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MicroRNA Binding Sites in Mitochondrial Genes are Associated with the Progression of Atherosclerosis

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Background & Hypothesis:
Cardiovascular diseases (CVD) represent a major health problem and they are the leading cause of death in developed societies. In recent years, it has been shown that mitochondrial dysfunction plays a key role in the triggering and progression of atherosclerotic lesions. It is shown that microRNA can regulate gene expression at the post-transcriptional level, so, in order to find possible targets for atherosclerosis therapy, we investigated the binding sites in the mitochondrial genome genes across different species of miRNA.

Methods:
A bioinformatic analysis of the mitochondrial genome data was performed. Full sequences of genes and miRNAs were obtained from the NCBI database and miRBase by using E-utilities API release 21. Auto search of binding sites was carried out using Mscanner software. The results were filtered to yield the matches with 90% identical nucleotides.

Results
The results showed MiRNA binding sites have been detected in mitochondrial genes, such as *MT-TRNF* (*hsa-mir-4284*), *MT-RNR2* (*hsa-mir-4485, hsa-mir-1973*), *MT-TRNQ* (*hsa-mir-2392*), *MT-TRNC* (*hsa-mir-4484*), *MT-COX1* (*hsa-mir-6723*), *MT-ND4L* (*hsa-mir-4461*), and *MT-ND5* (*hsa-mir-4463*). The entire set of mitochondrial DNA sequences revealed the relationship between atherosclerosis mutation (13050insC) in *hsa-mir-4463* of *MT-ND5* gene.

Discussion & Conclusion:
The microRNA *hsa-mir-4463* can be considered as a potential candidate that is involved in the regulation of the atherosclerosis progression.This research was supported by the Russian Science Foundation grant No: 15-15-10022.