Ice shelf creep rates and the flow law of ice

Sir—A suggestion[1] that creep measurements made on the Ward Hunt Ice Shelf, Canada, should provide needed information relevant to defining the flow law for ice, exposed the fact that such measurements had already been carried out[2]. Attempts to improve our knowledge of the flow law for ice have been under way for the past 30 years and the latest attempt[3] seems unlikely to be the last[2].

This communication is intended to point out that the data referred to in ref. 2 cannot easily be interpreted to provide information relevant to investigations of the flow law for ice. I will attempt here to summarize the major difficulties surrounding this problem.

Whilst the arctic ice shelves and ice islands are potentially able to provide a low (stress, strain rate) point on deformation maps for ice, it is of crucial importance to carry out the experiments in the right place and at the right time. For two major reasons neither of the known experiments[4,5] fulfill these conditions.

First, it has long been known that the internal structure of the arctic ice shelves and ice islands is extremely complex[6], and may vary significantly over relatively short distances. Power reflection coefficient data from airborne radar measurements[7] point to the existence of significant regional inhomogeneities in shelf structure. These variations occur in both crystallographic and chemical properties. In particular, two of the major ice types: sea ice, with large elongate crystals and iced firn with small equant crystals, may be contained in the same column, but in different proportions, depending on location. Crystal size, shape and optic axis orientation are all known to affect the creep properties of bulk ice[8]. Ice salinity may vary over a range of 15‰. The very significant effect on creep rate of the brine volume in the ice has recently been documented[9]. Thus, it is essential to site any experiment on flow law investigations at least where the structure of the shelf is known and preferably where it is least complicated.

Second, although most measurements of strain rate may be carried out with acceptible reliability, the determination of the accompanying stresses may not be, except in the simplest of cases[10]. The "point" at which the Ward Hunt Ice Shelf strain rate measurements[3] were made was < 1 km from the edge of an ice-locked island and < 4 km from the outer edge of the shelf. The geometry of the shelf in this region precludes a simple analytical stress solution. However, even if this problem were overcome (by finite element numerical modelling) yet another problem is present. The extremely mobile arctic pack ice impinges on the outer edge of Ward

Hunt Ice Shelf for the greater part of the year. There are periods when pack ice is thrust into and over shelf ice, as on ice island T3 (ref. 5). During such episodes, which may not be uncommon, significant compressive strains (and hence stresses) may be generated in shelf ice. During aftermath conditions on T3, an estimate of the compressive stress was $(0) - 0.01$ MNm^{-2} in the ice island, corresponding to $(0)-0.1$ MNm^{-2} in the pack ice[5]. It is now evident[9] that stresses in sea ice may exceed the latter value by an order of magnitude. Thus, for limited periods, the normal gravity expansive creep stresses (and accompanying strains) in thin ice shelves and ice islands, which are $(0) + 0.01$ MNm^{-2} (ref. 5) may be completely defeated, even though the long-term creep of the shelf ice may result in a net expansion[4]. Thus, the time span over which the flow law experiments are carried out is also of great importance. Then, one must evidently have to consider the relative effects of the different creep stages (primary, secondary and tertiary).

Experiments to simulate the creep of Ward Hunt Ice Shelf taking into account the structure and the sea ice back-pressure effect are now under way, using a finite element numerical model[11], and results shall be published shortly[12].

As some consolation to the array of difficulties presented here, it may be possible to avoid one of the major difficulties mentioned above. Part of the inner edge of Ward Hunt Ice Shelf flows in the form of a tongue into the entrance of an isolated fiord (Disraeli) which contains only passive fresh water ice. These conditions would seem to favour this as the best site for any flow law experiments. This leaves only the problem of the structural character of the shelf which, even if fully accounted for, does not allow easy comparison between these data the data[3] for the much thicker Antarctic ice shelves of entirely different structure[13].

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AIDS virus and HTLV-I differ in codon choices

Sir—The genomic pattern of choices between synonymous codons ("coding strategy") represents a fundamental evolutionary structure useful for distinguishing species[1], and great evolutionary times have been shown to be associated with substantial changes in coding strategy[2-4]. A rapid indication of the overall scheme of choices can be obtained by calculating the preferred triplet in each amino acid's set. Comparison between sequences or species is then possible by counting differences in preferred codons for the 18 amino acids with codon choices (methionine and tryptophan have unique codons except in mitochondria).

For instance, nuclear genes of mouse, rat and chicken have 16 to 18 preferences common with those of man. This is also an interesting index of the degree of imitation of host strategy by a virus or organelle. For example, when codon frequencies in the complete genome sequence of the AIDS (acquired immune deficiency syndrome) virus[5] are compared to those of all sequenced human nuclear genes[6], excepting the imune system, not a single common preferred triplet among the 18 cases is found. However, matching human T-lymphotropic virus type I (HTLV-I) preferences against those in man reveals 11 identical choices. Other retro-oncoviruses give similar results[4]. On the other hand, Visna lentivirus (VLV)[7] shares no common codon preference with man. With both VLV and AIDS virus, the various codons in each amino acid set have greatly different relative frequencies from human genes[4]. Thus AIDS virus and VLV do not at all imitate human (or mammalian) codon usage while HTLV-I does, to a degree. (Not as much as some other viruses, however, as the complete genome sequences of EBV and Ad2 each show 15 common preferred triplets with human mRNA[4].)

We now compare viruses among themselves. Perhaps surprisingly, HTLV-I and HTLV-III (AIDS virus) do not share any preferred codons, while VLV and AIDS virus coincide in all 18 cases. This suggests that the AIDS and Visna viruses have diverged relatively recently but that AIDS virus (or VLV) and HTLV-I are much more distantly related. Our results are compatible with those of Chiu et al.[7] and Sonigo et al.[8] who reported a close relationship in the genetic organization of VLV and AIDS virus. However, the present work concerns all three viral genes; in particular, we demonstrate that VLV-AIDS virus similarity is not limited to the pol gene and the common region between pol and env[4,7,8].

It does not necessarily follow that no individual genes in the host exhibit codon