

## Daedalus

## Solid cooling

The world's domestic refrigerators and air-conditioners all work on the same principle. A liquid is evaporated under low pressure, absorbing the latent heat of evaporation. Elsewhere the vapour is condensed under high pressure, returning that latent heat to a different system. The cycle then repeats. The snag is that the best fluid to use is a halocarbon, which damages the ozone layer. This wouldn't matter except that all refrigerators — especially those in cars — leak. New halocarbon is needed to top them up. So the whole halocarbon problem is merely one of bad plumbing.

Daedalus now has a way out: invent a solid working medium, which cannot leak, and the problem will go away. Most solids are so incompressible that only a small change of temperature with pressure seems feasible. Rubber, of course, warms when you stretch it, as the entropy of the molecules is increased. But Daedalus recalls that carbon nanotube is a valuable probe in an atomic-force microscope. If the force is excessive, the nanotube buckles and folds up totally. This solid collapse destroys the chemically resonant structure of the tube, but is fully reversible — remove the load and it springs straight and true again. Its resonance energy must be absorbed as heat in its collapse, and re-emitted in its recovery.

So DREADCO chemists are packing as much carbon nanotube as possible into a flexible solid, possibly rubber, looking for truly dramatic changes in temperature when the composition is deformed. A small bending or squashing should collapse the nanotubes strongly, so they lose their resonant energy and absorb heat. When the solid relaxes, the nanotubes will reform, lose energy as they reorganize, and deliver it as heat again. The result should be a working solid for a refrigerator.

A solid-state refrigerator poses unusual design problems. A big disc, cylinder or belt will carry the working solid, and will be rotated by a motor. Wheels on the periphery will deform it where cooling is desired, and release it to recover heat. The whole thing will be simple rather than efficient.

The DREADCO team reckon they will be lucky to get more than a few tens of watts of cooling; but with no plumbing to worry about, the new refrigerator should find a useful niche in the market. The automotive market is the obvious one. Efficiency is not very important, the device will not leak or stop working, and cooling power can be increased merely by speeding it up.

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in different parts of the world, including Africa. This view places special emphasis on the role of migration in transferring new mutations affecting important human genes arising in geographically isolated groups. More migrants came from Africa, where there were bigger populations, in which greater numbers of new mutations would arise. But do the inferences of differential migration that are essential to this view hold up to scrutiny?

Templeton and other proponents of multiregionalism have criticized Afrocentric interpretations as incomplete, and an inaccurate reflection of how modern populations are and have been structured; they claim that researchers are confusing history with geography. This problem is one of the reasons that an approach incorporating methods known as 'spatial autocorrelation' and 'multidimensional scaling' has gained popularity. Here, patterns of genetic variation are compared with those predicted from theoretical models, and then used to estimate parameters such as levels of inbreeding, natural selection and gene flow<sup>8</sup>. But this approach ignores certain information in the sequences themselves. So it has not been as useful as phylogenetic analysis for identifying a major event in the evolution of allelic lineages within a species — such as a large population 'bottleneck' (in which, at some point in time, comparatively few individuals of a species exist, and so genetic diversity is limited).

In human evolutionary studies, methods that are commonly used to identify differences between species are often extended to the study of variation within a species. Templeton sees this as a major shortcoming in the genetic approach to human evolution. He argues that some morphological traits would fail to show regional continuity between populations over time, if they are not under the strong influence of natural selection, and that gene flow from dispersing and expanding groups is balanced by the presence of random genetic drift (the random loss of alleles over time through small population size). In his view, an estimate<sup>9</sup> that only 90% of the haplotype trees in the nuclear genome demonstrate African roots is clear evidence that regionally isolated, archaic populations were not completely replaced by immigrants of ultimate African origin. Templeton attempts to break this impasse in understanding by showing that what is needed is an analytical tool favouring neither model on an *a priori* basis.

What assumptions lie behind his GEODIS analysis? First, a null hypothesis states that there would be no expected association between geography and a tree. Second, a plausible set of trees must be produced. Third, it is essential that the geographical sampling design is adequate. Also, the power of the analysis should increase if sampling includes greater numbers of unlinked regions of the genome — that is, regions inherited independently of others during

cell division. Do these assumptions match the application in this analysis?

Gene positions, or loci, on chromosomes 14, 16, 21, X and Y, and those in mitochondrial DNA, were chosen, representing a maximum scan of about 13% of the human genome. Sequences that recombine (those essential to pigmentation, the immune response, oxygen consumption and glycolysis) were considered equally with those that do not (maternal and paternal markers), and with the apparently non-functional pieces of DNA known as microsatellite markers that are inherited from both parents and are presumed to be neutral. Some of the analysis required the pooling of samples from individuals from different locations in order to perform the nested cladistic analysis, and sample size varied from 35 to 1,544 individuals.

It therefore comes as no surprise that evidence for range expansion, long-distance dispersal and isolation by distance varied in strength between the genetic loci sampled. In this respect, Templeton's analysis shows how our current understanding, based on loci that are non-concordant in pattern and process even in the same populations, limits certainty about a global reconstruction of human evolution.

Any tool that helps to clarify the magnitude of genetic drift, population migration or natural selection, and directs the researcher to what is needed (more donors, more sequence), is helpful. But perhaps Templeton was over-ambitious in the scale of his analysis. Most specialists would consider the reconstruction of the human population expansion into Polynesia to be a relatively simple task compared to what Templeton has attempted. But I know only too well that analysis of blood from 35 donors taken from just one island was insufficient to describe the major roots of diversity on that island, although the Polynesian expansion was quite recent. Perhaps we will need a demonstration that GEODIS reveals the composite picture agreed upon by archaeology, genetics and linguistics in this area of the world before we can settle on how to interpret the varied signals uncovered by Templeton's analysis on a global scale. ■

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1. Cavalli-Sforza, L. L., Menozzi, P. & Piazza, A. *The History and Geography of Human Genes* (Princeton Univ. Press, Princeton, New Jersey, 1994).
2. Templeton, A. R. *Nature* 416, 45–51 (2002).
3. Avise, J. C. et al. *Annu. Rev. Ecol. Syst.* 18, 489–522 (1987).
4. Posada, D., Crandall, K. A. & Templeton, A. R. *Mol. Ecol.* 9, 487–488 (2000).
5. Cooper, A. & Poinar, H. *Science* 289, 1139 (2000).
6. Harpending, H. et al. *Proc. Natl. Acad. Sci. USA* 95, 1961–1967 (1998).
7. Jorde, L., Bamshad, M. & Rogers, A. *BioEssays* 20, 126–136 (1998).
8. Bertorelle, G. & Barbujani, G. *Genetics* 140, 811–819 (1995).
9. Takahata, N., Lee, S.-H. & Satta, Y. *Mol. Biol. Evol.* 18, 172–183 (2001).