

the displayed spectrum¹ of the G9V star HR1232 yields a wavelength of 6,704.69 ± 0.28 for the feature nearest the lithium line, which is probably a blend of the 6,703.58 and 6,705.11 Å lines of Fe I whose mean, when weighted by the equivalent widths in the solar atlas⁴, is 6,704.23.

The lithium in V404 Cyg may be related to the fact that it is a binary with a period not too different from those of the RS CVn stars, which often show strong lithium lines despite their spectral types being about K0IV (ref. 5). But for RS CVn stars with $T_{\text{eff}} < 5,000$ K, the lithium abundance as given in Fig. 11 of ref. 5 is $\log N_{\text{Li}} \leq 1.8$ for 42 of 45 observed stars. For stars whose Li I line shows the same strength as 6,719 of Ca I, $\log N_{\text{Li}} \approx 2.5$, hence it is much more likely that V404 Cyg is a main-sequence star and neither a giant nor a subgiant. In addition, RS CVn stars are binaries consisting of a K giant or subgiant and a main-sequence star, not a compact star.

If our identification of the line at 6,708.0 Å as Li I is correct, a comparison with neighbouring lines indicates that the companion must have a lithium abundance near that of Pleiades stars of similar spectral type ($\log N_{\text{Li}} =$ about 2.5 on the standard scale of $\log N_{\text{H}} = 12$)². This

indicates that the age of the V404 Cyg system is of the order of 10^8 years because the lithium abundance is sufficiently uncertain that lithium might not have been depleted from the interstellar value at all.

Our confirmation that V404 Cyg is a dwarf adds weight to the model that places V404 Cyg at about 1.5 kpc from the Sun and an outburst X-ray luminosity near 3×10^{38} erg s⁻¹. This limits the possible models of the system. As discussed in ref. 1, the period of 6.5 days leads to an orbit which is too large for mass transfer to be taking place through the inner lagrangian point. Hence the model of V404 Cyg as a triple system with an unseen companion orbiting a black hole with a period near 6 hours becomes more likely.

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Bacteria and eukaryotes

SIR — The suggestions that eukaryotes should be renamed synkaryotes¹ or eukarya² should be strongly resisted. The purpose of biological nomenclature is not to describe taxa but to give clear, consistent and unambiguous labels to them: stability is highly desirable, and nomenclatural codes have always sought to discourage unnecessary changes. Neither of these changes has any merit whatever. Forterre¹ is mistaken in supposing that 'eukaryote' implies that eukaryotes are derived from prokaryotes. Eukaryote simply refers to their 'well-developed nucleus', an entirely correct description. But even if it were not, that would be no reason to change their name. Biological nomenclature is replete with descriptively inappropriate and misleading names of taxa that are retained because to change them would be confusing and impair information retrieval and effective communication. If I met a woman named Violet Green I would not ask her to change her name if she were neither colour.

For this reason I am opposed to the tendentious and illogical change of Archaeobacteria to Archaea². Archaeobacteria has been so long and widely accepted and understood that it seems undesirable to change it. The proposed change follows the more widespread rec-

ognition that Archaeobacteria are less old and much less distinct from eubacteria than Woese and Fox³ originally thought. One might have supposed that if this should prompt any change, it would be to Neobacteria, or better still to Metabacteria, as suggested long ago⁴ by those who never accepted the dogma that this group was as old as eubacteria. The proposed name of Archaea, and the even more confusing renaming of Eubacteria simply as Bacteria, seem designed to promote the oft-repeated but unjustifiable view that archaeobacteria are not bacteria at all but represent, as originally claimed, 'a new form of life'. Woese has mistakenly and repeatedly asserted that his recognition and firm establishment of the kingdom Archaeobacteria (certainly a great and important breakthrough) invalidates the classical distinction between prokaryotes and eukaryotes. But as archaeobacteria fall within the scope of prokaryotes and bacteria by every criterion as classically defined⁵, it does nothing of the kind.

If Forterre really does not like the term prokaryotes, because 'pro' does indeed have the connotation 'before', why does he not, instead of proposing a totally unnecessary new name, simply call them Bacteria, as they have been known for more than 100 years? The renaming of blue-green algae (a vernacular not a systematic name) as cyanobacteria made 'prokaryotes' simply a junior synonym for bacteria. More than 50

years ago, Prévot⁶ wrote, "*Pourquoi ne pas avoir le courage de dire: le Règne bactérien?*" I have therefore long adopted Bacteria as the formal scientific name for the superkingdom⁷, or empire^{8,9}, that includes the kingdoms Archaeobacteria and Eubacteria.

On the more substantive issue of whether bacteria are more primitive than eukaryotes, Forterre ignores the fossil evidence that they indeed are⁸. If he wishes his speculation that bacteria evolved by reductive evolution of eukaryotes (he actually says 'proto-eukaryotes', but I here take this vague term to mean 'first eukaryote') to be taken seriously, he should attempt to explain how they could have lost the cytoskeleton, endomembrane system and nuclear pores, as well as abolished mitosis and fused together their chromosomes into a circle and attached them to the plasma membrane, and drastically changed their DNA replication and segregation system. I have discussed⁹ the nature of the changes from the simpler bacterial cell to the vastly more complex eukaryotic one. Anyone who wishes to argue for the reverse ought to develop their hypothesis in enough detail for it to be shown to be mechanistically plausible (which I strongly doubt) and explain how it can be reconciled with palaeontological evidence^{8,9}.

The changes involved in forming a eukaryote from a bacterium are far more numerous and radical⁹ than those relatively much more trivial ones that separate eubacteria and archaeobacteria. For this reason the distinctions between bacteria and eukaryotes remain by far the most fundamental in the living world (other than the distinction between true, cellular organisms and viruses), and this primary division into two multikingdom empires (Bacteria and Eukaryota)^{8,9} is greatly to be preferred to a division into three domains². The latter has all the demerits of a one-character (one-molecule!) classification and ignores the numerous fundamental positive characters — both in genomic and in cellular organization^{7,9} — shared by all bacteria.

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