deeply integrated into the molecular fabric of these cells. These are precisely the features expected to be good evolutionary markers.

No properties support the Woese tree, including the "founding" ones upon which both the tree and classification were proposed, "membrane, cell walls, rRNAs and tRNAs"[1]. These "founding" properties are listed in Table 1. For example, 16S rRNA oligonucleotide catalogues indicate that the eubacterial pattern is different, but they do not identify which group the eubacteria are closest to. All of their characters are three-and-one and cannot support any tree. When judged by standard evolutionary procedures and tests, the same "founding" properties which prompted Woese's taxonomic proposal, fail to support his tree.

Ribosomal RNA sequences, as rapidly evolving molecular characters, are subject to artefactual analysis by parsimony. No matter what the correct tree, parsimony and other treeing algorithms can consistently predict a tree which, like Woese's places fast-clock groups (that is, eubacteria and eukaryotes) together[13]. When we analyse the rRNA sequence data using the method of phylogenetic invariants, which is insensitive to this artefact and independent of evolutionary rates, we find support for our eocyte/photocyte trees is significant at greater than the 99% level[14,15].

Woese claims that his proposed classification could be used with any tree. A classification that fits all trees is no classification at all. Consider the arginine deiminase pathway found in the photocytes (eubacteria and halobacteria). We interpret it as having evolved once in the photocytes. Woese's proposed classification, making it a property occurring in two "kingdoms," misdirected others to propose either (1) that it was invented twice, or (2) that it was laterally transferred between "kingdoms"[8]. An incorrect classification has great negative power to obscure and misdirect.

Science and not semantics, then, is the basis of our claims. We see no support for Woese's tree and taxonomic proposal from any molecular properties, whereas deep and fundamental properties support our eocyte and photocyte trees and classification. Viewed through the photocyte tree, membranes, biochemical pathways, and components of biochemical energetics are all natural and logical consequences of evolutionary history. Well integrated molecular biological and metabolic properties support the photocyte and eocyte trees and classifications. In the end, evolutionary connections, and not semantic ones, between organisms give theories true organizational and predictive value.

Table 1 Prokaryotic molecular properties

	Eubacteria	Halobacteria	Methanogens	Eocytes
	VALID BY PARSIMONY (Photocyte)			
Arginine deiminase pathway	+	+	-	-
Tetraether lipid	-	-	+	+
2Fe-2S ferredoxin	+	+	-	-
C40 carotenoids	+	+	-	-
Fatty acid esters	+	+	-	-
C50 carotenoids	+	+	-	-
Similar carotenoid synthesis pathways	+	+	-	-
Ribosomal 50S eocytic lobes	-	-	+	+
rRNA sequences	SEE DISCUSSION			
	IRRELEVANT BY PARSIMONY (Woese s characters)			
Ester lipids	+	-	-	-
Eubacterial cell walls	+	-	-	-
Eubacterial oligonucleotide catalogs	+	-	-	-
F-met initiator tRNA	+	-	-	-

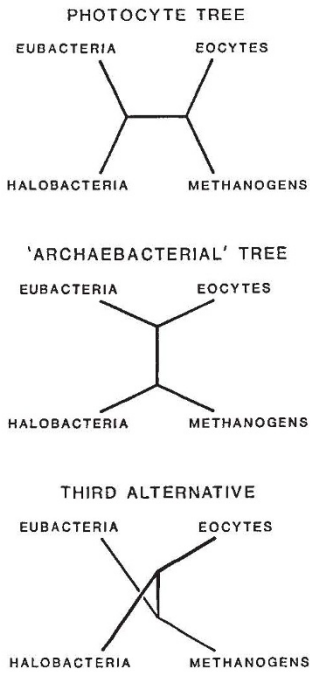

Fig. 1 All alternatives for linking the four prokaryotic evolutionary groups are represented in these three unrooted trees.

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Testis size and dizygotic twins

SIR—A recent article in *News and Views*[1] discussed R.V. Short's observations[2] on human testis size and dizyotic twin frequency in Asian, Indian, Caucasian and African ethnic groups.

Large testes were the first clinical feature to be associated with fragile X chromosome-linked mental retardation[3,4]. A mean testicular volume of 48 ml (range 15–127 ml, modal volume 35–40 ml) was observed[5] for adult white fragile X males in whom testicular volume was not a factor in ascertainment. The average testicular volume in unaffected Caucasian males is 20 ml. In an ascertainment of fragile X-affected kindred in Hawaii[6], it was noted that the mean testicular volume (22 ml) of pure Japanese males was less than that (39.5 ml) of pure Caucasian males. This reflected a previously observed difference between unaffected males of these ethnic origins.

A recent Belgian study[7] of 144 obligate female carriers of the fragile X led to the conclusion that such carriers have a high fertility, especially in those who are mentally subnormal (30%). An increase in the incidence of twinning was observed in the 642 progeny of 134 obligate carriers. Of 18 pairs of twins, 12 were dizygotic, and, in the remaining 6, the zygosity could not be determined. This incidence (1 in 35 births) is three- to-four-fold that of the expected incidence of twinning in Caucasians (1 in 80 to 1 in 140 births)[8]. This specialist fragile X-bearing population therefore would appear to express parallel variations to those already observed by your contributors.

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