

roosting. Animal rights activists will be pleased that no living birds were injured in the research, and that a hazard to wild birds was reduced.

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SIR—Not all bird droppings repel water on car roofs. In an attempt to support an insurance claim, a series of bird droppings were observed on various vehicles. It appeared in a limited series of eight sightings that only fish-eating birds' droppings have this effect: three seed-eaters, a fruit-eater and a crow had negligible repellent action. Three coastal seagulls, however, gave dramatic responses. I concluded that the cause is dietary oils: the high nitrate and acid content of most guano tends to wet rather than dry an exposed surface.

The repellent effect is seen more clearly on newer cars (post 1980) which have a polyurethane coating. Older baked paints have a less homogenous surface, and are, my insurers tell me, more liable to corrosion by any droppings.

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An alternative to archaeobacterial dogma

SIR—A recent *News and Views* report by Garrett, entitled "The uniqueness of Archaeobacteria", might more aptly have been titled, "The orthodoxy of Archaeobacteria", for it failed to report accurately the reasons that Archaeobacterial dogma is being challenged¹. The conflict at the EMBO Workshop on the Molecular Genetics of Archaeobacteria centred around two competing evolutionary trees. Each tree relates all known organisms from five major evolutionary groups. These trees are of fundamental importance because they describe the early history of all living life forms. If we are to understand molecular evolution, it is vital that we determine the correct tree.

A critical challenge facing molecular evolutionists is how to deal with both fast- and slow-clock organisms in different branches of the same tree. I believe the archaeobacterial tree is an artefact produced by greatly unequal rates in different arms of the tree. This type of situation has been analysed² and it has been found that under conditions of greatly unequal rates, fast-clock organisms will be placed with fast-clock organisms and slow-clock

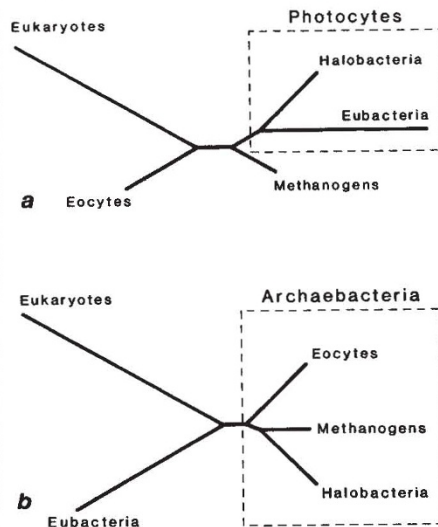


Fig. 1 *a*, The combined photocyte-eocyte unrooted evolutionary tree. *b*, The archaeobacterial unrooted tree.

ones with slow-clock organisms. The archaeobacterial tree places fast-clock organisms together, whereas our eocyte and photocyte trees do not.

Specially, we proposed the tree shown in Fig. 1*a*, based on our analyses of three-dimensional ribosome structure. Our tree makes two unique predictions that have important consequences. First, our data indicate that the eukaryotes are evolutionarily closest neighbours to the eocytes³. This would then explain the many eukaryotic properties of the eocytes, including the recent observations reported at Martinsried, that eukaryotes and eocytes both have similarly constructed ribosomal operons, in contrast to the common pattern which is found in eubacteria, methanogens and in halobacteria.

Our second proposal (shown at the right side of our tree), is that the eubacteria and halobacteria are evolutionarily closest neighbours⁴. Again, this was based on the three-dimensional structure of ribosomal subunits from the major groups. It also brings together all the photosynthetic prokaryotes, the halobacteria and the eubacteria, into a single group. As a result we called the larger group the photocytes and suggested that photosynthesis could have been a primitive property of the group.

The alternative archaeobacterial tree proposed by Woese and coworkers is shown in Fig. 1*b*. According to this tree, derived from sequence data, the slow-clock organisms on the right side of the tree are classified as the archaeobacteria. The two fast-clock organisms, indicated by long arms of the tree, are both on the left side of the tree. This is precisely the effect expected when evolutionary rates differ greatly in different branches of a tree. Hence, primary sequence data, as presently analysed, neither support nor disprove the archaeobacterial tree or any other tree.

Our tree, based on ribosome structure, appears to be insensitive to this effect, probably because three-dimensional structures are much more conserved than are primary sequence data. The best documented examples of this are provided by protein structures, determined by X-ray crystallography, that are well conserved between distant organisms and yet have primary sequences that have diverged so much that they are scarcely recognizable. Under conditions of lower absolute evolutionary rates it is known that trees will reflect the correct topology. Hence, three-dimensional structures, because they are better conserved than primary sequences, seem to be ideally suited for determining the deepest branching in the evolutionary tree.

Molecular evolution is on the way to establishing an accurate classification of organisms. This classification must be built on phylogenetically correct trees. I believe that the optimistic message that came from Martinsried was "let's wait and see which tree is correct". Time will reveal the correct tree and with it will come the correct classification at the kingdom level.

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Animal model for Epstein-Barr lymphoma

SIR—I was surprised to read in the *News and Views* section of the issue of 21 November 1985, an erroneous statement. A.J. Beale, in his piece "Epstein-Barr virus: Dream or reality of a vaccine" states that "Epstein *et al.* have developed an animal model of EBV-induced lymphomas in cotton-top tamarins (*Saguinus oedipus oedipus*)"¹.

In fact, Dr Thomas Shope and I and other colleagues developed this experimental model of lymphomagenesis by EBV in the early 1970s. It depended on the production of the high titred immortalizing B95-8 strains of EBV² and showing that the cotton-top marmoset was susceptible to induction of malignant lymphoma on inoculation with B95-8 virus³.

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