

عنوان مقاله:

In silico Analysis of Possible Novel RNA Interactions and Deleterious Single Nucleotide Polymorphisms Related to MSX γ , SHH, SMAD γ and TFAP γ
Genes Involved in Odontogenesis

محل انتشار:

مجله منابع ژنتیک, دوره 8, شماره 2 (سال: 1401)

تعداد صفحات اصل مقاله: 13

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خلاصه مقاله:

Identification of gene expression profiles, RNA interactions, gene regulation patterns, and single nucleotide polymorphisms (SNPs) is important for determining the molecular mechanisms underlying the normal odontogenesis and the pathology of oral and dental disorders. Therefore, this in silico study aimed to identify novel proteins, RNA interactions, and deleterious SNPs related to four major genes (MSX γ , SHH, SMAD γ , TFAP γ) involved in the odontogenesis process. After pathway enrichment and gene ontology analysis, the protein-protein, microRNA (miRNA)-mRNA, and miRNA-long noncoding RNA (lncRNA) interactions and networks were determined for the selected genes using integrated bioinformatics analyses. Moreover, the potential deleterious SNPs in the selected genes were identified and finally, their validation and implications on the structure of proteins were investigated by specific bioinformatics tools. The results of this study introduced UBE γ I, RNF γ 111, MYBL γ , and VEGFA as novel factors that may involve in odontogenesis. It was also found that the MSX γ , SHH, and TFAP γ A are targeted by hsa-miR-6775- δ p, hsa-miR-149-3p, and hsa-miR-432- δ p, respectively. Moreover, the hsa-miR-134- δ p regulated the SHH and TFAP γ A gene expression. LINC02035 and C3orf45 were also introduced as important lncRNAs that may involve in competitive endogenous RNA interaction with the SHH for binding to the hsa-miR-149-3p. Moreover, LINC00319, interacting with the hsa-miR-6775- δ p, indirectly regulated the MSX γ expression. We also identified various SNPs in the investigated genes that changed the normal structure and thus the function of their related proteins. This study, for the first time, introduces different new proteins, miRNAs, lncRNAs, and SNPs that may be important for normal odontogenesis and the pathology of oral and dental disorders.

کلمات کلیدی:

Bioinformatics analysis, lncRNA, miRNA, SNP, Tooth developmental genes

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