

mitochondrial genome of the ciliate protozoan *Tetrahymena pyriformis*⁸ and the unicellular green alga *Chlamydomonas reinhardtii*^{1,2} in which even more bizarre permutations have been uncovered. In *T. pyriformis* there are two large-subunit rDNA modules (separated by a tRNA gene) whose order is the reverse of that expected from their order in the RNA; and in *Ch. reinhardtii* there are four small-subunit and at least eight large-subunit rRNA modules interspersed with each other and with various protein-coding and tRNA genes (*b* in the figure). These are also 'illogically' scrambled among themselves. As before, abundant and separate large- and small-subunit mini-RNAs emerge from the single long transcript of the complex DNA unit, after removal of flanking sequences to form two networks typical of small- and large-subunit RNA secondary structures.

Boer and Gray^{1,2} point to an additional clue to unravelling rDNA evolution which derives from the potential of one of the three protein-coding genes (*b* in the figure) to give rise to a product that could function either as a reverse transcriptase or as an RNA maturase, given the similarity in sequence with open reading frames in group II introns involved with RNA processing in fungal mitochondria. The first activity suggests that the scrambled arrangement is a more recently derived feature reflecting haphazard insertions of complementary DNAs; the second could have been part of the machinery for the evolutionary removal of extraneous RNA lying between the modules, if indeed modules were once independently existing mini-genes. The first entertains the possibility that complex rearrangements were spread by internal (molecularly driven) events, whereas the second might have been a streamlining response to external (selective) pressures, extreme examples of which are the rDNAs in mammalian mitochondria which have lost several 'expansion segments'.

The concept of early modular organization predicts that first, each DNA module might have had a separate promoter and terminator; and second, enticingly, that each RNA module might have existed within separately functioning ribonucleoprotein particles not unlike present-day small nuclear RNAs and their associated proteins. With regard to the first prediction, in some organisms

the chief rRNA genes (*a* in the figure), including the 5S rRNA genes, can be separately transcribed, leading to the proposal⁹ that these were once independent units. These might have been intermediate steps in the process of assembling the smaller modules into more manageable units, as indeed might be the longer L7 and L8 pieces (*b*) consisting of mixtures of core and variable segments which are not further processed at the RNA level. The evolutionary end-point of this process would be present-day long rRNA genes co-transcribed from a single promoter whose variable (expansion) segments are unprocessed relics of intervening spacers that have become an integral part of large- and small-subunit rRNA secondary structures. With regard to the second prediction, a relationship between small eukaryotic and prokaryotic RNAs has been suggested recently by the finding¹⁰ of primary sequence and secondary structural similarities between 7S RNA and *Escherichia coli* 4.5S RNA.

As with all good biological stories, the situation is more complex than this. Experimental manipulations of expansion segments in yeast by R. Planta (personal communication) show that they are not all dispensable in the assembly and functions of ribosomes, although they lie in peripheral regions of the large- and small-subunit RNA secondary structures and do not seem to be associated with proteins. Furthermore, despite wide fluctuations in size and composition, often due to the continual gain and loss of short repetitive motifs of DNA by slippage, they form remarkably conserved secondary structures within kingdoms (as a consequence of compensatory mutations occurring in key stem regions)^{11,12} and are also coevolving as a set within any one species⁶. Their evolution might not be explicable solely on the basis of their being molecular fossils of unremoved rDNA spacers. There are arguments⁵ that some of them are more recent acquisitions, like many introns in protein-coding genes. Whatever the case, it is clear that there are some rDNA evolutionary paradoxes still looking for a solution. □

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Daedalus

Organic-vapour farming

PLANTS, says Daedalus, can extract a lot more from the atmosphere than carbon dioxide. Some roadside plants are usefully fertilized by the nitrogen oxides they capture from vehicle exhausts; and one report claims that office plants like chrysanthemums and spider-plants combat 'sick building syndrome' by taking up solvent vapours, formaldehyde, and carbon monoxide from the underventilated air. In principle, any enterprising green plant should gladly abandon photosynthesis to exploit such a ready-reduced source of carbon. So DREADCO's biologists are passing dilute radiolabelled organic vapours like alcohol and methane over a variety of plants, from tomatoes to rhubarb to privet, looking not just for absorption but for metabolic uptake. Now most plants, like most animals, have a resident flora of bacteria; in at least one case (the nitrogen-fixing bacteria in legumes) this relationship has deepened into a useful symbiosis. So to help things along the DREADCO team are dusting their plants with the methanotrophic bacteria which metabolize methane, simple hydrocarbons, and some of their derivatives. These organisms may have unsuspected collaborative talents. Some have recently been found living symbiotically in the gills of mussels near offshore oil platforms, helping the mussels to digest the local hydrocarbons. With good fortune, they will do the same for Daedalus's plants.

Daedalus has high hopes of his organic-vapour-metabolizing plants. Not only will they deodorize the depressing effluvia of high-tech offices, the fug-laden air of crowded parties, and the ominous smell of dentists' waiting rooms; they will clean up industrial air. As a final purification filter, a greenhouse of the new plants will wonderfully purify the slightly smelly and contaminated air discharged by most industrial processes. The resulting output of country-fresh air and useful vegetables will be a double improvement.

Even better, Daedalus hopes to develop strains of organic-trapping grass, shrubs, hedge plants, and so on, for planting in the environment at large. Particularly in polluted regions, they should have a powerful advantage over less accomplished species, and should spread vigorously. In bright sunlight they will photosynthesize carbon dioxide; under smoky skies they will make do with the smoke. At last the grim effluvia of industry will be integrated into nature. Daedalus even hopes that his plants will help to counter the growing contribution of atmospheric methane to the greenhouse effect. But even he has little hope of developing a strain of plant which will metabolize fluorocarbons, and save the ozone layer.

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Corrigendum

In the News and Views article by M.F. Perutz (*Nature* **336**, 202; 1988) it was implied that in a dimer of identical subunits related by a 2-fold symmetry axis, equivalence of the subunits is preserved only by rotations about and shifts along axes that are perpendicular to the 2-fold axis. In fact this is true for any pair of axes (one axis for each subunit) that are related by the same 2-fold symmetry axis as the subunits themselves.