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Data in Brief

Microarray analysis of microRNA expression in bone marrow-derived progenitor cells from mice with type 2 diabetes

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ABSTRACT

Bone-marrow derived vascular precursors are an important endogenous repair reservoir for vascular repair and neovascularization [1]. Therapies of stem/progenitor cells targeting on angiogenesis are considered hopeful solutions for tissue repair and regeneration. However, the dysfunction of patient-derived progenitor cells has been implicated in diabetes [2], which limited the efficacy of autologous cell therapies in the clinic [3,4]. MicroRNAs are important gene regulators whose functions remain largely unknown. In this project we reported the different microRNA expression profiles in bone marrow-derived progenitor cells from type 2 diabetic mice and their normal controls using microRNA array analysis. All microarray data are available at the Gene Expression Omnibus (GEO) at NCBI (http://www.ncbi.nlm.nih.gov/geo), under accession number GSE72616.

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Specifications	
Organism/cell line/tissue	Mouse bone marrow cells
Sex	Male
Sequencer or array type	MicroRNA microarray (μParaflo® Biochip Technology)
Data format	Raw
Experimental factors	Bone marrow cells cultured in endothelial growth medium-2 for 7 days
Experimental features	Bone marrow cells were isolated from type 2 diabetes mice (db/db) and their normal control litters (db/+). The cells were cultured in endothelial growth medium-2 for 7 days. Total RNA was extracted and subjected to microRNA analysis.
Consent	Not required.
Sample source location	N/A.

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE72616

2. Experimental design, materials and methods

2.1. Animals

Male db/db (BKS.Cg-m$^{+/+}$ Lepr^{db}/J) mice and their healthy control litters (BKS.Cg-m$^{-/-}$ Lepdb/− lean, db/+) at the age of 10–12 weeks were purchased from the Jackson Laboratory (Bar Harbor, ME). The animals were maintained under controlled environmental condition (12 h: 12 h light/dark cycle, temperature approximately 25 °C), and provided with standard laboratory food and water *ad libitum*. All animal procedures were performed according to Wayne State University Institutional Animal Care and Use Committee (IACUC) guidelines.

3. Bone marrow-derived progenitor cell culture

The important roles of bone marrow-derived progenitor cells have been demonstrated in previous reports [1,2]. However, they were found dysfunctional in diabetes [3,4]. To study the microRNA profile of bone marrow-derived progenitor cells, bone marrow mononuclear cells were isolated from the tibias and femurs of mice (n = 3 each group). The cells were plated on culture flasks coated with rat plasma vitronectin (Sigma-Aldrich) and maintained in Endothelial Growth Media (EGM-2, Lonza) in 37 °C, 5% CO_2. After 7 days of culture, the differentiating bone marrow-derived progenitor cells (BMPCs) as we identified in previous reports [5,6] were used for experiments.

3.1. MicroRNA array analysis

Total RNA was extracted from db/db BMPCs and db/+ BMPCs using miRNeasy Mini Kit (Qiagen). A total of 3 μg RNA each sample was sent to perform mouse genome-wide microRNA microarray analysis using μParaflo® Biochip Technology (service provided by LC Sciences) based on the latest version of the miRBase database (Sanger miRBase Release 21). In addition, multiple control probes are included in each chip

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for quality controls of chip production, sample labeling and assay conditions.

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