

tribute significantly to the N_2O flux in the upper few hundred metres. Within the oxygen-minimum zones, where most of the oceanic N_2O is concentrated⁶, the mechanism I propose might be dominant. Significant production might also occur through the mode favoured by Kim and Craig. However, the bulk of oceanic N_2O production could be through the nitrification–denitrification couple I propose.

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Ancient Arctic hunters

SIR—In 1989, a joint expedition from the Leningrad Institute of Archaeology and the Arctic and Antarctic Research Institute explored the ancient site on the Zhokhov isle (New Siberia isles, 76° N; Fig. 1). The existence of this remote site was known, but no details as to its dates

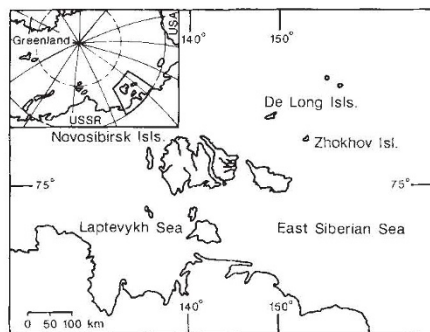


Fig. 1 Map of the Zhokhov isle region.

and type of occupation have previously been reported. Our data suggest that this area was occupied far earlier than has previously been thought.

The site we studied is in the southwest of the island, near the foot of a hill, which was probably used as an observation post or as a defence from the extreme weather. We found the remains of at least 13 dwellings within the site. The buildings were made of driftwood and covered by moss or sod. The walls were probably strengthened by vertical pieces of driftwood.

We excavated material from under one



Fig. 2. Bone implements found on Zhokhov isle. Double-edged (1,2) and one-sided (3–5) tools; bone points (6–8) and fragment of polished mammoth ivory specimen (9). Scale bar, 3 cm.

dwelling which provides information about the culture of the people who lived in the site. Various material was used for the making of stone tools. Different kinds of flint, silicated schiststone, halcedone and obsidian were used: undoubtedly, obsidian and scanty flint of high quality were imported. The techniques of processing the stone is typical of the mesolithic period.

We collected a series of massive mammoth-ivory and antler hoe-shaped tools, and found specimens of hunting implements: needle-shaped arrow points and fragments of large inset tools — both one-sided and double-edged (Fig. 2).

The fauna remains were examined by A. Kasparov at the Leningrad Institute of Archaeology. Most are from reindeer (50%) and white bear (45%). The rest of the bones we could define are from sea-mammals (such as walrus and seal), wolf and birds. Thus, there were two main species of prey. This specialisation of hunting is unusual.

We dated the site (processing of specimens was carried out by Y. Swejentsev at the Leningrad Institute of Archaeology); most wood and bone specimens examined define the age of the site as 7,000 to 8,000 years before present.

Thus, the finds on the Zhokhov isle are changing our notions about the time and extent of the mastering of the high Arctic by man. Our results suggest that the first migration to these territories happened even earlier.

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Provenance of HIV strains

SIR—Since your News report¹ on the experience of several laboratories, including mine, of accidental transmission of HIV in cell cultures, I have received some queries about whether any of our HIV isolates cannot be clearly distinguished from previously described strains. Of the viruses we have reported or distributed to other laboratories, CBL4 (HIV-1) and CBL20-24 (HIV-2) clearly differ from all previously described isolates^{2,3}, whereas CBL1 (ref. 4) is similar to both LAV-1 BRU and HTLV-IIIB.

As previously reported^{5–7}, monoclonal antibodies raised against CBL1 gag proteins do not distinguish between CBL1, BRU and IIIB, and gag sequence analysis revealed only minor nucleotide variation. Further sequence analysis provided by P. Highfield of Wellcome Laboratories (personal communication), representing in total 2,443 nucleotides in *env*, *tat* and *nef*, show that CBL1 has 98.0% amino acids in common with LAV-1 BRU and 97.8% with HTLV-IIIB (BH10 clone), whereas the similarity in the same regions between BH10 and BRU is 98.3%. The *tat* sequence was most variable, with 94.2% of the CBL1 sequence identical to both BRU and BH10, 83.7% to SF-2 and 74.4% to ELI.

On account of the close sequence relationship of CBL1 to LAV-1, HTLV-IIIB and the two University of Nebraska strains^{8,9}, I cannot exclude the possibility of cross-contamination during its isolation and subsequent adaptation to grow in T-cell lines — both LAV-1 and HTLV-IIIB were propagated in our laboratory at that time. But note that minor sequence variation can result in marked differences in the biological properties of the Nebraska strains⁹ and also of CBL1 compared with LAV-1 and HTLV-IIIB (refs 11, 12).

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