## Charles G. Kurland

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## CV

Charles Kurland received his PhD in Biochemistry from Harvard University in 1961, and did postdoctoral work at the Microbiology Institute of the University of Copenhagen. Since 1971, he has been a Professor of Molecular Biology at Uppsala University, Sweden. Professor Kurland has been a member of the European Molecular Biology Organization since 1994, and has represented Sweden on the Councils of both the EMBC and the EMBL (1989-1992). He has been chairman of several national councils and committees, and is a member of the Royal Science Society, Uppsala, the Royal Academy of Sciences, Stockholm, the Royal Academy of Sciences, Copenhagen, the Estonian Academy of Science, Tallinn, and the Royal Physiographical Society, Lund. Professor Kurland has published more than 170 scientific papers, among them a series of signal papers on the biochemistry and biophysics of the ribosome. His prominence in this field was witnessed by his contribution to the authoritative text ŒThe Ribosome1. Kurland's study of the E. coli ribosome is, however, but part of a career devoted to the molecular biology of bacteria, the most recent avenues of which have led him to study the evolution of endoparasitic bacteria and cellular organelles. Professor Kurland continues to be an enthusiastic promoter of molecular biology, whilst taking a keen interest in the communication of science to the public. As well as chairing the EMBO committee on Science and Society, he co-wrote the EMBO statement on genetically modified organisms and the public, which was published in February this year, and which is the starting point for the EMBO on-line discussion forum on GMOs.

## **CONTACT INFORMATION**

Charles Kurland, Ph.D. Munkarpsv. 21 SE 243 32 HOOR Sweden Fax (+46) 413 558746 Tel (+46) 413 558747 chuck@xray.bmc.uu.se Vanishing Genomes, Emerging Proteomes: Origins of Mitochondria

The genomes of mitochondria are miniscule and can encode as few as 2 proteins or as many as 67 proteins. Recent genomic sequence determinations with ?-proteobacteria such as Rickettsia and Bartonella have been useful aides to the analysis of mitochondrial origins. Phylogenies based on ribosomal RNA as well as mitochondrial proteins have shown rather clearly that mitochondria are sister clades of ?-proteobacteria such as Rickettsia.

The endosymbionts that were the direct ancestors of mitochondria were in all probability descendents of free living ??proteobacteria. These must have had genome sizes sufficient to code 1000 to 2000 proteins if the facultative endocellular parasite Bartonella is a reliable guide. Where have all these genes gone during the evolution of mitochondria?

Yeast has at least 400 mitochondrial proteins encoded in its nuclear genome. But of these only ca 50 can be identified with confidence as descendents of ?-proteobacterial ancestral sequences.

The largest group of proteins in the yeast mitochondrial proteome is in fact not made up of bacterial descendents. They are eukaryotic proteins with no allignable homologues in bacteria or in archaea. Some of the characteristic organelle-specific functions such as ATP export are carried out by such eukaryotic add-ons to the mitochondrial proteome.

The laboratories of Thorsness and Fox have demonstrated that there is a mechanism in yeast cells to transfer genes from mitochondria to nuclear genomes; the reverse process is not detectable. Such a biased transfer mechanism supported by mutations that can inactivate coding sequences in mitochondria would drive an evolutionary process in which genes would tend to be transferred from mitochondria to nuclei. Nevertheless, circa 1000 protein-coding sequences from the ancestral bacterial genome have simply vanished from mitochondrial lineages.

Thus, coding sequences of the ancestral bacterium that are not required by the organelle have vanished. A majority of the small number of bacterial proteins that remain has been transferred to the nucleus. In parallel, the proteome of an efficient ATP producing organelle has evolved within the nuclear genome of eukaryotic hosts.

Andersson, S. G. E., and C. G. Kurland. 1998a. Reductive evolution of resident genomes. Trends Microbiol. 6:263-268.

Berg, O. G., and C. G. Kurland. 2000. Why mitochondrial genes are most often found human genome. Nature Genetics 19: 19-24.

Karlberg, O., B. Canbaeck, C. G. Kurland, and S. G. E. Andersson. 2000. The dual origin of the yeast mitochondrial proteome. Yeast 17:170-187.

Kurland, C. G. and S. G. E. Andersson. 2000 Origin and Evolution of the Mitochondrial Proteome. Microbiol. Molec. Biol. Rev. 64: 786-820.

Thorsness, P. E., and T. D. Fox. 1990. Escape of DNA

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