

**RNA AND THE NATURE OF THE LAST COMMON ANCESTOR.** A. Becerra S. Islas, R. Hernandez-Morales and A. Lazcano, Facultad de Ciencias, Universidad Nacional Autonoma de México, 04510 México, D.F., MEXICO; email: abb@ciencias.unam.mx.

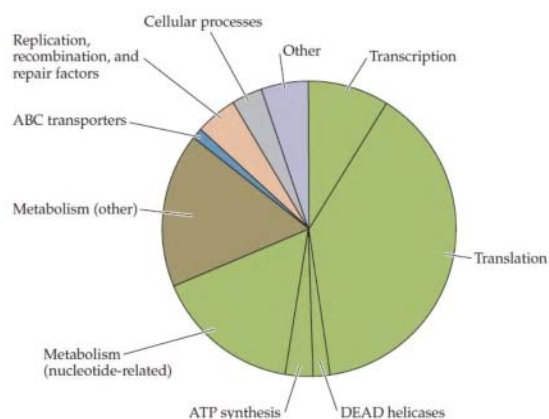
**Introduction:** Based on the three-domain phylogeny proposed by Woese and Fox in the early 1970s [1] that all living beings can be classified on one of three main cellular lineages (Archaea, Bacteria, and Eukarya), it is possible to reconstruct some of the characteristics of the Last Universal Common Ancestor or cenancestor.

Comparative genomics of organisms from the three domains has shown that the cenancestor was not a direct descendant of the prebiotic soup nor a primitive cellular entity where the genotype and the phenotype had an imprecise relationship (i.e., a progenote), rather it was an organism similar in complexity to extant cells. Quantitative estimates of its gene complement, may be hindered by ancient horizontal gene transfer events as well as by biases in genome databases and methodological artifacts [2].

Nevertheless, a significant number of the highly conserved genes are sequences involved in the synthesis, degradation, and binding of RNA, including transcription and translation [3].

The extraordinary conservation of RNA-related sequences supports the hypothesis that the last common ancestor was an evolutionary outcome of the so-called RNA/protein world. However, the chemical nature of the first genetic polymers and the catalytic agents that may have formed the hypothetical RNA world can only be surmised and cannot be deduced from comparative genomics or deep phylogenetics [2,3].

**References:** [1] Woese CR, Fox GE. (1977) *J. Mol. Evol.* 10:1–6, [2] Becerra, A., Delaye, L., Islas, S., & Lazcano, A. (2007) *Annu. Rev. Ecol. Evol. Syst.* 38:361–79, [3] Delaye, L., Becerra, A., Lazcano, A. (2005) *Orig Life Evol Biosph.* Dec;35(6):537-54.



Highly conserved protein domains [3]