



Figure 1 Alternative interpretations of core–mantle interaction as surmised from the tungsten isotope ^{182}W . Formation of the Earth’s core (left) results in separation of tungsten into the core along with iron, whereas its parent hafnium (^{182}Hf) remains in the mantle. **a**, In the preferred model of Scherstén *et al.*¹, the core forms early (some 30 million years after accretion of the Earth), with only mild separation of hafnium and tungsten. The core subsequently remains isolated from the mantle. **b**, An alternative model postulates very early core formation (say, within 5 million years), stronger hafnium–tungsten separation, and mixing at the core–mantle boundary which results in transfer of core material into the mantle. Both models could produce a modern mantle with a tungsten isotope anomaly of $\epsilon\text{W} = +2$, as assessed from rocks, such as those on Hawaii, that are produced by an ascending mantle plume.

made on exactly the same Hawaiian rock samples that displayed enrichments in ^{186}Os attributed to a contribution from the core, and there is no correlation between the ^{186}Os and ^{182}W isotopes.

The authors thus draw the most obvious conclusion — that lack of variation in the tungsten isotopes, and absence of a correlation with ^{186}Os , must mean that there is no contribution from the core in these Hawaiian hotspot samples. Nor, they believe, is there any such contribution in other, South African samples derived from the deep mantle (kimberlites) that they analysed. This is the simplest and most straightforward explanation of the data. The authors outline at least one way — recycling of oceanic plates in the convecting mantle — in which the ^{186}Os anomalies can be explained in the absence of ^{182}W anomalies.

This conclusion is an important one — it implies that the Earth’s core has remained perfectly isolated from the mantle since it formed, and that the only thing coming out of the core is heat.

However, there remain tantalizing clues that the story may not be so simple. Mantle concentrations of highly siderophile elements have long been known to be much higher than those predicted from the behaviour of such elements in high-temperature core-formation experiments². Most of these experiments were conducted at much lower pressures than those pertaining at the core–mantle boundary. So the mantle enrichment in highly siderophile elements might be merely the result of a higher pressure of core formation, and their different behaviour under such conditions.

Yet there is another possible model (Fig. 1b). It is conceivable that the differences in the ^{182}W abundances in the core and mantle are even larger than those modelled by Scherstén and colleagues. If the Earth’s core formed and removed tungsten from the mantle much earlier than previously

thought (say, within the first 5 million years of Earth’s formation), the core could have a depleted ^{182}W abundance as low as $\epsilon\text{W} = -4$, similar to that of some iron meteorites that are themselves the ancient cores of fragmented protoplanets^{7,8}. If so, then ^{182}Hf decay in the mantle over the next 60 million years will have produced an enormous anomaly in ^{182}W (perhaps as high as $\epsilon\text{W} = +30$ to $+35$). In this case, the only way to produce a modern mantle with a small ^{182}W anomaly ($\epsilon\text{W} = +2$) is to postulate very early core formation on the Earth, and then later transfer of some material from the core to the mantle over the next 4.5 billion years of Earth’s history⁹. Still, Scherstén *et al.* do outline a convincing case for isolation of the core from the remainder of the Earth, and their work should provide fertile ground for improved ^{182}W studies in all manner of rocks and meteorites.

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Evolutionary biology

Our relative genetics

David Penny

Data on the chimpanzee genome help in detecting differential selection on individual genes, and in judging whether normal microevolutionary processes are sufficient to account for human origins.

I ncreasingly accurate versions of the human genome sequence are being produced. But to find out what biologically makes us human we also need the sequenced genome of our nearest relative, the chimpanzee, to see whether there is anything in our genetic constitution that could not have arisen by well-understood genetic processes. Last month, a selected version of the chimpanzee genome was published by Clark *et al.* in *Science*¹. The group sequenced about 200,000 protein-coding regions, and combined them with human sequences to give over 20,000 chimp–human gene alignments. The mouse genome was then used as an ‘outgroup’, standard practice in this form of analysis, to leave 7,645 chimp and human genes for comparative analysis.

The fundamental issue here is Darwin’s

bold claim that “numerous, successive, slight modifications” are sufficient for all of evolution (Fig. 1). This can be paraphrased, in later terms, as “microevolution is sufficient to explain macroevolution”². The historical context is that evolutionary biology can be divided into two phases³: first, the acceptance in the 1860s that evolution (macroevolution) had indeed occurred; second, the realization in the mid-1900s that the processes of microevolution (natural selection working through genetics) were necessary for evolution to occur.

Over the past 30 years, with the rise of molecular biology, the search has been on for support for Darwin’s claim and to demonstrate the sufficiency², not just the necessity, of slight modifications in explaining macroevolution. The changes seen within populations and closely related species are by

definition 'slight modifications', and at the genetic level they take many forms — point mutations, small insertions, deletions and duplications of genes, chromosomal inversions and fusions, activation of transposable genetic elements of many kinds, and so on.

To test rigorously for the sufficiency of microevolution in human evolution, the full sequence of the chimpanzee genome will be necessary. But Clark *et al.*¹ make a good start on the task with their tests for the effects of natural selection on those genes that encode proteins. Use of the mouse genome as an outgroup allows estimates of the number of synonymous (silent) mutations and non-synonymous (replacement) mutations. The ratio of the two permits the potential identification of genes that have been under positive selection in humans as opposed to chimpanzees, and vice versa. Not surprisingly, selective changes occur in both the human and chimpanzee lineages (our common ancestor was neither chimp nor human).

One of Clark and colleagues' findings is that human enzymes for amino-acid breakdown (catabolism) have been under positive selection. This is concordant with the generally high proportion of meat (and thus protein) in the human diet, at least in comparison with the more herbivorous chimpanzee and gorilla. The increased capacity to break down amino acids is not surprising in another respect. For example, failure to catabolize phenylalanine has several adverse effects, including brain damage. Overall, the finding lends support to theories⁴ that an increased proportion of meat in the diet of early humans was important for an increase in brain size. Regardless of that, there could also be ethical implications. If early humans ate meat 'naturally', then for example being vegetarian could be considered a personal choice rather than a universal ethical decision. But all that can be claimed here is that scientific knowledge will be necessary, even if not sufficient, for solving such ethical questions.

Complex interactions are evidently occurring between the various genes involved in human olfaction⁵. The extensive results of Clark *et al.*¹ provide a wider picture of the consequences, which range from genes being under positive selection to those that have lost function (pseudogenes) — or those that may be in the process of losing function. These results illustrate how genome-wide information will stimulate new experiments, both at the level of gene expression and with the aim of making physiological comparisons. What, for instance, is the comparative sensitivity of humans and chimps to a range of olfactory stimuli? Do humans have an improved receptivity to odours from the increased proportion of meat and/or cooked foods in our diet? Such tests will allow us to see how genetic differences manifest themselves at the level of the organism, and we



Figure 1 The chimpanzee, our closest relative and a genomic test for Darwin's bold claim: "If it could be demonstrated that any complex organ existed, which could not possibly have been formed by numerous, successive, slight modifications, my theory would absolutely break down. But I can find no such case." (C. Darwin, Ch. VI, "Difficulties of the theory", *On the Origin of Species* 6th edn; 1872.)

can expect a burst of experiments to that end.

For the past 30 years, attempts to explain the differences between humans and chimps have centred on gene regulation⁶, rather than on the genes themselves. Those regulatory changes might be difficult to find in genome analyses, even though microarray experiments can now estimate changes in levels of gene expression⁷. But it is not clear whether genes with conserved, or with changed, levels of expression are the more important. Early in molecular-evolution studies it was assumed that differences in amino-acid sequences were the crucial ones. The neutral theory⁸ challenged this view and showed that the conserved regions of a gene were significant. The relative importance of conservation or change in gene expression remains to be evaluated. At the least, however, finding positive selection^{1,5,9,10} in many genes involved in metabolism and in physiology broadens our ideas on the role of selection in human and chimpanzee evolution.

A further example of what will be possible with full human and chimp genomes is accurate estimates of rates and variability of all the possible microevolutionary genetic changes. It is simple to estimate the number of mutations per year or per generation⁹. But good estimates of the date of divergence between chimpanzees and humans are essential in evaluating microevolutionary change, and the result depends on whether calibration points are used from within¹⁰, or outside¹¹, the primates as a group. But using a point (nucleotide) mutation rate of about 10^{-9} bases per year¹⁰, for a genome size of about 3×10^9 bases, still gives an average of well over one mutation per generation.

Given such information, a long-term issue might emerge: is the trend towards exact replacement rates of human reproduction (two offspring per female) genetically sustainable? If the proportion of deleterious and slightly deleterious mutations is significant, then exact replacement reproductive

rates might lead to eventual genetic decline¹². There is no short-term concern here: the planet's ecological sustainability is a much more immediate worry. But it is an indication of what questions might arise with firmer knowledge of our genetic evolution.

The results of Clark *et al.*¹, then, provide plenty of food for thought. However, there is much more to come: the entire chimpanzee genome is being sequenced by a publicly funded consortium¹³, and some data are already available through GenBank. The full sequence will be available later this year, and further comparative analyses should lead to a definite answer as to whether there is anything in the human genome that is not accounted for by the normal microevolutionary processes. Is there a genetic continuum between us and our ancestors and the great apes? If there is, then we can say that these processes are genetically sufficient to fully account for human uniqueness — and that would be my candidate for the top scientific problem solved in the first decade of the new millennium. ■

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