

the branch lengths to coelacanth and lungfish from their common ancestor are 0.27 and 0.65 amino-acid replacements per site, respectively, suggesting that the average rate of β -globin evolution in the lungfish lineage has been more than twice that in the coelacanth lineage, since their divergence. (These particular values come from comparisons with the Port Jackson shark as outgroup, with correction for multiple replacements⁴.) Comparisons between *Xenopus* and *Rana* of the β -globins expressed in larvae (average 44.7 amino-acid differences) and in adults (average 62.4) emphasize that the tadpole β -globins have also evolved slowly.

The neighbour-joining method⁵ is more appropriate than UPGMA, because it allows for unequal rates of evolution, and appears to be one of the most efficient algorithms for estimating the correct phylogeny⁶. This method suggests that the adult frog β -globins are orthologous to the fish proteins, and clusters lungfish with adult frogs (see figure), which is consistent with a result obtained from mitochondrial DNA². But this topology is not statistically reliable, as lungfish and frogs cluster in less than 60% of 1,000 bootstrap resamples. Thus, there are insufficient data to make firm phylogenetic statements. Gorr *et al.* conclude that in frogs the larval globin rather than adult form is orthologous to the fish sequences. Because the tadpole and coelacanth branches are both short, their observation that the β -globin of *Latimeria* is the most similar to tadpoles arises because both have undergone slow recent evolution, and not because they are the most closely related. Gorr *et al.* also used the maximum parsimony algorithm to support their conclusions, but this method also has a tendency to artefactually cluster long branches with long branches (and thus short with short)⁷.

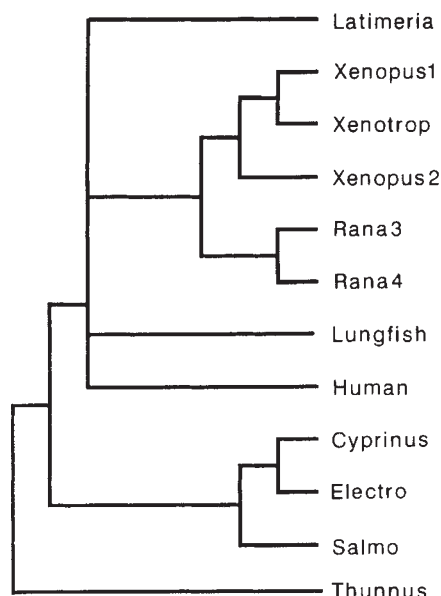
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SIR — Gorr *et al.*¹ claim to have found that the coelacanth is more closely related to tadpoles than are lungfishes. Their Fig. 2 contains a number of surprising and unprecedented groupings.



Evolutionary tree (PAUP, strict consensus⁷) based on analyses of amino acids and DNA data of haemoglobin chains. Names can be inferred from ref. 1.

Only one previous study², which was not based on cladistic approaches, aligned teleost fishes closely with the tetrapods. The new results¹ are at odds with morphological³ and molecular^{4,5} studies.

Several obvious problems in the analyses of their data prompted us and others (see the letter from Stock and Swofford, above) to re-analyse the data of Gorr *et al.* using parsimony⁷. To avoid potential problems of differences in alignment, only data presented in Fig. 1 of Gorr *et al.* have been used in our reanalysis. Ray-finned fishes are used as outgroup in agreement with virtually all phylogenetic hypotheses, which recognize that these fishes are only remote relatives of sarcopterygians³.

In our α -chain analysis we found three equally short evolutionary trees (TL=401, CI=0.803); the strict consensus of these three equally likely solutions is shown in the figure. The α -chain does not allow one to determine the relationships among sarcopterygian groups considered (human, tadpoles, coelacanth and lungfish). In our β -chain analysis we found three equally short trees (TL=427, CI=0.787), the consensus of which groups *Latimeria* closer to the larval, frog's haemoglobin. However, a trifurcation exists with that group and the human and the lungfish. The results of our reanalysis do not agree with the reported outcomes of Gorr *et al.*, even when the sequence data from sharks⁶ were included as outgroups. Reanalyses of amino acids demonstrate that neither the α - nor the β -chains of haemoglobin permit the inferences made in ref. 1.

DNA sequences contain more information than protein sequences, because the replacement of an amino acid

by another at a certain site may sometimes require more than one nonsynonymous substitution at the DNA level. Protein sequences of the β -chains were reverse-translated into DNA (IUPAC-IUB code) and subjected to parsimony analyses⁷. Two equally short trees (TL=514, CI=625) were found, the consensus of which is shown in the figure. Here, also, there is no support for the claims of Gorr *et al.*¹.

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No limit to global warming?

SIR — Ramanathan and Collins¹ have proposed a mechanism which limits the warming of the tropical Pacific Ocean in the present climate. I would like to make two points. First, atmospheric water vapour and cloud, and hence greenhouse trapping and cloud forcing, tend to be reduced in regions of atmospheric subsidence and enhanced in regions of ascent. This effect can be seen in Fig. 2a of ref. 1, where the rate of increase of the greenhouse effect with temperature is smaller than elsewhere between 290 and 298 K, corresponding to the regions of subsidence in the subtropics, and increases steeply as one moves to higher temperatures corresponding to the regions of ascent in the inter-tropical convergence zone. The central equatorial Pacific was a region of subsidence in April 1985 and a region of ascent in April 1987. Hence derivatives from these two years include these dynamical effects implicitly, as Ramanathan and Collins acknowledge, and they tend to enhance the more direct effects of increases in temperature. Indeed, the main region of ascent (and low-level convergence, precipitation and cloud) in the tropical Pacific appears to be linked to the region of maximum sea temperatures, rather than the magnitude of sea surface temperature *per se*². However it is not obvious that, once a region has changed from local descent to ascent, the dynamical