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Identification of miRNAome in myocardial infarction by high throughput sequencing

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Background: Myocardial infarction (MI) was the leading cause of death in worldwide. MicroRNAs (miRNAs) regulate gene expression at the post-transcriptional level and are known to play essential roles in various aspects of biological processes, including cell viability, proliferation, development and differentiation. The purpose of this study was to investigate difference of miRNA profiles between infarct zone and border zone in post-MI remodeling using the second generation sequencing.

Results: We induced MI by ligation of the left coronary artery (LAD) in rat. The miRNA profiles between infarct zone and border zone were compared in 14 days after MI using deep small RNA sequencing, and followed by bioinformatics analysis. It was found that 25,603,683 and 26,050,631 clean reads were obtained in infarct zone and border zone respectively, and 234 conserved known miRNAs and 5 novel potential miRNA candidates were identified. The digital expression profiling based on TPM (Transcripts Per Million) analysis of conserved miRNAs show that a total of 22 miRNAs were identified the most highly detected miRNAs (>1000 TPM) in the infarct zone and 27 miRNAs in the border zone. A total of 40 conserved microRNAs were significantly differentially expressed between infarct zone and border zone. Comparing with miRNA expression in the infarct zone, 29 miRNAs were up-regulated and 11 miRNAs were down-regulated in the border zone. In addition, 7283 annotated mRNA transcripts of selected miRNA were identified as putative target genes using microRNA Target Filter tool from Ingenuity Pathway Analysis (IPA) (Ingenuity Systems). IPA pathway analysis suggested that the differentially expressed miRNAs are involved in many molecular and cellular functions, such as Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Cellular Function and Maintenance, Cellular Development, Cell Death and Survival and so on.

Conclusions: Our findings contribute to understanding the role of differentially expressed miRNAs between infarct zone and border zone, which show that miRNAs are dynamically regulated in different regions of the heart during post-MI remodeling.

Biography

Chen was initially trained in Biochemistry and Molecular Biology during MS study in Huazhong Agricultural University, China. Since joining Key Laboratory for Regenerative Medicine, Ministry of Education, as a technical staff at Ji Nan University in 2008, he has been working on dissecting gene regulation mechanisms using cardiac microvascular endothelial cells as a model system. His current work is focus on the functional roles of miRNAs in regulating gene expression in ageing and myocardial infarction.

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