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# STZ로 유도된 당뇨성 신장질환 모델 쥐의 신장조직 내 유전자발현 변화 분석(RT2 프로파일링 기법의 활용)

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# Investigation of Gene Expression Changes in STZ-induced Diabetic Nephropathy using RT2-profilie Analysis

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**Objective:** We previously found that streptotzotocin (STZ)-injected rat shows pathophysiological features of diabetic nephropathy at 8 weeks post injection. So we carried out the RT2-profile experiment using mRNA from control (PBS-injection) and STZ-injected rat kidney to investigate the changes of gene expressions during these times.

**Methods:** Six-weeks-age Sprague-Dawley rats were subjected single time intraperitoneal injection of STZ (60 mg/kg). We checked the blood glucose level whether being increased more than 300 mg/dl in STZ-injected rats at 3 days after injection. At 8 weeks post injection, animals were sacrificed and then blood, urine and various tissues includeing kidney were collected for analysis. Total RNA were extracted from the kidney cortex region of these rats. RT2-profile experiment was performed using customized 96 well plate kit and Applied Biosystems 7500 real-time PCR machine according to manufacturer's instructions (QIAGEN, USA).

**Results:** Among the total 92 genes analyzed, the expressions of 20 genes were increased and those of 10 genes were decreased in STZ-injected group more than 2-fold compared with control group. We found that many genes increased in its expression which is related with 1)oxidative stress (ACE, ALDH1a1, ALDH2, NOS3, ATF3, TLR4, TGF-beta/smad), 2) autophagy (Atg3, Atg12, Atg7, Beclin1, lamp1), 3) ECM (ICAM1, VCAM1, MMP9, TGF/smad, IFN-g, fibronectin, MCP-1, and TLR-4) and 4) many cytokine genes, especially IL-10 gene up-regulated significantly with STAT family and SOCS family genes expression which are related with cytokine signaling and its inhibition respectively. Furthermore, we have assessed the gene network associated with ECM accumulation and subsequently, examined their reciprocal regulatory mechanisms.

**Conclusions:** We previously found that STZ-injected rat not only suffers from type I diabetes but also diabetic kidney disease of which features include mesangial expansion, fibrosis and inflammation at glomerular and tubular regions of kidney. In our present study we also found that the expressions of many genes related with oxidative stress, fibrosis and inflammation changed during the progress of renal dysfunction in STZ-injected rat. These genes are supposed to play crucial roles causing or protecting diabetic nephropathy progression. Therefore we will further investigate the functions of these genes alongside with identifying the signaling networks of these genes in diabetic nephropathy.

**Key Words:** 당뇨병성 신증, 스트렙토조토신, RT2-프로파일
Diabetic nephropathy, Streptozotocin, RT2-profile assay