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Expression of miR-17~92 Family of miRNA Clusters in Experimental model of Myocardial Infarction

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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 acute myocardial infarction.
Methods
For detection of miRNAs levels quantitative Real-time PCR was performed. RNA was isolated from Balb/c mouse hearts following myocardial infarction. Hearts were dissected into infarct area+infract border zone and to infarct non-adjacent areas. Sham operated animals served as control.
Results
Following myocardial infarction in Balb/c mice, both miR-25 and miR-17 were down-regulated (2.5 and 2 folds of down-regulation respectively) in the infarct area and infarct border zone but not in the infarct non-adjacent areas.
Conclutions
miR-17 and miR-25 are down-regulated in response to acute myocardial infarction in the infarct zone and infarct border zone. Further experiments are needed to elucidate the possible role of miR-17~92 cluster and it's paralogs in post MI processes.