

RNA World Remnants

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Abstract—The immediate objective of the project was to identify strategies to find additional examples of structural elements associated with non-coding regions of bacterial genome that have meaningful structures when transcribed into RNA.



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ASTROBIOLOGISTS WIDELY VIEW LIFE AS IT OCCURS ON Earth to have arisen from a predecessor “RNA World.” This conclusion is based in large part on the pervasive role RNA plays in modern living systems. The key element of the modern protein world is the ribosomal machinery which synthesizes proteins according to the genetic code. It is an RNA machine. The fundamental building blocks of DNA, the dNTPs, are not synthesized directly but are rather made by the reduction of ribonucleotides. The same ribonucleotides are precursors of a large variety of coenzymes. Moreover, RNA serves as the primer in DNA replication. Many catalytic RNAs are known to exist. Most recently, small microRNAs have been discovered to be pervasive in eukaryotic gene regulation.

When the first genomes were sequenced, researchers quickly observed that only a small number of operons were universally distributed, most of which coded for proteins that were associated with the ribosomal machinery. In essentially every case, these operons were known to be regulated by mechanisms that involved structures found upstream from the first gene when the mRNA was produced. Subsequently, additional riboswitches/riboregulator regions have been discovered and characterized.

Most bacterial genes are thought to be regulated by feedback mechanisms in which proteins bind to the encoding DNA and prevent or facilitate transcription. However, historically the RNA World would have been followed by an RNA/protein World in which RNA was the storage medium. Under such conditions, DNA level regulation would not be possible because of the absence of DNA. RNA-level regulation would thus be essential and once established as a working mechanism unlikely to be easily replaced. Hence, the list of genes that has RNA level regulation may define that portion of modern organisms that existed before DNA was established as the genetic material. As remnants of the late RNA World, structural elements found in leader RNAs can provide

at last, a picture of the true complexity of early organisms as well as insight into the relative age of various pathways and processes. Further, the structures found in these RNA regulatory regions may provide insight to the types of RNAs that were present in the late RNA World.

As a first step in identifying additional RNA World remnants, we identified all genes associated with protein synthesis. We next examined the distribution of each of these genes in all completely sequenced bacterial genomes. The genomic context of the widely distributed and hence likely oldest genes was examined in over 60 representative bacterial genomes in order to identify possible conserved operon structure. Approximately 20 gene clusters were identified and ranked by relative conservation of gene order. We are currently in the process of extracting and aligning the leader regions of these gene clusters in appropriate examples in order to facilitate a comparative search for conserved RNA level regulatory elements.

Publications

Fox, G. E. and A. K. Naik. “The Evolutionary History of the Ribosome,” in *The Genetic Code and the Origin of Life*. Ed. L. Ribas de Poplana. Landes Bioscience, 2004. Chapter 6, pp. 92-105.

Funding and Proposals

“RNA World Remnants in Bacterial Genomes,” NASA-Astrobiology: Exobiology and Evolutionary Biology July 1, 2005–June 30, 2008, \$288,268. The agency has indicated this proposal will be funded.

Fox, G. E. “Computational Identification of Riboswitches and Non-coding RNAs,” Co-investigators: R. Willson and Y. Fofanov. Texas Learning and Computational Center, April 1, 2005–Aug. 31, 2005, \$ 182,982 (*pending*).