

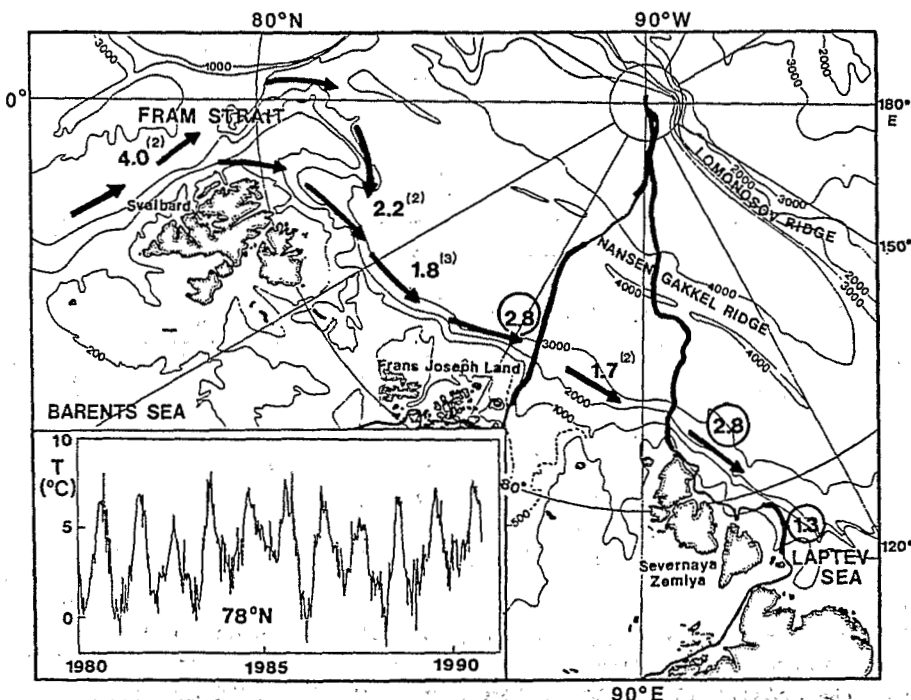
Warming in the Arctic

SIR — Climate models predict that global warming caused by the greenhouse effect will not be distributed evenly¹. The greatest temperature increase is expected for the polar and subpolar regions, with a relatively small change in the tropics. The polar regions may therefore be well suited to attempts to observe climate changes, but severe environmental conditions make it difficult to obtain such data, particularly in the case of the Arctic Ocean, which has a permanent ice cover and is thus virtually inaccessible to normal ocean-going vessels.

through turbulent mixing and diffusive fluxes.

Climatological² and synoptic data collected in 1987 (ref. 3) show that the maximum temperature in the Atlantic water decreased from about 4 °C in the ice-free Fram Strait to below 2 °C in the subsurface layer between Svalbard and Severnaya Zemlya. But our temperature measurements made in 1990 off Frans Joseph Land and north of Severnaya Zemlya had maxima of 2.8 °C, about a degree higher.

The ice thickness encountered during the



Maximum temperature in the Atlantic layer over the Eurasian Basin of the Arctic Ocean. Circled numbers, *Rossiia* observations along the tracks shown as bold lines. Other numbers are taken from the references given in brackets. The inset shows the maximum sea surface temperature in Fram Strait at 78° N during 1980–90.

During August 1990, the Soviet ice-breaker *Rossiia* carried a group of tourists from Murmansk to the North Pole, cutting across the Eurasian basin at longitudes 60° E and 95° E. Detailed observations of the ice were made as well as closely spaced temperature profile measurements in the upper 500 m of the water column, using expendable bathythermographs dropped in leads or small polynyas.

The Arctic Ocean water column consists principally of three layers: a cold and low salinity surface layer; a warm and salty Atlantic layer in the depth range 100–800 m; and the deep water below, being cooler and slightly fresher. The Atlantic layer derives from an inflow in the Fram Strait between Svalbard and Greenland and is the northernmost extension of the Gulf Stream–Atlantic current system. On its way north it loses heat to the atmosphere, and in or just north of Fram Strait subducts underneath the ice and polar water, continuing to lose its heat

cruise was 20–30% smaller than the climatological mean for the area⁴, although this might simply reflect that the vessel was taking the route of least resistance, avoiding thick old massives and other heavy ice features. It is of course not immediately clear whether the higher subsurface temperatures and the lower ice thickness already reflect a climate trend or just some normal interannual variability. The sparseness of the available data simply does not allow any such conclusion. Sea-surface temperature variability in Fram Strait is high, both on seasonal and interannual timescales. The year-to-year changes of 2 °C could mask any trends in temperature development. It seems clear, however, that there is a need for careful

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monitoring of the heat fluctuations in the Arctic, a region so vulnerable to changes in global climate.

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Clonal defence

SIR — Dye *et al.*¹ have criticized our clonal theory of parasitic protozoa² by pointing out that “clonality is the conventional wisdom” and that “sexual reproduction clearly occurs, [although . . .] may not be common in nature”. Unfortunately, they fail to understand the significance of our theory.

We are not denying that sexual reproduction may occur nor simply asserting that clonality may be a common mode of reproduction for parasitic protozoa, both of which are indeed well known. Our hypothesis is that parasitic protozoa have a clonal population structure, which in turn implies that sexual reproduction is very rare even on the evolutionary scale. The theory has momentous evolutionary as well as medical consequences. In *Trypanosoma cruzi*, for example, where the evidence supporting the hypothesis is overwhelming, the average genetic differentiation between two randomly sampled clones is greater than that between gorillas and humans. Generally, if the population structure is clonal it is not warranted to assume that any clone or a few of them may be representative of the species with respect to biological and pathological properties.

Walliker *et al.*³ argue that our theory is likely to be wrong with respect to the agent of human malaria *Plasmodium falciparum*. This may be so, but none of their four points will settle the issue. Because of the well-known fact that a sexual stage is required in the mosquito vector to complete the infection cycle, we were surprised that our analysis² of the limited data available supported a clonal population structure. In addition to a clonal population structure for the whole taxon, it is also possible that both biparental and uniparental lineages may coexist in nature — a phenomenon known to occur in many metazoa and plants.

The issue of the population structure of *P. falciparum*, as in the other protozoa, can be settled only by population-genetic evidence concerning the distribution of genotypes in natural populations. We reported the analysis supporting clonality as a challenge to those who work on *P. falciparum* to settle the

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issue, given its great biological and medical significance. We agree with Walliker *et al.*³ that allelic frequencies and the number of loci must be taken into account for estimating the probability of observed multilocus genotypes, and did this as best we could based on the scarce published evidence and obtained statistically significant evidence of nonrandom association between loci (Table 2 of ref. 2.).

Dye *et al.*¹ suggest that "analyses of protozoan clonality, particularly *Plasmodium*, will yield more convincing results if carried out on restricted geographic scales... not by making intercontinental comparisons...". We agree that more population-genetic data are needed: we could only analyse such data as have been published. But Dye *et al.* do not seem aware that the most convincing evidence for clonal population structure would come precisely from the observation of identical multilocus genotypes in geographically distant localities. Moreover, if such widespread genotypes exist, as seems to be the case in *Trypanosoma cruzi*,

for example, they are the ones that should most urgently become the subject of biological and medical research.

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Sea-level rise and earthquakes

SIR — Global sea level is believed to have risen at a mean rate of 1.7 ± 0.4 mm per year during the past 80 years¹. Several models suggest that sea-level rise is accelerating². To be of benefit to coastal communities, useful forecasts of sea-level rise can be made only by estimating the rise over decade or shorter timescales, which will require significant improvements in our misunderstanding of global ocean dynamics and much improved sea-level sampling of mid-ocean and Southern Hemisphere locations³.

As our ability to measure global sea level improves, it will become necessary to suppress the solid Earth input to global sea level, hitherto assumed to be an insignificant but steady contribution to sea-level change at decadal periods⁴. Although the net volume of the ocean basins increases slightly because the Alpine/Himalayan tectonic convergence zones are continental collisions, for example, the resulting reduction in global sea level is inferred to be less than 10 μ m per year. However, the sea-level perturbation from great oceanic subduction earthquakes is both significant and rapid. The Chilean earthquake in 1960 was accompanied by sea floor uplift and subsidence⁵ with a net reduction in ocean basin volume of more than 573 km³. This local reduction in ocean basin capacity causes an increase in global sea level of 1.7 mm, equal to the annual mean global sea-level rise from other causes. Similarly, the 1964 Alaskan earthquake⁶ was accompanied by a reduction in ocean basin capacity of approximately 250 km³ due to uplift, resulting in a 0.7-mm increase in global sea level. Offsets in tide gauge records following these events are obscured by daily and weekly oceanographic noise.

It is clearly important to remove the effects of submarine deformation accompanying subduction processes from future estimates of trends in sea level. This will require improved estimates of submarine co-seismic deformation, particularly in the far field and in the interseismic period. For example, the net long-term contribution to global sea level from subduction earthquakes is probably close to zero given reasonable models for post-seismic deformation and interseismic strain development. Thus global sea level must subside between great earthquakes. Because offshore postseismic and interseismic deformation data are unavailable for most tsunamigenic⁷ earthquakes, we are surprisingly ignorant of the true magnitude of this subsidence. Making the simplifying assumptions that coseismic sea-level uplift scales linearly with magnitude, and that interseismic deformation is linear in time between events, we infer a minimum sea-level lowering rate between historical earthquakes with magnitudes $M_w > 8.5$ of approximately 0.05 mm per year.

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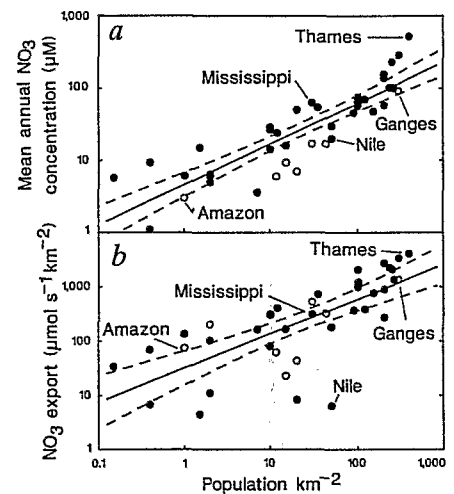
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Human influence on river nitrogen

SIR — The overabundance of algae in coastal waters is often blamed on excessive inputs of otherwise scarce nutrients such as nitrate and other forms of nitrogen¹. This nutrient overload originates primarily from rivers that discharge directly into an ocean^{2,3}. A key question, therefore, is what controls the amount of nutrients in, and exported from, coastal rivers? We now have quantitative evidence that, on a global scale, human population within a river's watershed is strongly related to the concentration of nitrate in rivers that discharge to coastal ecosystems.

We collected published data for 42 major rivers of the world (references available on



a, Average annual nitrate concentration in 42 rivers of the world against the corresponding human population density in the rivers' watersheds. Each point represents a different river; some major rivers have been labelled for comparison. O, tropical rivers ($\leq 23.5^\circ$ lat.); ●, all other rivers. Solid line, least squares regression: $\log[\text{NO}_3] = 0.56 \times \log[\text{Pop. Dens.}] + 0.67$ ($r^2 = 0.76$, $P < 0.00001$); dashed lines, 95% confidence intervals for the regression. b, Same as a, but for nitrate export. The regression line is $\log[\text{NO}_3 \text{ Export}] = 0.64 \times \log[\text{Pop. Dens.}] + 1.51$ ($r^2 = 0.53$, $P < 0.00001$).

request). The rivers chosen were restricted to those that large into an ocean and that had the appropriate data available — watershed population density, watershed area and mean annual nitrate concentration and water flow near the river mouth. The selected rivers appear to be representative of the world's rivers; mean runoff (flow per watershed area) is 13.2 litres $\text{s}^{-1} \text{km}^{-2}$ compared to a world mean value of 11.8 litres $\text{s}^{-1} \text{km}^{-2}$ (ref. 4). The rivers studied and their watersheds account for about 37% of global freshwater discharge to the ocean⁴.

A log-log regression of mean annual nitrate concentration plotted against human population density (part a of figure) shows a highly significant relationship ($P < 0.00001$) that explains 76% of the variation