Analysis of RNA-DNA interactome discloses the transcriptional dynamics of protein-coding genes

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The past few years have witnessed the development of a bunch of technologies for mapping genome-wide localization of chromatin-associated RNAs using proximity ligation. So far, most of the research in this area has been focused on non-coding RNAs and their functions in the nucleus, including transcriptional control, shaping of the 3D genome, and assembly/maintenance of functional nuclear compartments. In the present work, we used RNA-DNA interaction data from human K562 cells to study the transcriptional dynamics of protein-coding genes. Analysis of contact frequencies of different regions of mRNAs with the body of encoding genes allowed us to trace how mRNA is dragged behind the RNA polymerase during transcription and disengages from the gene after transcription termination. Our data support the model of co-transcriptional intron splicing, but not the hypothesis of the circularization of actively transcribed genes. In addition, we show that longer mRNAs are characterized by a higher proportion of cis to trans contacts, apparently due to a longer linkage with the parental chromosome in the course of transcription. Analysis of RNA-DNA interactome may become a useful tool in future studies of transcription mechanisms.

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