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Searching MiRNA Binding Sites in Metalloproteinase and Folate Cycle Genes

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Background & Hypothesis:
A bioinformatic search on miRNA methods allows to predict pre-miRNAs involved in the candidate genes of expression regulation during the development of atherosclerosis and determine their binding sites and the degree of binding to its target. The aim of this research was to determine and search miRNA binding sites in metalloproteinase and folate cycle genes during the development of atherosclerosis.

Methods:
The sequence of the matrix metalloproteinases genes (*MMP1*, *MMP3*, *MMP9*) and folate cycle genes (*MTHFR*, *MTRR*) were obtained from NCBI (http://www.ncbi.nlm.nih.gov/) using a set of scripts, IFITCH, which is designed for automatic data acquisition. MiRNA sequences were obtained from the miRBase website (http://mirbase.org/). Target for siRNA were taken from the miRTarBase website (http://mirtarbase.mbc.nctu.edu.tw/). Auto search of binding sites was carried out with Mscanner software. The results were filtered to yield the matches with 90% identical nucleotides.

Results:
MiRNA revealed the similarity index of minimum above 0.85. for *MMP1* gene—*hsa-mir-619*, *hsa-mir-3611* and *hsa-mir-5095* - 3 copies; for the *MMP9* gene—*hsa-mir-619* - 2 copies, *hsa-mir-1227*, *hsa-mir-1273g*, *hsa-mir-6800*, *hsa-mir-7155*, gene *MTRR—hsa-mir-574*, *hsa-mir-619* - 2 copies, *hsa-mir-4297*, *hsa-mir-1273g*, *hsa-mir-8485*. There were no miRNA revealed with a similarity index above 0.85 for *MMP3* and *MMP3* genes.

Discussion & Conclusion:
Hsa-mir-619 was detected in *MMP1*, *MMP9*, *MTRR* genes. These genes revealed a different number of polymorphisms for miRNA. The minimum number of SNPs was 1 (*hsa-mir-1273g*, *hsa-mir-574*, *hsa-mir-7155*, etc.), and the maximum number of polymorphisms have been found in the miRNA *hsa-mir-4297* and it was 8. This research was supported by the internal grant of the Southern Federal University №213.01-2015/003VG «The study of protein noncoding DNA elements in the structure of different genomes».