NEWS AND VIEWS

The cooling Earth

from Henry N. Pollack

WHAT can the exhaust of the Earth's heat engine tell about its internal workings and fuel? The exhaust is the heat lost from the Earth's interior, and the internal workings are the manner by which heat is transported upward from the deep interior. The fuel is thought to be principally nuclear, comprising the radioactive isotopes present in varying trace concentrations throughout the Earth.

Let us look first at the exhaust. The measurement of the heat flux over the Earth's surface is an endeavour of the last two decades, and the global survey is still only half complete. However, an important empirical rule, that heat flow varies inversely with crustal age, has enabled estimates of the heat flow to be made for the unsurveyed areas of the globe. At the present time the Earth seems to be discharging about 40×10^{12}W (ref. 1-3).

Does the engine run smoothly, or does it race or idle on occasion? How characteristic of recent Earth history is the present-day heat loss? Because the heat loss is strongly correlated with the age of the ocean floor, which in turn is related to oceanic crustal accretion rates that are known to be variable, it is likely that the heat flow has fluctuated in the past. Sprague and Pollack[4] have reconstructed the age distribution of oceanic and continental crust over the past 180 Myr and conclude that the heat loss has ranged between 39 and 52×10^{12}W, with an average of 43×10^{12}W, slightly higher than the present-day value.

The internal workings of the Earth engine are only weakly constrained by knowledge of the heat loss alone. The planetary thermal history models of 20 years ago were principally conductive models, in accord with the then prevailing view of an Earth without global scale horizontal movements. However, even before mobility became accepted in the 1970s, Tozer[5] argued that thermally-activated solid-state creep would, in response to thermally induced buoyancy, lead to large scale mobility within the Earth. The temperature dependent creep serves as a thermostat, with convection relieving the Earth of excessive heat by transporting it to the uppermost mantle where it makes the final journey to the surface by conduction through the upper horizontal boundary layer of the convection. This upper boundary layer comprises the plates of the lithosphere.

While the concept of solid-state thermal convection in planetary interiors is clear enough, a complete mathematical description of the process is difficult. The patterns of the Earth's topography, heat flow, gravity, and plate velocites provide surface constraints, but even so the broad features of the convection remain elusive. However, simpler quantitative treatments, which yield certain general characteristics of the convection system have recently been exploited[6-9]; collectively they are referred to as 'parameterized' thermal history models. At the heart of these analyses is the assumption, suggested by both theory and experiments, that the heat loss from a convecting system depends on the temperature difference driving the convection (the so-called Nusselt number — Rayleigh number relationship). The models yield the history of such properties as the mean temperature and viscosity of the mantle and the mean velocity and radial heat flux of the convective circulation over the lifetime of the Earth. The calculations all explicitly require the specification of the variation with time of the Earth's internal heat production, and thus a link is forged to the Earth's nuclear fuel and its characteristic rate of decay.

The existence of nuclear fuel in the Earth has been known ever since the discovery of radioactivity in rocks in the early part of this century. However, the abundance and blend of the fuel has been a subject of some debate. The principal heat-producing isotopes are ^{238}U, ^{235}U, ^{232}Th and ^{40}K, with respective half-lives of 4.47, 0.70, 14.0, and 1.25 billion years. Their abundances in the crust of the Earth are comparatively well known, and recognized to be significant enrichments over any possible primordial concentrations throughout the bulk of the Earth.

What then can be said of the primordial abundances of each of the principal isotopes? It was first pointed out in the 1950s that if the Earth had an isotopic endowment similar to that of the chondritic meteorites then the internal heat production would be just about adequate to supply the surface heat flow. However, the 'chondritic coincidence' as this near equilibrium between heat production and loss came to be known, was not without some inconsistencies as well. In particular, the relative proportions of U, Th, and K in chondrites are rather different from that in terrestrial rocks. If the primitive Earth were indeed chondritic, most of the uranium apparently now resides in the crust, while most of the potassium must be elsewhere, presumably deeper within the Earth. Wasserburg *et al.*[10] proposed an alternative primordial isotopic endowment which reflected the K:U:Th ratios found in the crust of the Earth. Yet a third approach has recently been put forward by Sleep[11] and by Stacey[12] who use the abundance of ^{40}Ar, a decay product of ^{40}K, to estimate the K abundance of the Earth. Their calculations indicate a K:U ratio even smaller than the model of Wasserburg *et al.* The significance of the K:U ratio resides in the much longer half-life of ^{238}U (the dominant uranium isotope) compared to that of ^{40}K. An Earth thermally evolving under the influence of long lived uranium and thorium has a slow and steady release of heat, with a decrease by only a factor of two or so during it's lifetime. A potassium dominated thermal evolution, such as would derive from the chondritic mix, is characterized by a more vigorous early history and an eight-fold decrease in internal heat production over the Earth's history. Thus the thermal and tectonic history of the Earth is closely tied to the blend of the radio-active fuel.

Now come the new family of parameterized thermal history models, and they tell a disquieting story, at least as far as deducing something of the Earth's primitive chemistry from the present-day heat loss. It appears that the heat loss derives not only from radiogenic heat, but also in part from 'initial' heat, that energy residual from the accretion of the planet and settling out of the metallic core. The

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calculated fraction of the present-day heat loss attributable to the initial heat appears to be highly model dependent; Schubert *et al.*[7] estimate that at least 15-35% of the heat flow is non-radiogenic, while Sharpe and Peltier[6] contend that it is not essential to invoke *any* radiogenic heat to understand the main thermal features of the Earth. Initial heat alone may be adequate to drive the Earth engine. Schubert *et al.* emphasize that while the amount of the non-radiogenic heat loss may be reasonably debated, a significant contribution to the total heat flow is unavoidable.

Some generalities do emerge from all the new thermal histories: 1) the Earth is and has been cooling, albeit very slowly, at a rate probably no greater then 100° C per billion years (the quintessential energy storage device!), 2) the cooling has been accompanied by a stiffening of the mantle and a slowing of the convective circulation, 3) the upper boundary layer of the convection, that part of the circulation moving horizontally at the Earth's surface and comprising the lithospheric plates, has thickened over the Earth's history. But if through these models we have learned a little of the functioning of the Earth's engine, it seems we know less than we thought about the Earth's primitive chemistry. The engine apparently will run on nearly any blend of fuel, and the thermal energy exhausted reveals little of the internal chemistry. The principal sources of geochemical insight, alas, must continue to be the continental and oceanic crustal rocks, salted with occasional bits of the mantle, and the much smaller collection of extraterrestrial samples; less help appears to be forthcoming from the Earth's heat than a generation of earth scientists had hoped for. □

The collagen gene family

from Ellen Solomon

COLLAGEN proteins occur as a family of molecules with closely related structures but varying tissue distributions. At least nine different genes code for protein with collagens unique features of a repeating pattern (every third amino acid is glycine) and large amounts of the unusual amino acids hydroxyproline and hydroxylysine.

The total number of genes in the family may be as high as fifteen or sixteen if some of the less well characterized chains are included, as well as the A,B,C, chains of Clq, and if some of the observed heterogeneity in sequence is due to different gene loci. These genes have almost certainly evolved by duplication and divergence of a common ancestral sequence, but nothing is yet known of their linkage. *c*DNA and genomic clones have been isolated from the chick proα_2(I) chain (Lehrach *et al. Proc. natn. Acad. Sci. U.S.A.* **75**, 5417; 1978; Sobel *et al. Proc. natn. Acad. Sci. U.S.A.* **75**, 5846; 1978; Vogeli *et al. Nucleic Acid Res.* **8**, 1823; 1980). Based on clones spanning 55 Kb of the chick genome, de Crombrugghe (National Institutes of Health) estimates that the proα_2(I) gene covers 40 Kb and that there are more than 50 intervening non-coding sequences that vary in size from 60-70 to 3-4,000 bp. These workers have analysed six coding regions in three separate regions of the helical portion of the molecule; five of these are 54 bp (18 amino acids). They propose that the helical portion of the collagen gene arose by duplication and divergence of a 54 bp sequence and that these regions diverged by the insertion or deletion of units of 9 bp — the basic (Gly-X-Y) repeat of collagen. Boedtker and colleagues (Harvard University) have analysed the codon usage for the amino acids in the α_1(I) and α_2(I) chains of Type I collagen and find that the usage differs significantly between the chains. Genomic clones of the sheep proα_2(I) have also been isolated (Schafer *et al. Nucleic Acids Res* **8**, 2241; 1980, and show at least 17 intervening sequences in 60% of the 3′ portion of the gene. Non-coding sequences are 300 to 1,600 bp, while the coding regions are 250 bp or less. Somatic cell genetic studies using species-specific DNA probes should soon clarify the location of some of the collagen genes and their possible synteney, if not linkage.

Haemoglobins (Weissman, Yale University), histones (Zweidler, Institute for Cancer Research, Philadelphia) and heat shock proteins (McCarthy, University of California, San Francisco) were discussed as representatives of rather different types of gene families, in regard to linkage and co-ordinate expression. Until the genetic map of the collagen genes is known it is obviously not possible to know if, as a family, it resembles any of these others. By analogy with the non-linked α and β genes, and the linked $\beta\cdot\delta\cdot\gamma\cdot$ genes of haemoglobin, will the proα_1(I) and proα_2(I) genes of collagen be unlinked and the proα_2(I,II,III,IV,) linked? Alternatively, will all the "collagenes" form a linked cluster as with the histones, or be scattered throughout the genome as with the actin, tubulin, and heat shock genes of Drosophila? As yet there is no information as to whether any of the collagen genes exist in multiple copies.

There are inherited connective tissue diseases which are likely to involve defects in collagen genes, such as Marfan's Syndrome and osteogenesis imperfecta and approaches towards their understanding were discussed. These diseases have eluded definition at the molecular level, largely because of the extreme difficulty of the protein chemistry. It was agreed that current DNA technology should be applied to defining these diseases, bearing in mind that in most cases there is no direct evidence for collagen gene involvement. It is not reasonable to clone collagen genes from individuals with connective tissue disorders without direct evidence that these genes are actually involved as the primary defect. A more general approach is needed whereby collagen gene mutations can be detected. One suggestion was to screen as many different patients as possible, with different diseases, by restriction mapping and Southern blots using collagen probes, and where appropriate tissue biopsies are available, by S1 mapping. Using these two techniques some types of mutations in the collagen genes could be detected. For results from either of these techniques to be meaningful, however, a great deal of data is needed regarding the degree of variation in these genes in the normal population. A second approach discussed at length was that of linkage analysis within families using the collagen gene probes and restriction site polymorphisms, as done by Kan and Dozy, for sickle cell anaemia (*Lancet* **ii** 910; 1978). The collagen diseases are rare, extremely heterogeneous, both clinically and genetically, and probably often represent new mutations. They are unlikely to have evolved by selection, as have some of the haemoglobinopathies, and it was therefore emphasised that each family would have to be screened with a set of restriction enzymes to find an appropriate polymorphism. The purpose of this type of analysis would be both to identify affected fetuses by prenatal diagnosis, and also to indicate the involvement of a collagen gene defect in those diseases.

Also discussed was the complexity of the genetics of a protein with as many enzymatic post-translational modifications as collagen. For example, mutations in different modification enzymes could lead to the same disease phenotype, and different mutations in the same enzyme could give dominant or recessive modes of inheritance.

The extensive post-translational modifications of collagen and proteoglycans, including removal of signal sequences, hydroxylation, glycosylation, disulfide bond formation, triple helix formation, and procollagen to collagen conversion was an important topic. Different types of collagen are modified to different extents and individual types of collagen show a degree of heterogeneity in their particular modification. Among the questions regarding modification, therefore, is to what degree individual primary amino acid sequences determine the position and extent of, say hydroxylation

A conference on 'Gene families of collagens and other proteins' was held from April 27-May 2, 1980 at CMDNJ — Rutgers Medical School. The organisers were D. J. Prockop and P. C. Champe.

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