

ancestor lacked it. A and B could have inherited it as a derived character from an intermediate ancestor or else could still have evolved it separately.

To appreciate that these are not just far-fetched theoretical alternatives, consider the two shared characters (knuckle-walking and thin dental enamel) that Martin<sup>10</sup> and Andrews<sup>12</sup> cite as (the sole) apparently derived morphological traits linking chimpanzees and gorillas and separating them from humans. Other anthropologists<sup>16</sup>, in disagreement with Martin and Andrews, suggest that proto-humans also practised knuckle-walking and then lost it, or that chimpanzees and gorillas evolved knuckle-walking (and thin enamel) independently. The same ambiguities apply to DNA sequences. For instance, the presence at  $\eta$ -globin position 5,153 of cytosine in chimpanzee and gorilla contrasting with adenine in human and orang-utan nominally suggests cytosine to be a shared derived trait linking chimpanzee and gorilla. But Miyamoto *et al.*<sup>1</sup> implicitly interpret it either as lost by proto-humans or else evolved independently by chimpanzee and gorilla. The  $\eta$ -globin sequences include three such features construed as pseudo-synapomorphies (at positions 5,153, 5,156 and 6,808) shared by chimpanzee and gorilla but not human or orang-utan — nearly half as many as the eight features interpreted as true synapomorphies (shared by chimpanzee and human but not gorilla or orang-utan).

The sole solution to this dilemma is to analyse a very large number of characters, as DNA/DNA hybridization in effect does (for example, by estimating about 32 million base-pair mismatches between humans and the 'other' two chimpanzees). Although interpretation of any single DNA sequence shared between A and B but not C or an ancestor is equivocal, a finding that A and B share many such non-coding sequences would identify common descent rather than independent evolution as the correct explanation.

Is sequencing or DNA/DNA hybridization the more useful technique? The latter has disadvantages for studying very distant taxa<sup>9</sup>. Neither is ideal for analysing relations of conspecific races or of very closely related species, which may differ too little in the nuclear DNA (but see refs 8, 9). Mitochondrial DNA, which evolves more rapidly than nuclear DNA, is better for such studies. But if one's interest is in the phylogeny of well-differentiated, not-too-distant species, DNA/DNA hybridization has two decisive advantages.

First, it measures the net sequence divergence between whole genomes, but sequencing can currently deal with only tiny fractions of genomes (about 0.0004 per cent in the study by Miyamoto *et al.*), and those fractions can vary in their evolution. Second, it offers higher accuracy and statistical power than is feasible with

sequencing. Felsenstein<sup>17</sup> discusses how to calculate the number of base pairs that must be sequenced to yield the same statistical power as a single DNA/DNA hybridization value, given the standard error of the latter. If one considers that newer techniques to sharpen DNA/DNA hybridization curves reduce the standard error<sup>8,9</sup> and that hybridization values are routinely measured in replicate (for example, 64 replicates for human  $\times$  common chimpanzee in ref. 2), more than 100,000 orthologous base pairs of human and common chimpanzee would have to be sequenced to achieve a similarly low standard error. Although it may some day be feasible to sequence so much material from two species, sequencing will remain a brute-force, indirect method to obtain a measure of total mismatches that DNA hybridization yields directly.

All this is not to say that measuring DNA sequences and other taxonomic characters is a waste of time. Sequencing is obviously essential if one is interested in the evolution of the particular gene sequenced, rather than in taxonomic relationships. The DNA/DNA hybridization technique increases rather than decreases the evolutionary interest of protein sequences and morphological traits, which formerly had to be used in circular fashion to infer both overall taxonomic relationship and the evolution of the studied trait. DNA/DNA hybridization can now be used to establish taxonomic relationships independently, so that evolution of proteins or anatomy can be established unequivocally. However, for the purpose of deducing phylogenies I expect that DNA/DNA hybridization will be the method of choice in future. Thus, I see the study by Miyamoto *et al.* not as the harbinger of even larger-scale brute-force sequencing efforts by taxonomists, but instead as resolving any lingering doubts that such efforts confirm the results of hybridization methods. □

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## Daedalus

### Bright noise

THE thermograph, which images a scene in surface temperature, has many medical and industrial uses. Daedalus is working on an instrument to image, not the heat given out by every point of a scene, but the sound. In effect it produces a sound-map of the scene.

Rather elegantly, the 'sonograph' will image the whole scene simultaneously in sound and vision. It has a lens with the same focal length for sound as for light. Daedalus calculates that such a lens can be made as a doublet, one element of which is the liquid perfluoroheptane, while the other is a mixture of 80 per cent helium and 20 per cent air. The liquid and gas elements are separated by a curved transparent membrane, its radius determined by the internal pressure; the front and rear faces are conveniently plane. For good focusing, its diameter should be at least a wavelength of the lowest sound to be imaged — more than one metre for middle C! The practicalities may dictate something smaller, with some sacrifice of bass resolution. The whole device will resemble a view-camera, with a ground-glass screen that the observer scrutinizes from under a black cloth.

To display the sonic image superimposed on the optical one, Daedalus will exploit the poetic phenomenon of 'the burning sea'. This luminosity of disturbed tropical sea water results from bioluminescent marine algae, like the dinoflagellate *Noctiluca miliaris*, which flashes when mechanically stimulated. An agar culture of *Noctiluca* on the focusing screen of the sonograph will flash brightly at those points of the image that are emitting sound. A stethoscope touched to such a point will reveal what the sound is.

Engineers should rush to buy sonographs. All the folklore of machine diagnosis by sound — the elusive rattle of loose parts, the squeak of dry bearings, the grinding of worn gears — will be reinforced by precise location of the noise. Silencing and sound-proofing will make giant strides: the sonograph will not only identify the real problem, but will show immediately the effectiveness of counter measures. The hi-fi fanatic will at last be able to image the 'sound stage' of his stereo equipment, and modify speaker positions and so on until his stethoscope reports every instrument of the orchestra in its proper place.

The sonograph will also have an impact on politics. Conference stewards will be able to identify distant hecklers, or insufficiently hysterical contributors to a standing ovation. In the televising of parliaments, it would usefully locate the sources of muttered backbench dissent. David Jones