

suggest an overall optical brightening of SN1987A, a property which is quite difficult to understand in models where the energy input is impulsive. Radioactive energy input (W. D. Arnett, preprint, 1987) will retard the decline and may even produce a slight increase in luminosity, so the light curve to date may not yet require pulsar input.

But if there is an embedded rapidly spinning pulsar, then by August 1987 SN1987A should have become several magnitudes more luminous than it was in March and should ultimately show a spectrum with an extremely hard and polarized continuum from the underlying nebula. The nebular magnetic field will be quite large, in the range of  $10^0$ – $10^2$  gauss. Soon after that a very short period pulsar should emerge. As radio luminosity is normally small and not a strong function of period, and the nebular plasma frequency will be large, a radio pulsar will not be detected<sup>25</sup>. In the case of the Crab nebula a significant fraction of the slowdown energy is seen as hard pulsed radiation, so we may expect X-ray and perhaps optical pulses in the millisecond range to be seen from SN1987A<sup>25</sup> by 1990.

The relatively specific predictions presented here (submitted 3 April 1987) allow one to test the hypothesis<sup>12–16</sup> that the SN1987A supernova is being driven by a central pulsar.

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- Paczynski, B. *IAU Symp.* No. 66 (eds Taylor, R. J. & Hessler, J. E.) 62 (Reidel, Dordrecht, 1974).
- Arnett, W. D. *IAU Symp.* No. 66 (eds Taylor, R. J. & Hessler, J. E.) 150 (Reidel, Dordrecht, 1974).
- Bethe, H. A. & Wilson, J. R. *Astrophys. J.* 295, 14 (1985).
- Burrows, A. & Lattimer, J. M. *Astrophys. J.* 307, 178 (1986).
- Woosely, S. F., Wilson, J. R. & Maygle, R. *Astrophys. J.* 302, 19 (1986).
- The Kamiokande-II Collaboration *Phys. Rev. Lett.* 58, 140 (1987).
- Bahcall, J. N., Dar, A. & Piran, T. *Nature* 326, 135 (1987).
- Colgate, S. A. & White, R. H. *Astrophys. J.* 143, 626 (1966).
- Bethe, H. A. & Wilson, J. R. *Astrophys. J.* 295, 14 (1985).
- Goodman, J., Dar, A. & Nussinov, S. *Astrophys. J.* (in the press).
- Falk, S. W. *Astrophys. J.* 226, L133 (1978).
- Chevalier, R. *Astrophys. J.* 251, 159 (1981).
- Ostriker, J. P. & Gunn, J. E. *Astrophys. J.* 184, 195 (1971).
- Rees, M. J. *Astrophys. J.* 6, L55 (1970).
- Bodenheimer, P. & Ostriker, J. P. *Astrophys. J.* 191, 465 (1974).
- Bisnovati-Kogan, G. S. *IAU Symp.* No. 66 152 (eds Taylor, R. J. & Hessler, J. E.) 152 (Reidel, Dordrecht, 1974).
- Gaffet, B. *Astrophys. J.* 216, 852 (1977).
- Symbalisty, T. M. D. *Astrophys. J.* 285, 729 (1984).
- Kulsrud, R. *Astrophys. J.* 163, 567 (1971).
- Friedman, J. L., Ispier, J. R. & Parker, L. *Astrophys. J.* 304, 115 (1986).
- Cutter, C. & Lindblom, L. *Astrophys. J.* 314, 234 (1987).
- McCray, R., Shull, J. J. & Sutherland, P. *Astrophys. J.* (in the press).
- IAU Circ.* No. 4352 (1987).
- IAU Circ.* No. 4356 (1987).
- Bahcall, J. N., Rees, M. J. & Salpeter, E. L. *Astrophys. J.* 162, 737 (1970).

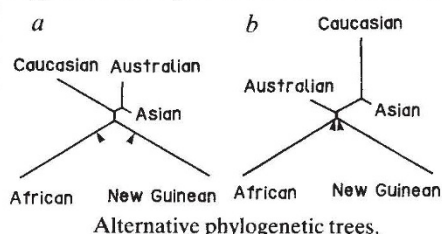
## Time and place of human origins from mt DNA data

SIR—Cann *et al.*<sup>1</sup> claim, from their mitochondrial DNA data, that the origin of current human populations was probably in Africa and that the time of divergence was about 200,000 years ago. We think however, that the place and the time of origin of *Homo sapiens sapiens* are difficult to estimate from their data.

The figure shows two phylogenetic trees obtained from the genetic distance data of Table 1 of ref. 1. These two unrooted trees were constructed by the neighbour-joining method<sup>2</sup> and both are equally the best of 15 possible topologies. Branch lengths are proportional to the estimated distances. Note that Africans and New Guineans cluster together in both trees. Although the branch separating these two populations from others is short in both trees, this clustering is supported by other tree-making methods such as UPGMA, Fitch and Margoliash's method, Farris' distance Wagner method, modified Farris method, and the transformed distance method (see ref. 3 for details of these methods). However, analyses of data from many nuclear loci show that New Guineans are clustered with Australians (Aborigines), instead of Africans<sup>4,5</sup>.

Arrows in the figure denote the points of the root, the common ancestor for all populations, determined by minimizing the variance of the distances from all populations. In this case, a rough constancy of the rate of evolution is assumed. Interestingly, there are two such points in both trees of the figure. If we accept this rooting procedure, not only Africans but also New Guineans can be the population that diverged first.

Without referring to the population phylogeny described above, Cann *et al.* focused their discussion on the gene phylogeny of mitochondrial DNA types (Fig. 3 of ref. 1). To give a tentative time scale, the rate of nucleotide substitution was assumed to be 2–4% per nucleotide site per million years. However, if we apply this rate to the data on hominoids<sup>6</sup>, the divergence time between humans and chimpanzees or gorillas becomes only 1.4–2.8 million years. A more reasonable estimate (0.71% per site per million years) has been obtained by Nei<sup>7</sup>. If we take this value, the divergence time of the point 'a' of Cann *et al.*'s Fig. 3 (ref. 1) becomes 400,000 years. This is in the middle of the supposed time span of *Homo erectus*, but



this may not mean that this alternative estimate of the rate is too small. Genetic polymorphism is expected in the ancestral human population and the mean coalescence time of alleles (mitochondrial DNA types) in this ancestral population can exceed one million years, if the average effective size and the generation time in the past have been 10,000 and 25 years, respectively<sup>7</sup>. Thus, there is no need to assume multiple colonizations.

In conclusion, we believe that data from mitochondrial DNA, which can be regarded as a single locus, are not enough by themselves to establish the branching pattern of human populations.

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- Cann, R. L. *et al.* *Nature* 325, 31–36 (1987).
- Saitou, N. & Nei, M. *Molec. Biol. Evol.* (in the press).
- Nei, M. *Molecular Evolutionary Genetics* (Columbia University Press, New York, 1987).
- Omoto, K. in *Molecular Evolution, Protein Polymorphism and the Neutral Theory* (ed. Kimura, M.) 193–214 (Springer, Berlin, 1982).
- Nei, M. in *Population Genetics and Molecular Evolution* (eds Ohta, T. & Aoki, K.) 41–64 (Japan Science Society Press, Tokyo, 1985).
- Ferris, S. D. *et al.* *Proc. natn Acad. Sci. U.S.A.* 78, 2432–2436 (1981).
- Takahata, N. & Nei, M. *Genetics* 110, 325–344 (1985).

## Varieties of sexual contact

SIR—May and Anderson report a wide variation in the estimates of  $\beta$ , the transmission probability for a single contact between a carrier of human immunodeficiency virus 1 (HIV-1) and a susceptible person<sup>1</sup>.

One explanation may lie in the failure of researchers, including May and Anderson, to distinguish between the various degrees of contact. In other words, it is not sufficient to ask how often new partners are acquired. One should rather inquire how often a new 'risk-partner' is acquired<sup>2</sup>. Moreover, a new risk-partner is anyone with whom one has had unsafe sex after having had unsafe sex with anyone else. This applies (perhaps repeatedly) even to one's regular partner in an otherwise exclusive relationship.

The problem is highlighted by the fact that male homosexual practices vary with different partners<sup>3</sup>. Because, for example, casual gay sex does not usually involve penetration, whereas casual heterosexual sex does<sup>4</sup>, any estimation of  $\beta$  which ignores this point may easily be in error by an order of magnitude.

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- May, R. M. & Anderson, R. M. *Nature*, 326, 137–142 (1987).
- Reece, G. J. *Modelling the Spread of AIDS*, (Social Research Unit, University College, Cardiff, 1987).
- McManus, T. J. & McEvoy, M. *Br. J. sex. Med.* 14(4), 110 (1987).
- Kinsey, A. C., Pomeroy, W. B. & Martin, C. E. *Sexual Behaviour in the Human Male* (Saunders, Baltimore, 1948).