

عنوان مقاله:

Bioinformatics prediction of long-non coding RNAs as expression regulatory candidates of genes involving in myelination

محل انتشار:

بیستمین کنگره ملی و هشتمین کنگره بین‌المللی زیست‌شناسی ایران (سال: ۱۳۹۷)

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خلاصه مقاله:

Multiple sclerosis (MS) is a chronic neuroinflammatory disease of the central nervous system, afflicting approximately ۲.۵ million people worldwide, and imposes a great personal and socioeconomic burden. In the most common form of MS, relapsing-remitting, the demyelinated lesions will undergo remyelination and result in remission, after each rout. But in the passing time, improvement during each remission wanes, and about ۸۰% of patients go on to develop secondary progressive multiple sclerosis, which shows accumulative disabilities. Therefore, understanding dysregulated mechanisms involved in repair of lesions and remyelination would be important in order to help to improve the quality of patient s life. CNTF, NTF۳, FGF۲, and PDGFC as secreted factors from astrocytes and affecting myelination, were chosen. All of the transcription factors (TFs) affecting these genes were searched. Using the UCSC database, the valid TFs, and using JASPAR database, the predicted ones with a high score were chosen. The TFs common among all of the target genes were chosen. Long non-coding RNAs (lncRNAs) related to these TFs were obtained using LncrnaTarget database and literature review. Exerting some criteria, like the studied role of candidate lncRNAs in inflammation or other neurodegenerative diseases, narrowed down the list of candidate lncRNAs as a possible regulator of transcription of target genes. Obtained data showed that about ۵ lncRNAs have the potential to affect the expression regulation of target genes. Differential expression and functional analysis of lncRNAs as the important factors involved in the regulation of gene expression would pave the way in understanding the impaired mechanisms of repair and remyelination

کلمات کلیدی:

Multiple sclerosis, Myelination, Long noncoding RNA

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