

Poster Presentations

[MS5-P45] Proteins Distinguish Three Structurally Distinct Ribosomes in Eukaryota.

William L. Duax, David Dziak, Alexander Merriman

Hauptman-Woodward Medical Research Institute, Buffalo, NY, USA.

We have been tracing species evolution via alignment of amino acids conserved in the folded core of ribosomal proteins in 8500 species for which complete Genomes have been reported. We have created a search vector that identifies 2905 eukaryotic proteins in the SwissProt/TrEMBL database as S19 or S15 and aligns them. Bacterial copies are consistently labeled as S19 while eukaryotic copies are labeled S19, S19e, S15 or simply hypothetical protein. Principal component or cluster analysis of the alignment reveals the presence of three distinctly different subsets of S19/15. The subsets have a common folded core and a few residues conserved in the core of all 8500 S19/15s (bacterial, eukaryotic and archaeal) responsible for maintaining the fold throughout evolution. Significant divergence in other residues in the folded core and additions at the N- and C- termini distinguish the three subsets from one another. One subset has some members biochemically characterized as mitochondrial. A second subset has some members biochemically characterized as chloroplastic. Characterized members of the third subset are identified only as being ribosomal protein S15. There is biochemical evidence for the existence of distinct mitochondrial, chloroplastic, and cytosolic ribosomes and reports that plants have all three forms and mammals have two. Our sequence analysis of the 21 ribosomal proteins of the small subunit allows us to determine species distribution of each of them. In general we find that only certain classes of viridiplante have three different S ribosomal proteins, most mammals and archaea have only one copy of each ribosomal protein and fungi are exceptional in having mitochondrial and cytosolic ribosomal proteins. The mitochondrial S19/15 is

homologous with the S19 in alpha-proteobacteria consistent with biochemical evidence that an alpha-proteobacteria was the mitochondrial endosymbiont. The cytosolic S19 in fungi are homologous in length with S19 in Metazoa and Archaea suggesting that archaea evolved after a gene duplication in fungi or a fungal precursor.