Obesity is associated with depot-specific alterations in adipocyte DNA methylation and gene expression

The present study aimed to identify genes exhibiting concomitant obesity-dependent changes in DNA methylation and gene expression in adipose tissues in the mouse using diet-induced obese (DIO) C57BL/6J and genetically obese ob/ob mice as models. Mature adipocytes were isolated from epididymal and inguinal adipose tissues of ob/ob and DIO C57BL/6J mice. DNA methylation was analyzed by MeDIP-sequencing and gene expression by microarray analysis. The majority of differentially methylated regions (DMRs) were hypomethylated in obese mice. Global methylation of long interspersed elements indicated that hypomethylation did not reflect methyl donor deficiency. In both DIO and ob/ob mice, we observed more obesity-associated methylation changes in epididymal than in inguinal adipocytes. Assignment of DMRs to promoter, exon, intron and intergenic regions demonstrated that DIO-induced changes in DNA methylation in C57BL/6J mice occurred primarily in exons, whereas inguinal adipocytes of ob/ob mice exhibited a higher enrichment of DMRs in promoter regions than in other regions of the genome, suggesting an influence of leptin on DNA methylation in inguinal adipocytes. We observed altered methylation and expression of 9 genes in epididymal adipocytes, including the known obesity-associated genes, Ehd2 and Kctd15, and a novel candidate gene, Irf8, possibly involved in immune type 1/type2 balance. The use of 2 obesity models enabled us to dissociate changes associated with high fat feeding from those associated with obesity per se. This information will be of value in future studies on the mechanisms governing the development of obesity and changes in adipocyte function associated with obesity.

General information

State: Published
Organisations: Department of Systems Biology, DTU Multi Assay Core, Department of Biotechnology and Biomedicine, DTU Multi Assay Core, Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, University of Copenhagen, BGI-Shenzhen, National Institute of Nutrition and Seafood Research, University of California at San Francisco
Authors: Sonne, S. B. (Ekstern), Yadav, R. (Intern), Yin, G. (Ekstern), Dalgaard, M. D. (Intern), Myrmel, L. S. (Ekstern), Gupta, R. (Intern), Wang, J. (Ekstern), Madsen, L. (Ekstern), Kajimura, S. (Ekstern), Kristiansen, K. (Ekstern)
Number of pages: 10
Pages: 124-133
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Adipocyte (Philadelphia)
Volume: 6
Issue number: 2
ISSN (Print): 2162-3945
Ratings:
- Web of Science (2018): Indexed yes
- Scopus rating (2017): CiteScore 2.33 SJR 0.914 SNIP 0.67
- Web of Science (2017): Impact factor 3.029
- Web of Science (2017): Indexed yes
- Scopus rating (2016): CiteScore 1 SJR 0.956 SNIP 1.205
- Scopus rating (2015): SJR 0.289 SNIP 0.362
- Original language: English
- Epididymal adipose tissue, Gene expression, Global DNA methylation, Inguinal adipose tissue, Obesity
- Electronic versions: 15_5_2017_Obesity_is.pdf
- DOIs: 10.1080/21623945.2017.1320002
- Source: Findit
- Source-ID: 2357781844
- Publication: Research - peer-review › Journal article – Annual report year: 2017