we obtained values of α significantly larger than 0.5 for both categories. Indeed, only the human embryonic myosin heavy chain sequence lacks the long-range correlations ($\alpha = 0.47$). Thus, we find no consistent difference in α for the intron-containing versus the intronless sequences.

Owing to the considerable deviation of our data from those of ref. 1, we draw attention to the following. We tested the correctness of our computer program (which is based on the equations (1) and (2) of ref. 1) with artificial sequences of variable lengths, produced with the aid of a random-number generator, and obtained $\alpha \sim 0.5$ as expected. Second, we realized that the double-logarithmic (log–log) plot of the function $F(l)$ (as used in Fig. 2 of ref. 1) may easily distort some features of the displayed data. This is clearly illustrated by the two representations shown in the figure for the bacteriophage λ sequence (48,502 base pairs). Note that the log–log plot (*a* in the figure) gives the value $\alpha = 0.53$ (which coincides with the corresponding value of ref. 1) if one takes into account only the first 20–30 points of $F(l)$.

The figure also shows that the log–log plot of $F(l)$ exhibits a significant curvature, demonstrating that $\alpha(l)$ is not a constant. This interesting finding is characteristic for most of the DNA sequences investigated. Additionally, we find that most sequences exhibit a positive curvature (for example the bacteriophage λ sequence) whereas others exhibit a negative curvature. (Note that 15 of the 24 sequences analysed by Peng *et al.* encode myosin heavy chains, and that not even these share a similar value of α.) Thus we can conclude that a well-defined fractal power exponent α does not usually exist for a DNA sequence.

It has been proposed that the long-range correlations in intron-containing sequences may be caused by repeated segments in introns[3–5]. Our results clearly demonstrate that long-range correlations are not unique to introns; see also refs 6 and 7. The explanation for these correlations in DNA sequences remains a challenge.

C. A. Chatzidimitriou-Dreismann*
D. Larhammar
Department of Medical Genetics, Uppsala University, Box 589, S-751 23 Uppsala, Sweden

1. Peng, C.-K. *et al. Nature* **356**, 168–170 (1992).
2. Voss, R. F. *Phys. Rev. Lett.* **25**, 3805–3808 (1992).
3. Li, W. *Int. J. Bifurc. Chaos* **2** (1), 137–154 (1992).
4. Li, W. & Kaneko, K. *Europhys. Lett.* **17**, 655–660 (1992).
5. Maddox, J. *Nature* **358**, 103 (1992).
6. Nee, S. *Nature* **357**, 450 (1992).
7. Prabhu, V. V. & Claverie, J.-M. *Nature* **359**, 782 (1992).

* Permanent address: Iwan-N.-Stranski Institute, Techn. Univ. Berlin, D-1000 Berlin 12, Germany.

Early T-cell development

SIR — The report by Molina *et al.*[1], showing a profound block in thymocyte development in mice lacking the p56^{lck} tyrosine kinase gene, deserves special attention. This work, as well as illustrating the crucial role of this T-cell specific tyrosine kinase in thymocyte differentiation, might also indicate the relevance of the expression of the β-chain of the interleukin-2 receptor gene during early T-cell development.

In T cells, p56^{lck} interacts and transduces signal(s) delivered through the β-chain of the receptor for interleukin-2 and through the CD4 and CD8 coreceptors[2]. The impairment in thymocyte maturation in Lck-deficient mice reflects the inability of any of these molecules to transduce their signal(s). Because both CD4- and CD8-deficient mice have normal thymic architecture and no decrease in the number of thymocytes[3], the most obvious candidate responsible for the observed phenotype in Lck-deficient mice is the interleukin-2 receptor β-chain. These three molecules (CD4, CD8 and the β-chain) are known to participate in T-cell differentiation. Although CD4 and CD8 signals are important during positive selection, the interleukin-2 receptor β-chain is thought to be involved in the prior phase of expansion of earlier thymocyte subpopulations. Thus, the interaction of interleukin-2 with the receptor β-chains constitutively expressed by freshly isolated prothymocytes promotes their differentiation into functionally competent T cells[4].

We have previously reported the analysis of β-chain expression (in the absence of the α-chain) in the most immature T-cell precursors[4]. These studies revealed that pro-T cells isolated from neonatal thymus express higher amounts of β-chain molecules than mature T cells isolated from peripheral blood lymphocytes. By contrast, double-positive thymocytes (the stage at which positive selection of T cells takes place), have few, if any, β-chain molecules on the surface. Interestingly enough, only those differentiation stages characterized by the absence of expression of CD3, CD4 and CD8 and by the expression of the β-chain genes are the ones affected by the developmental blockage observed in Lck-deficient mice.

This, together with the fact that the developmental profile of expression of p56^{lck} parallels that of the interleukin-2 receptor β-chain gene during T-cell differentiation[5], suggests that the phenotype seen in Lck-deficient mice is indicating the essential function(s) *in vivo* of the β-chain molecules during the early expansion and differentiation phase of T-cell development. This view can only be confirmed, of course, by examination of β-chain deficient mice.

Jose C. Gutierrez-Ramos
The Center for Blood Research, Inc., Boston, Massachusetts 02115, USA
Maria Luisa Toribio
Carlos Martinez-A
Centro de Biologia Molecular del CSIC, Universidad Autonoma de Madrid, 28049 Madrid, Spain

1. Molina, T. J. *et al. Nature* **357**, 161–163 (1992).
2. Hatakeyama, M. *et al. Science* **252**, 1523–1528 (1991).
3. Rhaemtulla, A. *et al. Nature* **353**, 180–184 (1991).
4. Toribio, M. L. *et al. Nature* **342**, 82–85 (1989).
5. Perlmuter, R. M. *et al. J. Cell Biochem.* **38**, 117–126 (1988).

Caliche and the carbon cycle

SIR — Kern and Schlesinger[1] infer that there would have been a decrease in carbonate carbon storage on land (as caliche/calcrete in soils) since the last glacial maximum, due to a substantial decrease in the global area of desert and semi-desert[2]. They suggest that this may have offset part of the increase in organic carbon storage which seems to have occurred since that time. However, they do not point out that these two types of reservoir are not really comparable in terms of their roles in the global carbon cycle.

For example, there is a fundamental difference between the ways in which inorganic caliche and organic carbon tend to interact with atmospheric CO_2. An organic reservoir can release its carbon back into the atmosphere as CO_2 when it undergoes oxidation, while a caliche reservoir will tend to weather by taking up more CO_2 to form bicarbonate, when climatic conditions change to favour this. Thus, when a caliche reservoir shrinks due to weathering, it is mainly taking up CO_2 from the atmosphere (and contributing the resulting hydrogen carbonate, via river water, to the oceanic reservoir), while an organic carbon reservoir shrinking due to oxidation will tend to be releasing CO_2 into the atmosphere.

It is interesting to consider that at around the beginning of the present interglacial, both the shrinking caliche reservoir and the expanding organic reservoir would have been taking up CO_2 in parallel from the atmosphere. One can only guess at the quantitative and qualitative effects which these combined CO_2 sinks, together with the enhanced silicate and carbonate weathering sinks of glacial sediments and loess, had on the time course of the atmospheric CO_2