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Genome regulation by long non-coding RNAs

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Regarding the human genome, only 2-3% of it translates into proteins, whereas 97-98% of the genome is comprised by sequences that are not translated, and thus defined as "dark DNA" that appear as non-coding RNAs (ncRNAs) and are interrelated to the regulation of gene expression. Long ncRNAs (lncRNAs) consist of more than 200 nucleotides and are derived from various regions in the genome (Mercer, Dinger, & Mattick, 2009; Wilusz, Sunwoo, & Spector, 2009). Several lncRNAs create RNA–protein, RNA–DNA and RNA–RNA complexes that are associated with chromatin modifications and lead the transcription factors to specific genomic DNA targets. Another function of lncRNAs is the regulation of the mRNA translation levels by interfering with miRNAs. For that reason, they are associated with various diseases, such as cancer, myocardial infractions, and Alzheimer's disease (Jarroux, Morillon, & Pinskaya, 2017; Ma, Bajic, & Zhang, 2013). The basic functions of ncRNAs are imprinted in the process of: 1) translation; 2) splicing; 3) replication; and 4) gene regulation (Mattick & Makunin, 2006). Remarkably, alternative splicing allows the human genome to direct the synthesis of more proteins than expected from the 20,000 genes encoding proteins (Black, 2003). For that reason, the analysis of lncRNAs functions in gene expression and genome regulation is pivotal. Using big data processing, recording potential repeated motifs and epigenetic modifications in splicing sites, and examining the interactions of lncRNAs with the chromatin remodelling complexes could lead to the discovery of lncRNAs that constitute potential drug targets and leading to more specialised and personalised treatment.

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