrations of soluble reactive phosphorus and dissolved organic carbon. In lakes, possessing high concentrations of chlorophyll *a*, intact bacteria, and rates of bacterial production, viruses-to-bacteria ratios were established. Authors concluded that viral abundance in the Antarctic lakes was determined by the trophic status of the lake and the resultant abundance of intact bacterial hosts. Viral abundance in two large ultraoligotrophic freshwater lakes (Lake Druzhby and Crooked Lake) in the Vestfold Hills, Eastern Antarctica, ranged from  $0.16$  to  $1.56 \times 10^9 \text{ particles l}^{-1}$  and bacterial abundances ranged from  $0.10$  to  $0.24 \times 10^9 \text{ cells l}^{-1}$ , with the lowest bacterial abundances noted in the winter months (S awstr om *et al.*, 2007). Virus-to-bacteria ratios (VBR) were consistently low in both lakes ranging from 1.2 to 8.4.

Lysogenic bacteria were determined by induction with mitomycin C. In Lake Druzhby and Crooked Lake, lysogenic bacteria made up between 18% and 73% of the total bacteria population. Bacterial production ranged from  $8.2$  to  $304.9 \times 10^6 \text{ cells l}^{-1} \text{ day}^{-1}$  and lytic viral production ranged from  $47.5$  to  $718.4 \times 10^6 \text{ virus-like particles l}^{-1} \text{ day}^{-1}$ . In the winter months, there was a high contribution from viruses when  $> 60\%$  of the carbon supplied to the dissolved organic carbon (DOC) pool (i.e., autochthonous sources), originated from viral lysis while during the summer  $< 20\%$  originated from viral lysis.

Madan *et al.* (2005) investigated viral and microbial loop dynamics in three saline lakes: Highway Lake (salinity of  $4\text{‰}$ ), Pendant Lake (salinity of  $19\text{‰}$ ), and Ace Lake (salinity of  $18\text{‰}$ ) in order to assess the importance of viruses in extreme, microbially dominated systems. VLP showed no clear seasonal pattern, with high concentrations occurring in both winter and summer, ranging from  $0.89 \times 10^7 \pm 0.038$  to  $12.017 \times 10^7 \pm 1.28 \text{ ml}^{-1}$ . VLP abundances was connected with lake productivity based on chlorophyll concentrations. Pendant Lake, the most productive of the three lakes, supported the highest bacterial biomass, while the virus-to-bacteria ratios were higher in Ace Lake (range  $30.58 \pm 3.98$  to  $80.037 \pm 1.6$ ). The heterotrophic nanoflagellates of Highway Lake (dominated by the marine choanoflagellate *Diaphanoeca grandis*) showed a positive correlation with VLP. Highest rates of lysogeny - up to 32% in Pendant Lake and 71% in Ace Lake - were detected in winter and

spring, while there was no or lower lysogeny in the summer (Laybourn-Parry *et al.*, 2007).

In winter, VLP persisted in cold, dark water. High VLP concentrations and high VBR indicated that viruses, most of which were bacteriophages, are a major habitant within the microbial communities in extreme saline lakes. Variability in abundance of VLP, VLP decay rates, and prokaryotic mortality due to viral infection were determined in three Antarctic areas: Bellingshausen Sea, Bransfield Strait, and Gerlache Strait (Guixa-Boixereu *et al.*, 2002). VLP abundance showed very small spatial variability in the three areas and decreased from the surface to the bottom. Low seasonal variability in VLP abundance was found when comparing each area separately. Prokaryotic mortality due to viral infection was always higher than the one due to bacterivores.

To comprehend the nature of virus-host interaction in the sea, Sullivan *et al.* (2005) sequenced and characterized DNA genomes of three marine phages. One of them is podovirus and the other two are myoviruses. The marine phages are similar to two terrestrial phages, T4 and T7, which infect *Escherichia coli*, but also carry genes that appear specially adapted to infecting photosynthetic bacteria *Prochlorococcus* in nutrient-poor oceans. All three cyanophages contain photosynthetic-related genes and, thus, the virus helps the host maintain photosynthesis during infection. Toparceanu and Negoita (2007) investigated water samples from Lasermann Hills. The latter samples contained algal virus-like particles (PBCV). Some of them were identified and sequenced: chlorovirus (PBCV-1), 331 kb, 375 genes, with host *Chlorella*; Ectocarpus siliculosus virus (ESV-1), 336 kb, 231 genes, with host *Ectocarpus siliculosus*; coccolithovirus (EHV-86), 407 kb, 472 genes, with host *Emilliana huxleyi*. In these viruses 14 ancient genes were detected. The scientists revealed also prasinovirus (MPV-1), with host *Micromonas pusilla*, primnesiovirus (CBV), with host *Chrysochromulina brevifilum*, and rhabdovirus (HAV-1), with host *Heterosigma akashiwo*. Lopéz-Bueno *et al.* (2009) indicated that the genetic structure of an Antarctic lake viral community revealed unexpected genetic richness distributed across the highest number of viral families. Antarctic virus assemblage had a large proportion of sequences related to eukaryotic viruses, including phycodnaviruses and single-stranded DNA (ssDNA) viruses not previously identified in aquatic environments. The authors revealed that the transition from an ice-covered lake in spring to an openwater

lake in summer led to a change from ssDNA to a double-stranded DNA-virus-dominated assemblage, which is possibly a seasonal shift in host organisms.

Borriss *et al.* (2003) isolated three host-specific bacteriophages from Arctic sea ice and melt pond samples collected north-west of Svalbard (Arctic). They belonged to the tailed, double-stranded DNA phage families *Siphoviridae* and *Myoviridae*. Their bacterial hosts exhibited the greatest similarity to the species *Shewanella frigidimarina*, *Flavobacterium hibernianum*, and *Colwellia psychrerythraea*.

As an unusual discovery could be considered the isolation by R. Cavicchioli and coll. (Yau *et al.*, 2011; Pyper, 2011) of a virophage, a virus that attacks viruses, from an extremely salty Organic Lake in Eastern Antarctica, named Organic Lake Virophage (OLV). It was established that this virus kill phycodnaviruses (Zablocki *et al.*, 2014).

### **Impact and Importance of the Studies on Antarctic Viruses**

Studies on the levels of virus-induced mortality in Antarctica manifested the greatest impact of viral infection occurred under oligotrophic conditions in alpine lakes (Murray and Eldridge, 1994; Laybourn-Parry *et al.*, 2001; S awstr om *et al.*, 2007). A higher virus-to-bacteria ratio has been showed for eutrophic waters (Bratbak *et al.*, 1990). Viruses in Antarctica influenced biochemical and ecological processes as nutrient cycling, bacterial and algal biodiversity, algal bloom control, and genetic transfer.

Antarctica provides a good source of new organisms and model virus-host associations. They are often trapped in glacial ice and subglacial lakes. Conditions in Antarctica create the selection pressures including temperature, nutrient limitation, desiccation, and non-ionizing radiation. Specific environmental stress on microbial population communities can be used in observations of global climatic changes. Infectivity of free viruses may be lost by solar radiation (Suttle and Shen, 1992; Wommack *et al.*, 1996). Viruses participate in the maintenance of species diversity and genetic exchange.

By processes of lysogeny and pseudolysogeny the phage population may be maintained. Viruses in Antarctic lakes play an important part in controlling microbial community dynamics. High abundances of VLP occurred in lakes with high concentrations of soluble reactive phosphorus and dissolved organic carbon. Sullivan *et al.* (2005)

showed that marine phages, living in lakes and controlling the microbial dynamics, possess genes that appear specially adapted to infecting photosynthetic bacteria *Prochlorococcus* and, thus, the virus favours the host photosynthesis during infection. López-Bueno *et al.* (2009) revealed that the viruses in lakes have a great flexibility of DNA expressing in case of transition of single-stranded DNA to double-stranded DNA-virus-assemblages in dependence of season - spring or summer.

Observations on viruses in Antarctica are important for their diversity and systematics. Comparison of detected viruses with well-known viruses using modern methods reveals some differences in cell structures: protein and nucleic acids. All this allows determination of the new species unknown in temperate geographic regions. These investigations are contributions in virus systematic and microbial ecology. Distribution of viruses in Antarctica may elucidate their migration, potential reservoirs, and hosts. Observations on viruses would explain the processes of virus infection, survival, pathogenicity, and medicine.

Investigations in the Antarctic area contribute in another highly fundamental scientific domain. Researchers on one of the subglacial lakes, Lake Ellsworth, situated in West Antarctic Ace Shelf, believe some of these isolated lakes could be home to microorganisms unknown to science, potentially holding secrets to the origine and limits of life on Earth. This knowledge could in turn hold clues about the possible conditions for extraterrestrial life, in locations such as the bodies of water through to exist beneath the surfaces of ice moons of Saturn and Jupiter (Pearce, 2012).

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