

MicroRNAs IN ATHEROSCLEROSIS: ALTERED EXPRESSION AND DIAGNOSTIC POTENTIAL

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[ENGINEERING OF BIOMATERIALS 148 (2018) 76]

Introduction

MicroRNAs are a group of small, non-coding RNAs, occurring in all species. MicroRNAs are very important regulators of protein coding genes expression. Incorrect regulation of gene expression by microRNA is the cause of many diseases.

Materials and Methods

Peripheral blood mononuclear cells were obtained from patients with atherosclerosis. miRNA levels were determined using next generation sequencing, NGS (S5 XL ThermoFisher Scientific technique). Statistical analyses identified differences between normal and patients samples. miRNA expression profiles that associate with atherosclerosis were established. A variable was considered statistically significant if $p < 0.05$. All statistical calculations were performed using the R software.

Results and Discussion

Differential expression analysis revealed around 30 microRNAs with highly significant changed expression in patients ($P < 0.0001$), in comparison to healthy individuals. Around 20 out of those microRNAs were showed to be related to atherosclerosis for the first time and were embodied in patent application No. P. 424674. Moreover, around 40 high confident gene targets were determined for found microRNAs using predictive target annotation databases and confirmed in transcriptomic analysis of study participants.

Conclusions

We have found significantly differentially expressed miRNAs in atherosclerosis. Recognition of dysregulations in microRNA regulatory network, associated with atherosclerosis development, allows to discover new mechanisms involved in etiology of this disease and enables to establish novel biomarkers, providing new diagnostic and therapeutic opportunities.

Acknowledgments

This study was funded by The National Centre for Research and Development (NCBR) in the program STRATEGMED III (project no. STRATEGMED3/303570/7/NCBR/2017).