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Expression of miR-17~92 Family of miRNA Clusters in Experimental Atherosclerosis

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Background
MicroRNAs (miRs) are small non-coding RNAs that regulate a wide range of physiological and pathophysiological processes. miRNAs regulate gene expression by interacting with target mRNAs at their 3` untranslated region, leading to translational repression or mRNA degradation.
The polycistronic microRNA cluster miR-17~92 comprises seven mature micro-RNAs and has two closely related paralogs: miR-106a~363 and miR-106b~25. Studies revealed a critical role of these miR clusters in heart and lung development, tumor angiogenesis, hematopoiesis, immune functions and postnatal vascularization.
We sought to investigate the expression profile of individual genes from the miRNA family: miR-17 and miR-25, in experimental model of atherosclerosis.
Methods
For detection of miRNAs levels, quantitative Real-time PCR was performed. RNA was isolated from aortas of 9 month old ApoE knockout mice, which harbor heavy atherosclerotic lesions. Six weeks old ApoE mice served as control.
Results
In experimental atherosclerosis, miR-25 showed a >10 folds down-regulation in the aortas of old ApoE knockout mice compared with young ApoE knockout mice, whereas miR-17 showed no comparable change in expression.
Conclutions
Marked down-regulation in miR-25 expression is associated with the progression of atherosclerotic lesions in ApoE knockout mice. Further experiments are needed to elucidate the possible role of miR-17~92 cluster and it's paralogs in the initiation and progression of atherosclerosis.