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## **Microarray profiling of gene expression patterns in glomerular cells of astaxanthin-treated diabetic mice: a nutrigenomic approach.**

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We have demonstrated that astaxanthin reduces glomerular oxidative stress as well as inhibits the increase in urinary albumin in diabetic db/db mice. The aim of the present study was to determine the gene expression patterns in the glomerular cells of the diabetic mouse kidney, and to investigate the effects of astaxanthin on the expression of these genes using a high-density DNA microarray. The diet administered to the astaxanthin-supplementation group was prepared by mixing a control powder with astaxanthin at a concentration of 0.02%. Glomerular cells were obtained from the kidneys of mice by laser capture microdissection. Preparation of cRNA and target hybridization were performed according to the Affymetrix GeneChip eukaryotic small sample target labeling assay protocol. The gene expression profile was evaluated by the mouse expression set 430A GeneChip. Array data analysis was carried out using Affymetrix GeneChip operating and Ingenuity Pathway analysis software. Comparison between diabetic db/db and non-diabetic db/m mice revealed that 779 probes (3.1%) were significantly affected, i.e. 550 probes were up-regulated, and 229 probes were down-regulated, both at levels of  $\geq 1.5$ -fold in the diabetic mice. Ingenuity signal analysis of 550 up-regulated probes revealed the mitochondrial oxidative phosphorylation pathway as the most significantly affected canonical pathway. The affected genes were associated with complexes I, III, and IV located on the mitochondrial inner membrane, and the expression levels of these genes were decreased in mice treated with astaxanthin as compared to the levels in the control mice. In addition, the expression of many genes associated with oxidative stress, collagen synthesis, and transforming growth factor-beta signaling was enhanced in the diabetic mice, and this enhancement was slightly inhibited in the astaxanthin-treated mice. In conclusion, this genome-wide nutrigenomics approach provided insight into genes and putative genetic pathways that are thought to be affected by stimulation by high-glucose concentrations. In addition, the present approach may help us gain a better understanding of the genes and pathways involved in the anti-diabetic mechanism of astaxanthin.

