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Data in Brief

Genome-wide profiling to analyze the effects of high fat diet induced obesity on renal gene expression in mouse with reduced renal mass

Zhibo Gai *

Department of Clinical Pharmacology and Toxicology, University Hospital Zurich, Rämistrasse 100, CH-8091 Zurich, Switzerland

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A B S T R A C T

To assess the relationship between a reduced nephron number and a particular susceptibility to obesity-induced renal damage, mice underwent uninephrectomy (UNX) followed by either normal chow or high-fat diet (HFD) and were compared with sham-operated control mice. Analysis of gene expression in the mouse kidney by whole genome microarrays indicated that high fat diet led to more changes in gene expression than uninephrectomy. However, the combination of UNX and HFD additionally altered the effects of obesity on gene expression pattern. Here we describe in details the contents and quality controls for the gene expression and related results associated with the data uploaded to Gene Expression Omnibus (accession number GSE53996).

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Direct link to deposited data

Deposited data can be found here: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE53996.

Experimental design, materials and methods

Uninephrectomy and kidney function data

Male C57/BJ mice aged 6 weeks were randomly assigned to uninephrectomy (UNX) or sham procedures and fed with a high fat diet (D12331; ResearchDiet, NJ, USA) or control chow diet (Provimi Kliba). Mice were divided into 4 groups of 6: Sham-chow, UNX-chow, sham-HFD and UNX-HFD. For uninephrectomy, the left kidney was surgically removed via a left paramedian incision on the back under anesthesia. The adrenal gland was carefully freed from the upper pole of the renal capsule before the renal pedicle was ligated and the kidney removed. For sham surgery, the kidney was manipulated without ablation. All mice were sacrificed under anesthesia 20 weeks after surgery and the kidneys were harvested. Half of the kidney from each animal was snap frozen in liquid nitrogen and stored at −80 °C for RNA and protein extraction. All protocols conformed to the Swiss animal protection laws and were approved by the Cantonal Veterinary Office in Zurich, Switzerland. Kidney functions of the different treatment groups are checked and described in Table 1. Both urine albumin/creatinine ratio and urine H2O2/creatinine level are increased in mice fed with HFD for 20 weeks. Moreover, albumin and H2O2 levels were significantly higher in the UNX group after 20 weeks of the high fat diet, indicating much severer kidney damages in such a treatment group.

Microarray and gene expression analysis

RNA was extracted from the frozen kidney using RNeasy Microarray Tissue mini kit (73304, Qiagen, Germany), followed by column DNase digestion to remove any contaminating genomic DNA. RNA samples from 4 mice per group were subjected to microarray analysis. Briefly, 100 ng of total RNA was reverse-transcribed into double-stranded cDNA, which was linearly amplified and labeled with Cy3 dye. Following quantification using a Nanodrop spectrophotometer (Witec, Luzern, Switzerland) and quality assessment with Agilent 2100 Bioanalyzer.
Normalization

Data analysis was carried out with R/Bioconductor [2]. The processed intensities and normalized across samples were loaded by using quantile normalization implemented in the Bioconductor package preprocessCore [3]. Differential expression was computed using the limma package [4]. More details on analysis methods can be found at http://fgcz-bfabric.uzh.ch/wiki/tiki-index.php?page=app.two_groups.

Table 2 Microarray analysis of mRNA expression levels in kidney tissue of the four treatment groups.

| Cooperation between groups | Number of differentially expressed genes |
|---------------------------|------------------------------------------|
| UNX-chow vs. sham-chow    | 157                                      |
| UNX-HFD vs. sham-HFD      | 136                                      |
| Sham-HFD vs. sham-chow    | 2441                                     |
| UNX-HFD vs. UNX-chow      | 2581                                     |

Summary of differentially expressed genes between groups. Cut off 1.7-fold, \( p < 0.05 \).

Discussion

We described here a unique dataset of mouse kidney disease model with obesity. This dataset is composed of genome-wide gene expression profiling data measured by Agilent platform. We showed that obesity induced proteinuria and oxidative stress in mice fed a HFD, and these changes were further enhanced by uninephrectomy. Furthermore, gene-profiling analysis of differentially expressed genes in the kidneys from each group revealed the synergistic effects of obesity and uninephrectomy. The altered expression of genes responsive to hypoxia is consistent with the increased urinary \( \text{H}_2\text{O}_2 \) levels in UNX-HFD mice.

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