The regulated retrotransposon transcriptome of mammalian cells

Abstract

Although repetitive elements pervade mammalian genomes, their overall contribution to transcriptional activity is poorly defined. Here, as part of the FANTOM4 project, we report that 6–30% of cap-selected mouse and human RNA transcripts initiate within repetitive elements. Analysis of approximately 250,000 retrotransposon-derived transcription start sites shows that the associated transcripts are generally tissue specific, coincide with gene-dense regions and form pronounced clusters when aligned to full-length retrotransposon sequences. Retrotransposons located immediately 5' of protein-coding loci frequently function as alternative promoters and/or express noncoding RNAs. More than a quarter of RefSeqs possess a retrotransposon in their 3' UTR, with strong evidence for the reduced expression of these transcripts relative to retrotransposon-free transcripts. Finally, a genome-wide screen identifies 23,000 candidate regulatory regions derived from retrotransposons, in addition to more than 2,000 examples of bidirectional transcription. We conclude that retrotransposon transcription has a key influence upon the transcriptional output of the mammalian genome.

http://www.nature.com/ng/journal/v41/n5/abs/ng.368.html