The Crafoord Prize 2003

The Royal Swedish Academy of Sciences has decided to award the Crafoord Prize in Biosciences 2003 to Professor **CARL R. WOESE**, *University of Illinois, Urbana, Illinois, USA: "for his discovery of a third domain of life"*

From Carl Linneaus to Carl R. Woese

Two major streams of biological thought are united in the work of Carl R. Woese. One of these is Carl Linneaus' (knighted von Linné) vision of a universal natural system of taxonomy for organisms (a taxonomy is the classification of organisms according to their relationship). The other is that of molecular genetics as initially envisioned by Watson, Crick and Gamov. They conceived a universal scheme based on the structure of DNA to describe how the genetic information for the structures of proteins is encoded in nucleic acid sequences. Woese provided the connection between these two seemingly separate fields of biology by employing the nucleic acids of the rRNA molecules themselves to make taxonomic comparisons and to derive phylogenetic order, i.e. summarize the evolutionary history in a phylogenetic tree.

The ribosome – a centrally placed informer

The choice of rRNA for this work was not gratuitous. In Woese's view the evolution of gene expression in general and the ribosomal mechanism for protein synthesis, in particular, is the defining process in the origin of cells. Thus, there is a universal ribosome-based translation mechanism and a universal genetic code that relates all organisms to each other, Archaea (the domain proposed by Woese himself, based on his findings), Bacteria and Eukaryotes alike. In Woese's view, the ribosome mechanism and the genetic code first evolved in a primitive population of organisms, collectively referred to as the progenote. Accordingly, the progenote population is identified as the common ancestor of modern organisms. Archaea, Bacteria and Eukaryotes diverge from this common progenote ancestor and they evolve by the selection of advantageous mutations in Darwinian lineages.

The sequence changes created by mutations in genes that define the evolution of species can be detected by sequence analysis of the nucleic acids of the DNA-molecule, or that of the RNA which is transcribed from DNA, or of the amino acids that constitute the end product, i.e. the proteins. Thus, these co-linear molecules are all related to each other by the Watson Crick base pairing rules and by the genetic code. In principle, the evolutionary sequence changes in any particular gene from any clade of organisms can be ordered in a natural phylogeny. If the analyzed sequence is present in all organisms, the resulting phylogenetic reconstruction should be universal.

Woese focused on rRNA as a molecular marker because of its unique biological and molecular attributes. First among these is its universality. Second, is its central role in protein synthesis. The universal role in protein synthesis is expected to constrain sequence variation among the rRNA molecules of different organisms. Likewise, a requirement to interact precisely with many different proteins in the functional ribosome will constrain sequence evolution for rRNA. For these reasons sequence evolution of rRNA is expected to be unusually conservative. Indeed, evolving proteins in general

turn out to be much more "volatile" than rRNA. This, in turn makes the rRNA marker an unusually robust phylogenetic probe for studying long evolutionary distances.

Likewise, rRNA genes are most often found in multiple copies in genomes of both prokaryotes and eukaryotes. In other words, horizontal transfer would not be as great a problem for phylogeny based on rRNA as it is for phylogeny based on proteins. Indeed, this distinction has been verified by the fact that out of all the thousands of sequenced rRNA genes in public databases, no genome has been found to contain alien rRNA sequences completely replacing the original rRNA complement. Two examples are known in which partial alien replacements are observed. In contrast there are reliable reports of dozens, perhaps hundreds of alien proteins transferred to organisms by Horizontal Gene Transfer.

The obscured diversity of microorganisms

Woese's choice of rRNA as the molecular "window" through which to view the evolution of life on this planet was a wise one, indeed. He has introduced and developed a tool that has revolutionized medical microbiology, epidemiology and microbial ecology. However, it may be more important that Woese's work has greatly changed our perception of biodiversity. Indeed, reflecting on the universal rRNA phylogenetic tree (figure 1) leads inevitably to the insight that our planet's biota is totally dominated by microorganisms.

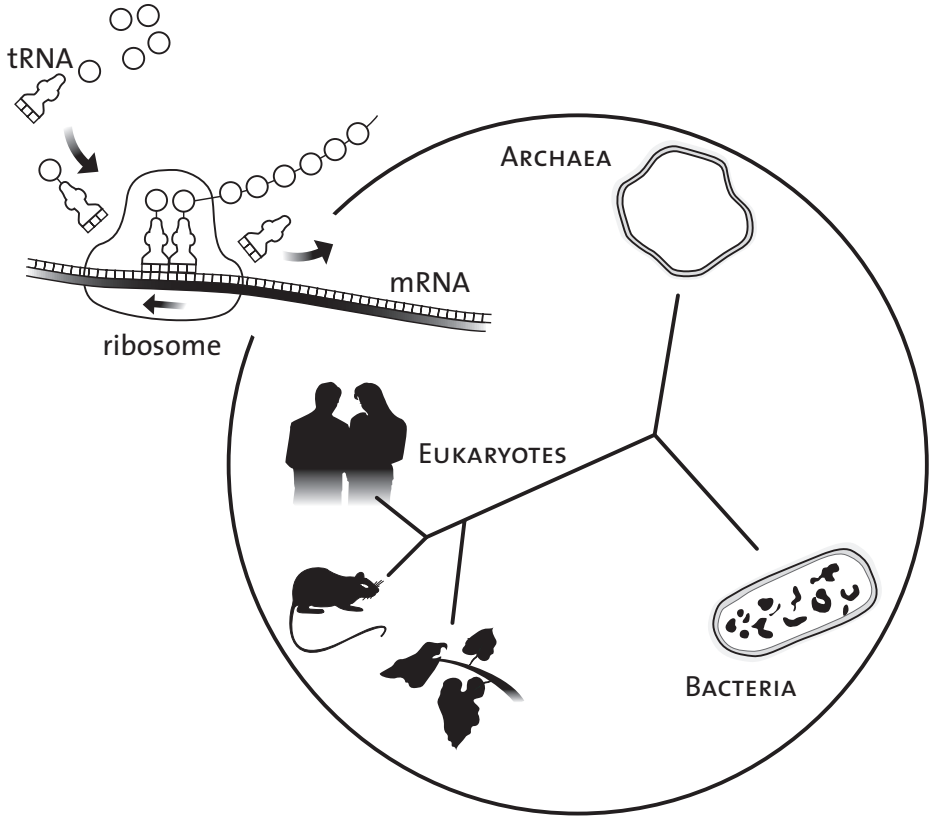

Figure 1. Woese realized that the ribosomes held the key for a proper construction of a phylogenetic tree of the main domains of life. The ribosomes interpret the messenger RNA molecules (mRNA) carrying the instructions from the DNA of the cell, and together with transfer RNA (tRNA) construct the proteins encoded in the genome. Woese showed that the nucleic acid sequence in the ribosomes, which themselves to a large extent consist of RNA, can be used to construct the tree.

In conclusion it seems appropriate to cite Edward O. Wilson (Crafoord Laureate 1990). ”In an ecological sense, the animals of rain forests and the abyssal benthos occupy opposite ends of the earth; one could say that they dwell on two planets. Their environments are as physically different as possible and their biotas share not a single species of plant or animal. Yet all the diversity they contain may be dwarfed by that of the bacteria, organisms that saturate the two extreme environments and every other place on earth. It is a common misconception among both biologists and non-biologists that bacteria are relatively well known because they are so important in medicine, ecology and molecular genetics. The truth is that the vast majority of bacterial types remain completely unknown, with no name and no hint of the means needed to detect them.” Elsewhere, Wilson has written ”If I could do it all over again, and relive my vision in the twenty-first century, I would be a microbial ecologist”. A more fitting tribute to Carl R. Woese is difficult to find.

Short biography

Carl R. Woese was born in 1928 in Syracuse, New York, USA. He studied at Amherst College and at the University of Rochester before completing a PhD in Biophysics at Yale University in 1953, where he also did his post-doc. He became Professor in Microbiology at the University of Illinois at Urbana in 1969 and holds the Stanley O. Ikenberry Endowed Chair at the same university since 1996.

Suggested reading

Carl R. Woese
www.life.uiuc.edu/micro/woese.html

Classification and phylogenies
www.eti.uva.nl/Database/WBD/paper/Paper.html
www.pbs.org/opb/intimatestrangers/treeoflife/puzzle.html

The Crafoord Foundation:
www.crafoord.se

The Crafoord Prize

The Crafoord Fund was established in 1980 by a donation to the Royal Swedish Academy of Sciences from Anna-Greta and Holger Crafoord. The purpose of the Fund is to promote basic scientific research worldwide in the following disciplines: Mathematics, Astronomy, The Geosciences, the Biosciences (with particular emphasis on Ecology) and Polyarthritis. The prize was awarded for the first time in 1982 for Mathematics and has since been awarded annually to one discipline at a time, taking turns according to the list stated above. Both an international prize and research grants to Swedish scientists are awarded among the sciences mentioned. The prize amounts to USD 500 000.

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