

Alternative splicing and RNA selection pressure — evolutionary consequences for eukaryotic genomes

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Abstract

Genome-wide analyses of alternative splicing have established its nearly ubiquitous role in gene regulation in many organisms. Genome sequencing and comparative genomics have made it possible to look in detail at the evolutionary history of specific alternative exons or splice sites, resulting in a flurry of publications in recent years. Here, we consider how alternative splicing has contributed to the evolution of modern genomes, and discuss constraints on evolution associated with alternative splicing that might have important medical implications.

<http://www.nature.com/nrg/journal/v7/n7/abs/nrg1896.html>