Chapter 24

Evolutionary Asides 24.4--Noncoding DNA evolved to control gene expression in vertebrates

Vertebrate genomes contain a few million conserved noncoding regions (CNCs) that evolved more slowly than DNA that does not have a function. The slower rate of evolution of the CNS is consistent with a functional role for the sequences, which is now proposed to be regulating gene expression A subset of CNCs is located near genes and regulates the expression of the genes. Sorting out when different CNCs gained a regulatory function was inferred by aligning the genomes of 40 vertebrates. Then for the subset of CNCs of interest, sequences were compared to determine when the rate of base pair substitution had slowed down to the point that it was reasonable to conclude that the CNC had begun to function as a regulatory element.

Genes regulated by the CNCs were categorized as coding for development, transcription factors, receptor binding, and posttranslational protein modification. A fascinating evolutionary pattern emerged from this comparison of whole genomes. About 600 to 300 mya, regulatory factors that encode transcription factors, plus genes that otherwise influence development, arose. Between 300 and 100 mya receptor-binding genes came under regulatory control and only recently have proteins that regulate the posttranscriptional modification of other proteins gained their own transcriptional regulation.