



An anthropologist asks why Neandertals cannot make up part of the ancestry of modern humans, even if their genes are not evident: "Perhaps we should slow down and consider a...parsimonious explanation for why Neandertals seem so human-like...." Acid rain is said to still be a major problem for natural ecosystems, unlikely to be improved by a free-market approach to regulation. A reader expresses concern about whether natural and evolutionary history may be overlooked in molecular studies. And an evolutionary mechanism called the Handy-Dandy Kitchen Device is proposed.

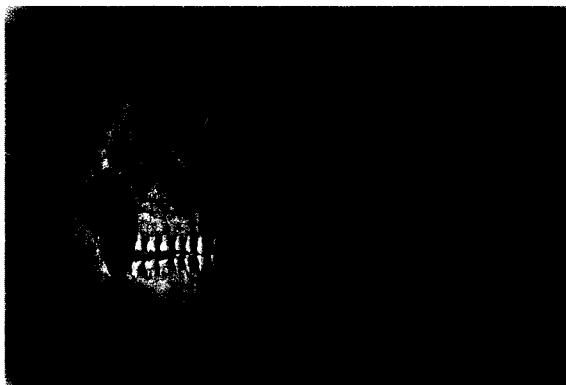
Neandertals: Not So Fast

Constance Holden (Special Section, Archaeology, 20 Nov., p. 1456) cites evidence indicating that Neandertal mitochondrial DNA (mtDNA) shows they had been a distinct branch from the human tree for a half-million years (Research News, 11 July 1997, p. 176) and refers to the debate about why, if Neandertals are so similar to us, they became extinct just at the time of their "technological golden age." Of course, all populations alive at that time are now extinct, so the question is whether the Neandertals became extinct without issue. This is a behavioral matter if we assume that behavior and biology are linked together, rather than being unlinked, as they are between human populations today. This assumption requires that Neandertals were a distinct and separate evolutionary line.

Holden contends that the mtDNA shows this, but for this interpretation of the ancient mtDNA (1) to be correct, one must assume that (i) the history of the Neandertal mtDNA lineage segment is a population history, (ii) constantly accumulating mutations are the sole cause of mtDNA evolution, and (iii) the mutation rate of mtDNA is known with sufficient accuracy to date the putative split. Belief in the Eve theory of modern human origins is the most important prerequisite for these assumptions (2), because it ties mtDNA history to population history through the explanation that low-mtDNA diversity in humans comes from a recent population-size bottleneck at the beginning of a new species.

But this interpretation is not obviously correct. The mtDNA observations are insufficient to resolve issue of whether they were a separate evolutionary line. For instance, a different reason why we may not find many of their genes is that, if Nean-

dertals made up 25% of the ancestry of all modern humans (3), there is a better-than-50% chance that all their mitochondrial genes would have been lost because of drift (4). This calculation assumes a slow, or phylogenetic, rate of change for mtDNA. If the rate was 100 times faster, as intergenerational studies now suggest (5), Ne-



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andertal genes could not have been lost by drift, but then there would have been ample possibility for them to have evolved into the modern genome through mutations (6). Most important, the star-shaped genealogy of the human mtDNA genome reveals a history of selection (6), and post-Neandertal selection in human mtDNA renders all of these phylogenetic interpretations meaningless.

Perhaps we should slow down and consider a more parsimonious explanation for why Neandertals seem so human-like in brain size and anatomy, the speech-related details of the hypoglossal canal, hyoid bone anatomy, burial behavior, hunting prowess, and invention of a true Upper Paleolithic industry in Europe. If it looks like a duck and quacks like a duck....

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cently estimated from anatomical considerations that Neandertals must have made up at least 25% of the ancestry of modern Europeans; if so, their contribution to all modern humans would be much smaller [J. Hawks in *Human Evolution: Abstracts of Papers Presented at the 1997 Cold Spring Harbor Symposium on Human Evolution*, L. Cavalli-Sforza, Ed. (Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1997), p. 81.]

3. M. Nordborg, *Am. J. Hum. Gen.* **63**, 1237 (1998).
4. L. Loewe and S. Scherer, *Trends Ecol. Evol.* **12**, 422 (1997); T. J. Parsons, D. S. Muniec, K. Sullivan *Nature Genet.* **15**, 363 (1997).
5. K. Hunley and A. Merriwether, paper presented at the 1998 meeting of the Human Biology Association, Salt Lake City, Utah, 31 March to 1 April 1998.
6. J. Hey, *Mol. Biol. Evol.* **14**, 177 (1997); C. A. Wise, M. Sraml, S. Easteal, *Genetics* **148**, 409 (1998).

Solving the Acid Rain Problem

We applaud the successful application of flexible regulatory mechanisms in combination with a free-market approach in lowering the costs of reducing sulfur emissions to the atmosphere (R. A. Kerr, *News Focus*, 6 Nov., p. 1024). However, we have serious misgivings about solving the acid rain problem by the trading of sulfur emissions based only on a free-market approach. A trading program that cuts U.S. emissions, but allows continued amounts of damaging deposition on sensitive ecosystems would miss the point.

The major question to be resolved is whether the 1990 Clean Air Act Amendments will reduce significantly atmospheric deposition of sulfur and nitrogen compounds to sensitive ecosystems, such as in the Appalachian and Adirondack Mountain regions and eastern Canada, and, more important, whether these ecosystems can recover after inputs are reduced.

The information available to us does not support Kerr's statement that "with some significant exceptions, lakes and forests are on the road to recovery." Indeed, recent articles suggest that the expected recovery of natural ecosystems has not been observed (1). Also, Kerr does not mention acid NO₃ deposition, yet this is a large and growing component of the acid rain problem in eastern North America. At Hubbard Brook Experimental Forest (HBEF), New Hampshire, with the longest, continuous record of precipitation chemistry in North America, currently about 45% of the acidity is contributed by nitric acid, and it will be the dominant acid in precipitation by the early 2000's if present trends continue (2). There is no cap on total U.S. NO_x emissions. Also, Kerr does not mention the dry deposition of acidifying gases and particles, which can contribute 30% to 50% of total acid deposition, whether as sulfur or nitrogen (3).

The idea of "sweeter rain" is supported in Kerr's article by a figure that is not accurate for the locations with which we are

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familiar (for example, HBEF). Since 1983, there has been no significant change in the pH of precipitation at HBEF, yet the figure would suggest otherwise.

Currently, there is much interest and debate about trading CO₂ emissions in the free market. As control strategies are considered, it will be important to recognize the fundamental difference in biogeochemical effect of sulfur and carbon emissions. Carbon dioxide is a major greenhouse gas, so its concentration and mixture throughout the atmosphere are critical, whereas acidifying gases and particles of sulfur contribute to the acid rain problem when they are deposited to the Earth's surface, after being transported in the atmosphere (4). Thus, the location of emission sources is much less critical for CO₂ than for SO₂ emissions in causing environmental change.

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3. *Clean Air Status and Trends Network (CASTNet) Deposition Summary Report (1987-1995)*, (EPA/600/R098/027, U.S. Environmental Protection Agency, QST Environmental Inc., Gainesville, FL, 1998).
4. Obviously, CO₂ also interacts dynamically with organisms and with Earth's surfaces; SO₂ can be a phytotoxicant at high concentrations in the atmosphere, and aerosols can affect global warming.

The Context of Molecular Data

Elizabeth Pennisi, in her article about the *methuselah* gene regulating life-span in *Drosophila* (News of the Week, 30 Oct., p. 856) includes a quote from molecular geneticist Cynthia Kenyon: if this process "happens in both worms and fruit flies, you have to be crazy to think it won't happen in vertebrates." Although likely an impromptu comment from Kenyon, the immediate conclusion and the underlying thought are troubling.

First, the referenced flies and nematodes are animals with short life-spans and highly regulated development, making them valuable model systems, but possibly unrepresentative of their respec-

tive phyla. Additionally, both taxa may be more closely related than previously suspected, as some evidence suggests they are members of a larger grouping within the Protostomia, the Ecdysozoa (1). Thus, a *methuselah*-type gene may simply be a shared character of the Ecdysozoa and not relevant to deuterostomes.

Second, I am concerned that natural and evolutionary history are often overlooked in such extrapolations from molecular data. I see this attitude reflected in an increasing number of undergraduates. Many important strides, such as the Modern Synthesis, were achieved by scientists integrating theory and laboratory studies with natural history observations (2). Natural selection generally acts at the level of the organism (3), so we ignore the context in which the organism operates at our peril.

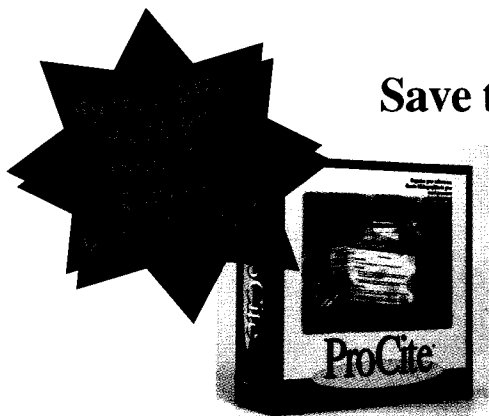
Whether from natural or laboratory systems, data need to be evaluated in terms of the contributing organisms' overall biology. Otherwise, we as a society may begin missing both forest and trees for all the cells, mitochondria, and genes.

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