Viruses are the most numerous and diverse biological entities in the oceans, with numbers (~10⁷-10⁸/ml) often exceeding those exhibited by their bacterial hosts (~10⁶/ml) by several orders of magnitude (1). Bacteriophages are found wherever microbial life is present and play a significant role in aquatic ecosystems. They affect microbial abundance, production, respiration, diversity, genetic transfer, nutrient cycling and particle size distribution. Viral infection is a stochastic process and depends on the abundance of viruses and hosts (1). Theoretical considerations regarding this mechanism suggest that viruses might selectively kill the most abundant members of the prokaryotic community and, in so doing, they influence species richness (3). A number of studies support this hypothesis (4). More recently, virus-mediated genetic exchange through generalized transduction as an additional mechanism potentially involved in shaping prokaryotic community structure has received attention as well (2).

In this work, we studied, using a transmission electron microscope, the phage community structure from Potter Cove, a small fjord located in the southwest of 25 de Mayo (King George) Island, South Shetland Islands, Antarctica. Surface water samples (35 liters) were aseptically collected on surface during an Antarctic summer campaign in 2008 and serially filtered onto 1.5 μm, 0.2-μm-pore-size filters (140 mm diameter; MSI, USA fiber glass and cellulose acetate, respectively), and Zeta Plus (an electropositive membrane). Adsorbed viruses were eluted from filters by using 1M NaCl and ultrasound. Particles were then negatively stained for microscopic study.

Figure 1 shows the bacterial infection by a podovirus particle. At sample collection time, the infection appears to be a frequent event because the probability of obtaining this picture could be very small if the viral prevalence was low. We can propose that, at least in summer, Potter Cove marine water could be inhabited by a large podoviral population. Furthermore, the ecological role of this highly prevalent viral population has to be studied in the future.

REFERENCES

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