Data in Brief 6 (2016) 899–902

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Gene expression microarray data from human microvascular endothelial cells supplemented with a low concentration of niacin

Jennifer M. Hughes-Large, Nica M. Borradaile *

Department of Physiology and Pharmacology, Schulich School of Medicine and Dentistry, Western University, London, Ontario, Canada

ARTICLE INFO

Article history:
Received 17 September 2015
Received in revised form
11 December 2015
Accepted 20 January 2016
Available online 3 February 2016

Keywords:
Vascular biology
Endothelial cells
Niacin
Lipids

ABSTRACT

The systemic lipid modifying drug, niacin, can directly improve human microvascular endothelial cell angiogenic function under lipotoxic conditions, possibly through activation of niacin receptors "Niacin receptor activation improves human microvascular endothelial cell angiogenic function during lipotoxicity" (Hughes-Large et al. 2014). Here we provide accompanying data collected using Affymetrix GeneChip microarrays to identify changes in gene expression in human microvascular endothelial cells treated with 10 μM niacin. Statistical analyses of robust multi-array average (RMA) values revealed that only 16 genes exhibited greater than 1.3-fold differential expression. Of these 16, only 5 were identified protein coding genes, while 3 of the remaining 11 genes appeared to be small nuclear/nucleolar RNAs. Altered expression of *EFCAB4B*, *NAP1L2*, and *OR13C8* was confirmed by real time quantitative PCR.
© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

Specifications table

Subject area	Vascular biology
More specific subject area	Endothelial cell biology
Type of data	Tables

* Corresponding author.
E-mail address: nica.borradaile@schulich.uwo.ca (N.M. Borradaile).

http://dx.doi.org/10.1016/j.dib.2016.01.039
2352-3409/© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

How data was acquired	Affymetrix GeneChip RNA Microarray, RMA and statistical analyses, real time quantitative PCR
Data format	Filtered, analyzed
Experimental factors	Human microvascular endothelial cells were incubated with growth media containing either vehicle control (water) or niacin for 24 h.
Experimental features	RNA isolation, global gene expression analyses, and real time quantitative PCR.
Data source location	London, Ontario, Canada
Data accessibility	Data is within this article.

Value of the data

- A global gene expression analysis of human endothelial cells treated with niacin.
- These data may be useful for comparison with microarray data from other cell or tissue types treated with niacin.
- Genes identified as differentially expressed in this data set could be included in further studies of the direct effects of niacin on the vasculature.

1. Data

Affymetrix GeneChip microarray analyses of mRNA isolated from human microvascular endothelial cells (HMVEC) following 24 h treatment with 10 μM niacin revealed significantly ($P < 0.05$) altered expression of only five protein coding genes at a fold change of greater than 1.3 (Table 1). Changes in the expression of *EFCAB4B, NAP1L2*, and *OR13C8* in response to niacin treatment were confirmed by real time quantitative PCR. We also observed altered expression (> 1.3 fold, $P < 0.05$) of 3 non-coding sequences in HMVEC treated with niacin (Table 2), which appear to be small nuclear or nucleolar RNAs (snRNA and snoRNA). Our experiment was conducted using arrays consisting of predominantly coding transcripts (GeneChip Human Gene 1.0 ST, Affymetrix), and was not optimized to rigorously detect changes in the expression of small non-coding sequences.

2. Experimental design, materials and methods

2.1. Endothelial cell culture and treatments

Primary HMVEC (Lonza) were maintained in Medium 199 (Life Technologies) supplemented with EGM-2MV SingleQuots (Lonza), and subcultured as recommended by the supplier. For experiments, cells from three independent subcultures from a single donor were used. Cell monolayers at 80% confluence were incubated for 24 h with experimental media supplemented with either cell culture grade water as vehicle control (Life Technologies) or 10 μM niacin (Fluka BioChemika) solubilized in cell culture grade water. A total of six samples (three vehicle control, three niacin treated) were generated for subsequent gene expression analyses.

2.2. RNA Isolation, quality assessment, probe preparation and GeneChip hybridization

Total RNA was prepared as previously described [1]. Cell monolayers were harvested using trypsin and lysed with QIAshredder columns (Qiagen). Total RNA was isolated using an RNeasy Mini Kit (Qiagen), and eluted with nuclease-free water. RNA was stored at −80 °C for 1 week prior to microarray analyses.

All subsequent sample handling, labeling, and GeneChip (Human Gene 1.0 ST arrays) processing was performed at the London Regional Genomics Center (Robarts Research Institute, London, Ontario,

Download English Version:

https://daneshyari.com/en/article/175026

Download Persian Version:

https://daneshyari.com/article/175026

Daneshyari.com