Palmer LTER: Spatial distribution of viruses in the Palmer LTER region

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Viruses have been identified as dynamic components in several aquatic environments including marine and fresh waters (Bergh et al. 1989; Klut and Stockner 1990; Proctor and Fuhrman 1990), marine and freshwater sediments (Paul et al. 1993; Maranger and Bird unpublished data), and polar sea ice (Maranger, Bird, and Juniper in press). High abundances and rapid changes in viral abundance (Bratbak et al. 1990) along with rapid viral decay rates (Heldal and Bratbak 1991) suggest that viruses may play an important role in controlling microbial populations. Viruses are also thought to be involved in carbon transfer within the microbial loop (Bratbak et al. 1992); however, their quantitative role in carbon and nutrient cycling has not been fully established.

Viruses have previously been observed in the southern oceans and abundances have been reported for the Drake Passage (D.C. Smith et al. 1992) and for the coastal waters of Paradise Harbor (Bird, Maranger, and Karl 1993). During cruise 94-01 of the R/V *Polar Duke* (January 1994), we enumerated viruses from surface water samples taken at each station of the Palmer Long-Term Ecosystem Research (LTER) transect lines 300, 400, 500, and 600 (Waters and Smith 1992). Our objective was to determine onshore-to-offshore gradients in viral abundance and to compare these results with other physical, chemical, and microbiological characteristics of the surface waters. Viruses were counted in different size classes by head capsid diameter [less than 30 nanometers (nm), 30–60 nm, 60–80 nm, greater than 80 nm) to determine changes in the viral community composition between sites. Depth profiles of virus samples were taken at the endpoint stations (nearest to and farthest from shore) of each transect line.

Virus samples were fixed with electron microscopy (EM) grade glutaraldehyde (2.5 percent final concentration), stored in polypropylene vials at 4°C, and prepared on board the R/V *Polar Duke* as soon as sea conditions were calm. Water samples were concentrated using AMICON microconcentrators (10,000 molecular weight cutoff filter) in a microcentrifuge. Viruses from these concentrated water samples were then pelleted directly onto 400-mesh formvar-coated copper EM-grids using an EM-90 rotor in a Beckman airfuge for 30 minutes at 100,000 × g. Once removed, the grids were floated on a drop of filtered (0.02-micrometer) distilled water to remove salts.

Grids were stained with uranyl acetate (2 percent final concentration) for 30 minutes. Viruses were counted directly by transmission electron microscopy at high magnification (90,000×). Virus particles were identified on the basis of shape, size, and staining properties. Our criteria for virus

identification were quite strict because high abundances of colloidal particles similar in shape and size to virus particles have been reported in the southern oceans (Wells and Goldberg 1994).

Viral abundances ranged from 3.2×10^5 to 1.7×10^6 viruses per milliliter (mL^{-1}) (coefficient of variation of each mean was approximately 30 percent) in the surface waters of the region studied (figure 1). Peaks of viral abundances appeared at stations 40 (nearest to shore), 100, and 120 whereas the lowest abundances observed were at stations 60 and 180. Comparisons of these trends with other physical, chemical, and microbiological variables will be made as they become available.

An interesting observation is that the viral population, as classified by head capsid diameter, appeared to be quite variable among sampling stations (figure 2*A* and 2*B*). Viruses are largely species-specific and, thus, spatial distribution is influenced by the bacterial community itself. Therefore, a difference in the viral population might imply a difference in the species composition of the bacterial community or a difference in the numerically dominant species of bacterium at different stations. It should not be assumed that all the viruses observed were bacteriophage; it is possible that some were algal viruses. No methods to discern between algal and bacterial viruses in natural systems exist at present, however.

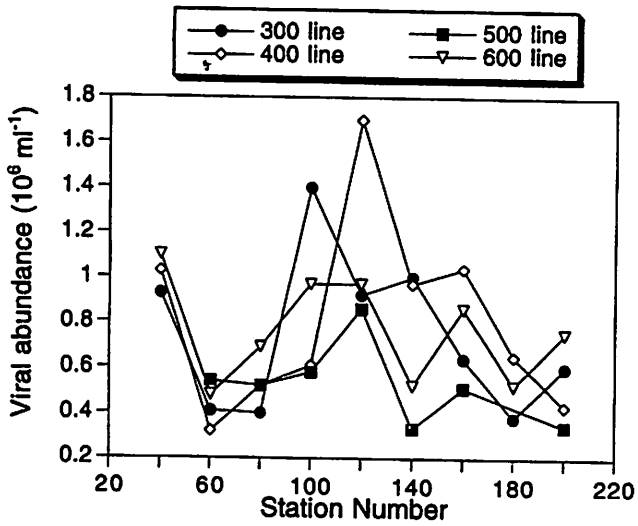

Figure 1. Viral abundances (in millions of virus particles per milliliter) in the surface waters of the transect lines 300, 400, 500, and 600 of the Palmer LTER study region in the southern oceans during January and February 1994. Station number represents distance from shore in kilometers.

Viral abundances were consistently lower in the surface waters of the vertical profiles (figure 3*A–D*). Low concentrations of viruses in near-surface waters have been observed in Paradise Harbor (Bird et al. 1993) during the austral spring. A surface reduction in virus particles, however, was not observed in the Drake Passage during the austral winter (D.C. Smith et al. 1992). This reduction in virus concentration in the summer might indicate that virus accumulation is inhibited by increased ultraviolet (UV) radiation at the surface (R.C. Smith et al. 1992; Suttle and Chan 1992), resulting in either lower production rates or higher loss rates. UV radiation may damage viral DNA or proteins, rendering infectious viruses defective, or it may destroy viruses directly by photolysis. The reduced number of viruses observed in the surface waters of the Palmer LTER region could also be due to differences in mixed layer depths between our study region and the Drake Passage. Viruses may be more abundant in the surface waters in areas where there is a deep well-mixed layer. In this case and relative to more stratified waters, the residence time of viruses at the surface will be reduced as a result of mixing and, consequently, so will their exposure to UV light. A simpler alternative explanation is that viral loss rates are high as a result of rapid sedimentation rates due to bubble scavenging and adhesion to particles. Adsorption to marine snow particles has been shown to be a major factor in controlling viral loss at lower latitudes (Suttle and Chan 1992). A consistent subsurface peak of viruses was observed between 20 and 60 meters in the water column. The peak of viruses appeared closer to the surface at the nearshore stations (figure 3*A* and 3*C*) and deeper in the water column at the offshore stations (figure 3*B* and 3*D*).

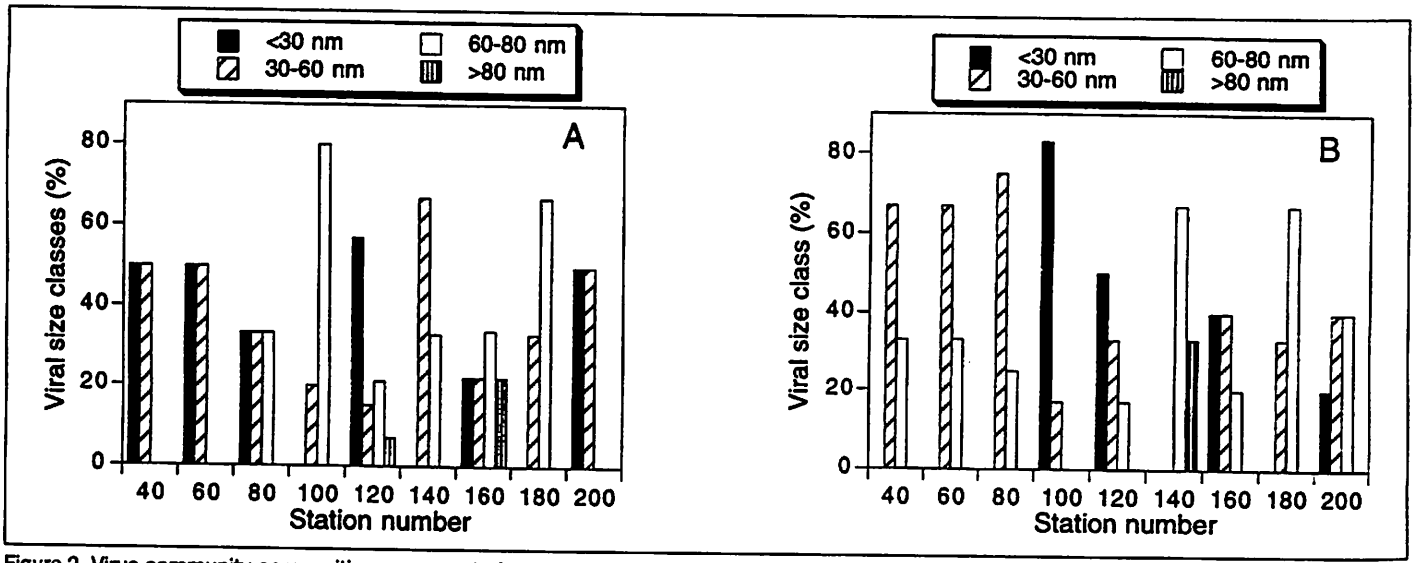

Figure 2. Virus community composition, represented as a percentage of head capsid diameter size classes, for the onshore-to-offshore stations of the (*A*) 400 transect line and the (*B*) 600 transect line.

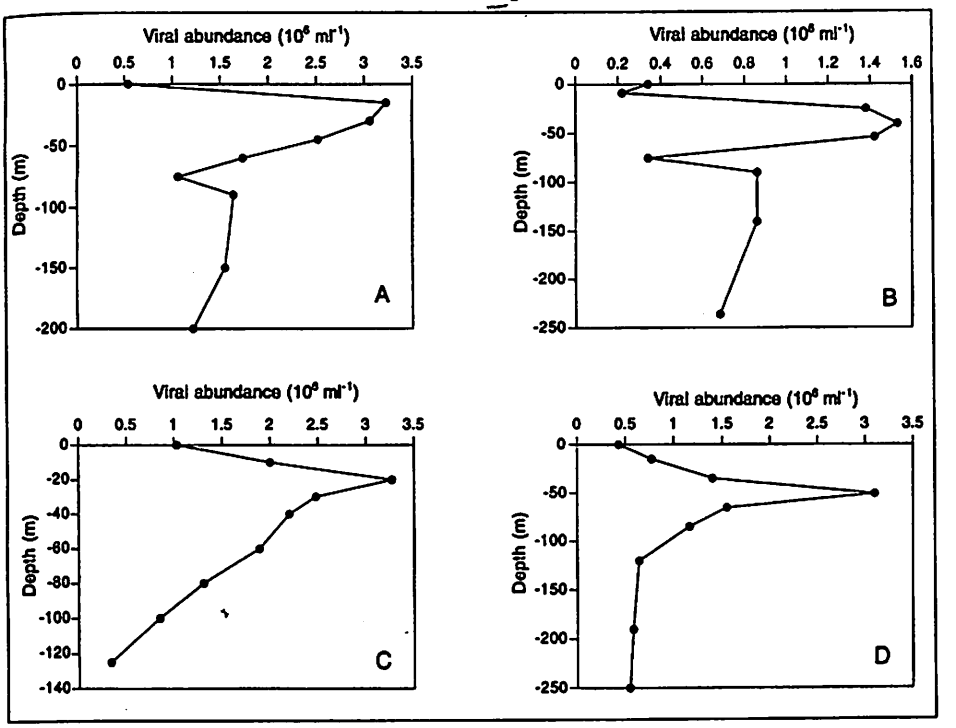

Figure 3. Profiles of viral abundance in the upper 200 meters of the water column of LTER station number (*A*) 500.060, (*B*) 500.020, (*C*) 400.040, and (*D*) 400.200.

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