Molecules in the Focus of Next Generation Biology: Short and Long Non-Coding RNAs (ncRNAs)

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The effects of non-coding RNAs on the regulation of gene expression are researched.In our project by using bioinformatics methods, we aimed to specify the importance of possible similarities and differences of short and long non-coding RNAs in binding to the target gene and determine the conserved and functional areas of these RNAs and identify the genes which are among the target proteins of drugs in use, whose orthologs are available in C.elegans and which are associated with the development of cardiovascular system in RNAi scanning tests. We identified the gene (EPB41L3) targeted mostly by siRNA by analyzing 147 different siRNAs from the database of siRNA. We developed software called SEQUENCE-SEARCH-FIND in order to identify other genes that these siRNAs would be able to target in genome. We determined that not only the exon regions but also the promoter regions of the lncRNAs whose conservation level is less than miRNAs are conserved. Moreover, we believe that we supported the hypotheses defending that the non-coding RNAs are not transcriptional noise by determining that there are some binding sequences which belong to the transcription factors having a role in cardiovascular diseases in these preserved promoter regions. These results also point to the importance of tight regulation of lncRNA expression and highlight their potential as candidate diagnostic and therapeutic targets. We identified the drugs that have a potential to be used in cardiovascular diseases by taking the genes associated with the cardiovascular system into consideration as a result of the scanning tests performed with RNAi in C.elegans. For a different purpose, the clinical phases of drugs which are successful in pre-clinical experiments will be completed much faster and at lower costs.

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