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## On the Roles of Repetitive DNA Elements in the Context of a Unified Genomic-Epigenetic System

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**ABSTRACT:** Repetitive DNA sequences comprise a substantial portion of most eukaryotic and some prokaryotic chromosomes. Despite nearly forty years of research, the functions of various sequence families as a whole and their monomer units remain largely unknown. The inability to map specific functional roles onto many repetitive DNA elements (REs), coupled with the taxon-specificity of sequence families, have led many to speculate that these genomic components are “selfish” replicators generating genomic “junk.” The purpose of this paper is to critically examine the selfishness, evolutionary effects, and functionality of REs. First, a brief overview of the range of ideas pertaining to RE function is presented. Second, the argument is presented that the selfish DNA “hypothesis” is actually a narrative scheme, that it serves to protect neo-Darwinian assumptions from criticism, and that this story is untestable and therefore not a hypothesis. Third, attempts to synthesize the selfish DNA concept with complex systems models of the genome and RE functionality are critiqued. Fourth, the supposed connection between RE-induced mutations and macroevolutionary events are stated to be at variance with empirical evidence and theoretical considerations. Hypotheses that base phylogenetic transitions in repetitive sequence changes thus remain speculative. Fifth and finally, the case is made for viewing REs as integrally functional components of chromosomes, genomes, and cells. It is argued throughout that a new conceptual framework is needed for understanding the roles of repetitive DNA in genomic/epigenetic systems, and that neo-Darwinian “narratives” have been the primary obstacle to elucidating the effects of these enigmatic components of chromosomes.

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