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Data in Brief

MicroRNA expression profiles of human left ventricle derived cardiac cells in normoxic and hypoxic conditions

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ABSTRACT

Studies in the cardiovascular research field have demonstrated the vital roles of microRNAs for proper cardiovascular development and functional maintenance. The involvement of aberrant microRNA expression leading to ontogenesis of cardiovascular diseases lends further support of the regulatory role of microRNAs in heart function. Hypoxic insult is one of the major factors that trigger downstream signal cascades which contribute to the pathogenesis of hypoxic/ischemic-related heart diseases. Here, we report the microRNA expression profile in human cardiac-derived cells subjected to 120-h hypoxic treatment. By comparing with the normoxic control state, we identified microRNAs differentially expressed in cardiac cells subjected to hypoxic challenge. MicroRNA microarray data are available at NCBI under the GEO accession number, GSE55387.

Specifications	
Organism/cell line/tissue	*Homo sapiens*/HCMa
Sex	N/A
Sequencer or array type	miRCURY LNA microRNA Array, v.11.0 — hsa, mmu & rno
Data format	Raw and processed
Experimental factors	Normoxia vs. hypoxia
Experimental features	MicroRNA profiles of cardiac cells in normoxic and hypoxic conditions
Consent	Allowed for reuse citing original author
Sample source location	Singapore

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE55387.

2. Experimental design, materials and methods

2.1. Introduction

Adequate oxygen is essential for the proper function of cardiovascular tissues. Studies in various heart disease models have shown that reduced oxygen supply to the heart leads to alteration of myocardial gene expression [1]. Hypoxia-induced microRNA signatures in various cell lines, including tumor, vascular, and stem cells have been widely studied [2,3]. However, there is limited information on the microRNA profile in human cardiac-derived cells. Herein, a human left ventricle-derived cell line (HCMa) was selected for the microRNA microarray study on the basis of two vital characteristics. Firstly, the HCMa cells were shown to express cardiac lineage markers including Sarcomeric α-Actin. Secondly, the HCMa cells consistently manifested hypoxia-induced elevated BNP/ADM responses as typically observed various heart diseases, including heart failure and acute coronary diseases. The goal of this work is to provide a global view of the microRNA expression profile in human-derived cardiac cells after sub-chronic hypoxic treatment.

3. Experimental design, materials and methods

3.1. Human left ventricle derived cardiac cells

Human left ventricle-derived cardiac cells, HCMa, were obtained from ScienCell and cultured according to the manufacturer's protocol [4]. For hypoxic challenge, cells were placed in a chamber connected to an OXc system (BioSpheric). The chamber was installed in a SANYO O_2/CO_2 incubator (MCO-18M) maintained at 5% CO_2, and 37 °C. The oxygen level for hypoxic chamber was set at 0.2% O_2.

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3.2. RNA sample preparation

Total RNA was extracted from cells using TRIzol reagent (Invitrogen). The RNA samples were treated with DNase I (Invitrogen) prior to subsequent analyses. Total RNA quantity and quality were determined by spectrophotometric (NanoDrop) and RIN analysis on the bioanalyzer (Agilent). To obtain the global view of microRNA expression profile, microRNA microarray analysis was performed by pooling equal amounts of total RNAs obtained from 3 RNA samples in 3 independent experiments.

3.3. MiRNAs microarray

RNA labeling and hybridization for miRCURY LNA™ Arrays were performed according to the manufacturer's protocol (Exiqon). The microarray chips were then washed and scanned using InnoScan700 microarray scanner (Innopsys) with Mapix® Ver4.5 software (Innopsys).

3.4. Microarray data analysis

Microarray data were exported to Microsoft Excel for filtering and basic analyses. Median signal intensity readouts from each microRNA specific probe were extracted for further comparison. The cut-off value for signal intensity readout was set at 100, and values below 100 were excluded from subsequent analyses. For miRCURY LNA microRNA Array v.11.0, the levels of individual microRNAs were detected using 4 probes. Student's t-test was applied to compare the difference of 4 signal intensity readouts for individual microRNAs between experimental groups (normoxia vs. hypoxia), and microRNAs with significant difference between experimental groups ($p < 0.05$) were included for further analysis. The average median signal intensity readouts for individual microRNA were normalized by the average intensity value obtained for U6-snRNA-2. Differentially expressed miRNAs were selected based on the relative fold change ≥1.2 and ≤ −1.2 [4].

4. Discussion

MicroRNA microarray technology has provided a high throughput method to provide a global view of the microRNA expression profile in target tissues/cells. Nevertheless, the ability to evaluate and select the most promising candidate entities from the large amount of microarray data for subsequent investigations remains a major challenge. Here, we describe an analysis procedure adapted from previous publications whereby Microsoft Excel was used for initial candidate microRNA selection [5]. Using this method, approximately 80% of the microRNAs of interest selected were subsequently verified using RT-qPCR method. In a separate study, the putative regulatory effect of microRNA-100 on natriuretic peptide receptor 3 was further demonstrated using various biochemistry methods [4].

As revealed from the analyzed result, 145 microRNAs were found differentially expressed in the human cardiac cell comparing the normoxic state with hypoxic challenge ([4], GSE55387). By publishing the details of sample preparation and the data analysis procedure, we aim to contribute this valuable information to support further work by the research community who may not have the resources to conduct the upstream work in a similar field of interest. The list of the microRNA entities provided in our work could be used for further pathway analyses using free online algorithms, such as DIANA miRPath v.2.0 [6] or commercial software such as ingenuity pathway analysis (IPA). The regulatory effects of the microRNAs listed and their predicted target genes would require further validation from functional studies using in vitro and in vivo platforms.

Conflict of interest

The authors declare that there are no conflicts of interest.

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