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Abstract

The $\sigma^{70}$ subunit of the bacterial RNA polymerase holoenzyme is responsible for specific binding to the –10 and –35 promoter motifs. It has been shown that selection acts to remove –10 and –35 consensus sequences in both coding and noncoding regions, implying that it is disadvantageous to maintain misplaced sites that can strongly bind $\sigma^{70}$ and interfere with proper gene expression. Here we analyze 56 bacterial genomes and show that the numbers of non-consensus, potential $\sigma^{70}$ binding sites in both regulatory and non-regulatory noncoding regions deviate significantly from the random expectations based on base composition, di- and tri-nucleotide contents in a majority of eubacteria. This implies that, not only is there selection for maintaining high densities of potential $\sigma^{70}$ binding sites in regulatory DNA, but there is also selection against these sites in non-regulatory DNA. The often overlapping binding sites in regulatory DNA likely confer some subtle survival advantage, even though experimental evidence suggests only one or a few of these sites are actual transcription initiation sites. Remarkably, we find that the degree of selection against potential $\sigma^{70}$ binding sites in non-regulatory DNA correlates positively with rate of growth, adaptive codon bias and number of tRNA genes. This is evidence that the efficiency needed for faster growing bacteria can only be achieved by reducing spurious RNA polymerase binding to false sites, and that transcription and translation efficiencies are both optimized at a genome-wide level to permit faster growth.