Lipid metabolism associated genes in the visceral fat tissues after losartan treatment in the fetal programming rat model

Objectives: Maternal undernutrition or overnutrition during pregnancy can have negative consequences for the health of children born to these pregnancies, but the physiological mechanisms are not completely understood. Recent studies on the effect of long-term or severe food restriction (FR) have revealed that many genes are dynamically modulated by this condition. The purposes of this study were to define the global gene expression profile in response to FR and clarify changes of gene expressions after losartan treatment.

Methods: Rats were divided into three groups: the control (C) group, the food restriction (FR) group and the losartan (L) group (FR plus losartan 5 mg/kg/day orally). Pregnant rats were fed a reduced diet (50 % FR) in the L groups for 21 days. Losartan was ingested during the postnatal period (4-20 week) in the L group. Rats were sacrificed at week 5. Visceral fat tissues were obtained. Using high-density oligonucleotide microarrays, the differential gene expression profiles were compared in visceral fat tissues among three groups.

Results: The amount of visceral fat was significantly higher in the FR group compared with the C group and significantly lower in the L group compared with the FR group. There was a subset of 12 genes which were preferentially expressed at 2-fold or higher in the L groups compared to the FR group. And, there was a subset of 22 genes which were preferentially expressed at 2-fold or higher in the L group compared to the C group. This subset contained numerous genes involved in the inflammatory response, immune response, lipid metabolism, cell adhesion, cell migration, cell differentiation, apoptosis, cell growth, transport, cell proliferation, transcription and signal transduction. Fat acid synthase, leptin, endothelin (ET), angiotensinogen, ET receptor type A, adiponectin, carnitine palmitoyltransferase-1 and insulin-like growth factor binding protein-3 gene were significantly expressed in the visceral fat tissues by microarray analysis.

Conclusions: Losartan may have potential for preventing apoptosis, inflammation and lipid metabolism in the offerings of animals under FR. Microarray analysis can help to identify changes of gene expressions in FR state after losartan treatment.