GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Oligonucleotide microarray analysis reveals dysregulation of energy-related metabolism in insulin-sensitive tissues of type 2 diabetes patients

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Genet. Mol. Res. 13 (2): 4494-4504 (2014)
Received January 14, 2013
Accepted June 10, 2013
Published June 17, 2014
DOI http://dx.doi.org/10.4238/2014.June.17.1

ABSTRACT. Impaired insulin action within skeletal muscle, adipose tissue, and the liver is an important characteristic of type 2 diabetes (T2D). In order to identify common underlying defects in insulin-sensitive tissues that may be involved in the pathogenesis of T2D, the gene expression profiles of skeletal muscle, visceral adipose tissue, and liver from autopsy donors with or without T2D were examined using oligonucleotide microarrays and quantitative reverse transcriptase-PCR. Compared with controls, 691 genes were commonly dysregulated in these three insulin-sensitive tissues of humans with T2D. These co-expressed genes were enriched within the mitochondrion, with suggested involvement in energy metabolic processes such as glycolysis and gluconeogenesis, fatty acid beta oxidative, tricarboxylic acid cycle,

and electron transport. Genes related to energy metabolism were mostly downregulated in diabetic skeletal muscle and visceral adipose tissue, while they were upregulated in the diabetic liver. This observed dysregulation in energy-related metabolism may be the underlying factor leading to the molecular mechanisms responsible for the insulin resistance of patients with T2D.

Key words: Oligonucleotide microarray; Insulin-sensitive tissues; Type 2 diabetes; Energy metabolism

