

A natural system of organisms

SIR—For a remarkably long time after the publication of Linnacus's *Systema Naturae* (1758) only two branches of systematics were generally recognized: zoology and botany. Fungi and even bacteria were traditionally looked after by botanists and studied in botany departments. In due time, primarily because of their medical importance, the bacteria were recognized as different from higher organisms and eventually it was realized that the fungi had nothing particularly in common with the plants. Making use of these insights, Whittaker¹ suggested recognizing five kingdoms of organisms (Animalia, Plantae, Fungi, Protista and Monera) and this proposal was widely adopted.

In an article published in June, Woese *et al.*² correctly pointed out that a system that assigns the same rank to five higher taxa that differ from each other so unevenly is highly unbalanced and therefore unsatisfactory. Instead, they proposed to recognize three 'domains' of organisms, the Bacteria, the Archaea and the Eucarya. Unfortunately, in this arrangement the previous imbalance is replaced by a different one. The ranking in the classification suggested by Woese *et al.* is based entirely on the amount of difference in ribosomal RNA, ignoring the enormous evolutionary step from the prokaryotes to the eukaryotes. I would like to propose a new classification of the living world based on that second consideration.

The difference in structural organization between prokaryotes and eukaryotes is an order of magnitude greater than the relatively small difference between the Archaeobacteria and the Eubacteria. As important as the molecular distance between Archaeobacteria and Eubacteria may seem to a specialist, as far as their general organization is concerned, the two kinds of prokaryotes are very much the same. By contrast, the series of evolutionary steps in cellular organization leading from the prokaryotes to the eukaryotes, including the acquisition of a nucleus, a set of chromosomes and the acquisition, presumably through symbiosis, of various cellular organelles (chloroplasts, mitochondria and so on), results in the eukaryotes in an entirely novel level of organization. This new organization has had fundamental consequences for the further evolution of the eukaryotes, including diploidy, sexuality and meiosis.

This was surely the most drastic change in the whole history of the organic world. It seems that the fundamental difference between prokaryotes and eukaryotes, originally pointed out by Chatton¹, should be made the basis of the first great classificatory division in the system of organisms. Using the categorical term 'domain'

proposed by Woese *et al.*, one could adopt a division of the organic world into two great domains, the Prokaryota (Monera) and the Eukaryota.

The specialists of the Prokaryota will have to decide what rank (category) to choose for the Archaeobacteria and Eubacteria, either subdomain or kingdom. Ranking them as subdomains would permit ranking the two divisions of the Archaeobacteria as the kingdoms Crenarchaeota and Euryarchaeota. As far as the domain of the Eukaryota is concerned, instead of recognizing the customary four kingdoms, it might be advisable to recognize two subdomains on the basis of grade of organization, the largely unicellular Protista and the multicellular 'Metabionta', containing the Fungi, Metaphyta and Metazoa.

Everyone realizes that the Protista are as heterogeneous a lot (or more so) as the three kingdoms of the Metabionta together. I have little doubt that the specialists will in due time break them up into a considerable number of kingdoms, but by recognizing the subdomain Protista one emphasizes that these organisms represent a definite evolutionary grade, a definite stage in the development of the derived multicellular Metabionta. Many of these protists combine characteristics (such as mobility) traditionally ascribed to animals, with other characteristics (such as photosynthesis) traditionally ascribed to plants. Others have characteristics not found in any of the multicellular taxa. Eventually, when molecular research is further advanced, it will be possible to determine exactly which of the protist genera or families gave rise to the higher animals and plants.

There is considerable disagreement among taxonomists as to methodology and theory of macrotaxonomy. Cladists favour Hennig's 'general reference systems', in which taxa that have given rise to descendants (ex-groups) are broken up and removed from the classification as being 'paraphyletic'. Cladists would probably not recognize those prokaryote taxa that participated in the evolution of the eukaryotes. They would certainly reject recognition of the Protista, which includes the ancestors of various metaphytic and metazoan groups.

A basic classification of the living world will be used not only by specialists but also by nontaxonomists and lay people. They will be more comfortable with the classical concept of classification⁵ with its recognition of the traditional grouping of protists, fungi, metaphytes and metazoans. Grade of evolutionary development, as well as organizational similarity, are stressed in this arrangement, which also agrees with the traditional information-retrieval

system that has been in use for so many years. A classification based on these considerations would be as follows:

- Domain Prokaryota (Monera)
 - Subdomain Eubacteria
 - Subdomain Archaeobacteria
 - Kingdom Crenarchaeota
 - Kingdom Euryarchaeota
- Domain Eukaryota
 - Subdomain Protista
 - Subdomain Metabionta
 - Kingdom Metaphyta (plants)
 - Kingdom Fungi
 - Kingdom Metazoa (animals)

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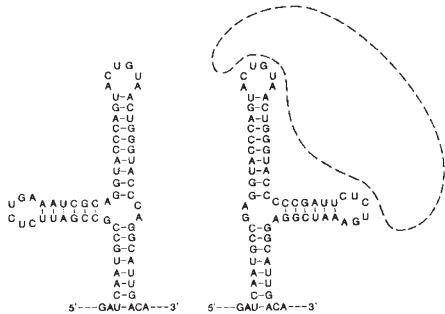
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Ambidextrous RNA

SIR—John Galloway, in his discussion in *News and Views*¹ of Brown and Wolpert's paper² on asymmetry in development, states that molecular determinants are unlikely to be involved. He points out that the structure of individual proteins is either right- or left-handed and that gene mutation could not readily produce a change in handedness, and also that the primary structure of nucleic acids cannot be ambidextrous.

But if one considers the secondary structure of nucleic acids it is easy to see that RNA molecules, or parts of such molecules, could exist in left- or right-handed forms. Simply hypothetical examples are shown in the figure. The base sequence of the stem of the two molecules is the same, and the sequence of the side



Right- and left-handed RNA structures. The sequences of bases in the stem and the side arms are the same, but the latter are inserted at different positions while retaining the same sequence polarity. The orientation of the bases in the terminal loops are different in the two molecules, so a specific protein (dashed line) may bind to one and not the other. Alternatively, different proteins might bind to each molecule.