

These antisera showed high NA against HTLV-III_B and HX10, but NA against HXB2 and HXB3 was substantially lower in every case (Table 2). Neutralizing activity of antiserum to Sub2 against HTLV-III_B and HX10 was seen at dilutions of $\geq 1:2048$ to $\geq 1:4096$, but NA against comparable inocula of HXB2 and HXB3 was lost at dilutions of $\geq 1:23$ to $\geq 1:281$. A murine monoclonal antibody to HTLV-III_B-derived gp120 (96-16) displayed similar specificity. In contrast, goat antisera against recombinant gp160 derived from the biologically inactive BH8 molecular clone (IMM-6) showed NA against HXB2 that was 64 times as high as NA against HTLV-III_B. The amino acid sequence of HXB2 differs from that of HX10 in the Sub2 region at only two positions (289 and 305), and those of BH8 and HXB3 differ at these same locations, including the presence of arginine or lysine instead of serine (representing a single nucleotide change) within a possible cysteine loop structure (20) that lies in the amino-terminal portion of Sub2 (Fig. 2).

In a series of competition experiments, we used synthetic oligopeptides spanning the RP135 or RP136 regions containing residues at the 289 and 305 positions corresponding to those of HX10, HXB2, or HXB3 (Fig. 2 and Table 3). Sera G2935 and 987 completely inhibited infection by HTLV-III_B in the absence of RP136 but showed no inhibition from control values when RP136 was added. In contrast, inhibition by a patient serum (HS-25) was not blocked by RP136. Peptides 51.4 and 80-1 (corresponding to HX10 at position 305) were significantly more effective than 51.20, 51.4.20, 80-2, or 80-3 (peptides containing either threonine or glutamine at position 289 but with arginine or lysine instead of serine at 305 as in HXB2, HXB3, and BH8) in blocking the neutralizing effects of G2935 and 987 on HX10 infection, supporting the conclusion that a change at the 305 position is sufficient to account for the observed restriction of NA in heterologous sera.

Although it is unlikely that differences in areas other than the *env* region are responsible for this restriction of NA, conceivably changes in other genes might alter gp120 processing, presentation, or stability (21). Also, differences at distant sites in gp120 or gp41 could induce conformational changes in the RP135 region. Finally, while there was no difference in the average titers of the panel of human sera against these viruses, suggesting HXB2 and HXB3 are not intrinsically more resistant to neutralization, such might not be the case for the specific goat antisera studied.

Our data suggest that a single amino acid change in the virus envelope may result in profound changes in recognition by neutralizing antisera, and extend the previous concept of type-specificity of neutralization (20) to differing variants of a single isolate. This suggests that the group-specific NA of some human sera could be directed against a large number of type-specific determinants, as well as conserved epitopes. This could have important implications for vaccine development. Inability to demonstrate protection by candidate vaccines after challenge with homologous virus isolates could represent the selection of minor clonal variants not well recognized by the immunized host (22, 23). Only the use of cloned HIV-1 variants will permit direct evaluation of the hypothesis that neutralizing antibodies are capable of protecting against HIV-1 infection.

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Acoustical Detection of High-Density Krill Demersal Layers in the Submarine Canyons off Georges Bank

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High-density demersal layers of krill have been detected in the submarine canyons off Georges Bank by means of a high-frequency, dual-beam bioacoustical technique. Krill densities in these demersal layers were observed to be two to three orders of magnitude greater than the highest densities observed in water-column scattering layers. Such abundances may help explain the unusually high squid and demersal fish production estimates attributed to the Georges Bank ecosystem.

EUPHAUSIIDS TYPICALLY PLAY A MAJOR role in the economy of pelagic marine ecosystems. In the productive waters of the North Atlantic, the species *Meganyctiphanes norvegica* provides an important link in the food chain between lower trophic level plankton and higher trophic level consumers, including decapod crustaceans, squids, fishes, marine mammals, and birds (1, 2). Early Norwegian whalers referred to *M. norvegica* as krill, a term that has now been expanded to encompass all species of euphausiids (3). A feature of krill ecology that makes them particularly vulnerable to successful exploitation by higher trophic level consumers is their tendency to form highly aggregated distributions (1, 2, 4). Krill

aggregations have been categorized into four basic types: patches, shoals, swarms, and schools, with the last two types corresponding to high-density aggregations of more than 1000 animals per cubic meter (2). Such high-density aggregations of *M. norvegica* have been reported, but those reports have been of surface swarms often associated

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anic regions, these scattering layers may coalesce in a high-density layer at the bottom when the krill migrate downward in the morning, thereby greatly concentrating the animals present (11). In addition, the topography of the submarine canyons may cause a funneling effect that would further concentrate the animals at the canyon bottom (12).

Better documentation of the spatial extent and temporal persistence of high-density demersal layers of krill will be essential for assessing the importance of these layers in high-latitude marine ecosystems (13). The Georges Bank ecosystem provides a good example. Georges Bank is one of the world's most productive fishing grounds (14-17), and krill are an important but variable dietary component of the Bank's commercially important squid and demersal fish stocks, including long- and short-finned squid, cod, flounder, haddock, hake, pollock, and redfish (1, 18-20). Recent analyses of secondary production on Georges Bank indicate that the levels of zooplankton and benthic production there are insufficient to support the high levels of squid and demersal fish production (16, 21). Hypotheses suggesting that there are high trophic efficiencies within the ecosystem do not seem to explain this discrepancy (16). A more plausible hypothesis is that squid and demersal fish stocks on Georges Bank are subsidized by exploiting krill production in the canyons and deep waters surrounding the Bank (22). Although krill rarely intrude on the shallower parts of Georges Bank, many squid and demersal fishes seasonally inhabit the deep, surrounding waters (23). Closer examination of the spatial and temporal coupling between predator and prey populations will determine the viability of this hypothesis. If it proves correct, then the excess squid and demersal fish production associated with Georges Bank may be attributed to the existence of high-density demersal layers of krill in the deep, surrounding waters.

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