

عنوان مقاله:

Phylogenetic Analysis of Three Long Non-coding RNA Genes: AK082072, AK043754 and AK082467

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خلاصه مقاله:

Now, it is clear that protein is just one of the most functional products produced by the eukaryotic genome. Indeed, a major part of the human genome is transcribed to non-coding sequences than to the coding sequence of the protein. In this study, we selected three long non-coding RNAs namely AK082072, AK043754 and AK082467 which show brain expression and local region conservation among vertebrates. Thus, the sequences of these genes are appropriate for phylogenetic analysis. In order to evaluate the evolutionary and molecular trend of lncRNAs in vertebrates, phylogenetic analysis and natural selection process were analyzed during evolution. The nucleotide sequences of selected long non-coding RNAs from different vertebrates were aligned and the phylogenetic trees were constructed using Neighbor Joining method with maximum sequence differences of 0.75. Our analysis of nucleotide sequences to find closely evolved organisms with high similarity by NCBI-BLAST tools and MEGA7 showed that the selected sequence of AK082072 in human and *M. fascicularis* (macaque) were placed into the same cluster and they may originate from a common ancestor. In addition, the human sequence of AK082467 and AK043754 had the closest similarity with cow. Also, bioinformatic analysis showed that the dN/dS ratio is lower than 1 for all three genes which demonstrates purifying selection for the longest predicted ORF of each lncRNA. Together, these results indicate that lncRNAs act as regulatory genes that have important roles in development.

کلمات کلیدی:

Natural selection, Long non-coding RNA, Phylogenetic tree, Common ancestor, Development

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