Overexpression of p53 due to excess protein *O***-GlcNAcylation is associated with coronary microvascular disease in type 2 diabetes**

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Short Title: p53 and endothelial function in Diabetes

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Category of the Manuscript: Original Article

Supplemental Figure 1. Endothelium-dependent relaxation in coronary artery is attenuated in TH mice compared to Wt mice. Isometric tension experiments were conducted using 3rd order coronary arteries to assess EC-dependent relaxation using acetylcholine (ACh) or EC-independent relaxation using papaverine (Pap). Nmice=4 per group. Data are presented as mean ± S.E. **P*<0.05 vs. Wt. Statistical comparison between dose-response curves was made by two-way ANOVA with Bonferroni post hoc test.

Supplemental Figure 2. Inhibition of p53 by p53 siRNA increases tube formation in diabetic HCECs. Control siRNA or p53 siRNA was transfected into diabetic HCECs using lipofectamine RNAiMAX reagent. Forty-eight hours later, cells were used for the experiment. **A**: Western blot analysis showing p53 protein level in ECs after siRNA transfection in a dose dependent manner. **B**: Western blot image (left) showing p53 protein levels after transfection of control and p53 siRNA in ECs at 100 nM. Summarized data (right) showing protein level of p53 (n_{experiments}=6 per group) normalized by the protein level of actin. Data are expressed as mean \pm SE. **P*<0.05 vs. control siRNA (Cont-siRNA). Unpaired Student's *t*-test was used for comparing two experimental groups. **C**: Summarized data of tube formation in control HCECs (C-HCEC) treated with ContsiRNA (100 nmol/L, n_{experiments}=5), diabetic HCECs (D-HCEC) treated with Cont-siRNA (n_{experiments}=4), and D-HCEC treated with p53-siRNA (100 nmol/L, n_{experiments}=5). *#P*<0.05 vs. D-HCEC + Cont-siRNA. Data are mean ± SE. Statistical comparison among three groups was made by one-way ANOVA with Bonferroni *post hoc* test.

Supplement Table 1. Antibody list.

Supplement Table 2. Human coronary endothelial cell.

Note: All commercially-available T2D cells were purchased at the time the studies were performed.

Supplement Table 3. Mouse p53 signaling pathway PCR array result. Gene names of which mRNA levels were altered in TH mice and restored by chronic PFT administration are listed.

Wt + Vehicle, n_{mice} =5; TH + Vehicle, n_{mice} =4, TH + PFT, n_{mice} =5. Data are presented as mean ± S.E. One-way ANOVA was carried out to determine the significance between groups.

Supplement Table 4. Primer information used for real-time PCR

1. Supplementary methods for supplemental figures/tables

Isometric tension measurement in coronary arterial ring (Supplemental Figure 1)

Isometric tension measurement in isolated coronary arteries (CAs) from mice was performed as described previously1-6. Briefly, third-order small CAs were dissected from the hearts and then cut into 1-mm segments. The CA rings were mounted on a myograph (DMT-USA, Inc. Ann Arbor, MI, USA) using thin stainless wires (20 μm in diameter) and the resting tension was set at 0.1 g. CAs were allowed to equilibrate for 45 min with intermittent washes every 15 min. After equilibration, each CA ring was contracted by superfusion of $PGF_{2\alpha}$ to generate similar contraction level in all groups. Acetylcholine (ACh) or papaverine (Pap, a phosphodiesterase inhibitor) was administrated in a dose-dependent manner (1 nmol/l to 100 μmol/l).

p53-siRNA transfection in diabetic HCECs (Supplemental Figure 2)

Downregulation of p53 in diabetic HCECs was achieved using p53 siRNA (siRNA ID# s606, Thermo Fisher Scientific) and lipofectamine RNAiMAX reagent (Thermo Fisher Scientific). Specific protein knockdown was verified with Western blotting 48 hours after transfection.

RT2 profile PCR array (Supplemental Table 3)

mRNAs from MCECs were isolated using the miRNeasy Mini Kit (QIAGEN, Chatsworth, CA). First-strand cDNA was synthesized using a RT2 first-strand kit (QIAGEN). Pathway-focused gene expression analyses were performed using RT2 Profile PCR Arrays (Mouse p53 Signaling Pathway PCR Array, PAMM-027ZA, QIAGEN). The results from the PCR array were analyzed done based on manufacturer's instructions. Each array contained five housekeeping genes and we used beta actin to normalize other gene expression levels. The transcript levels of Gene of Interest (GOI) were quantified according to the cycle threshold (ΔCt) method. Ct values > 35 were not included in the analysis and were considered as negative.

Statistical analysis

Statistical analysis was performed using SigmaPlot 14 (Systat Software, Inc.). Data were presented as mean ± S.E. One-way ANOVA was used for multiple comparisons. Statistical comparison between dose-response curves was made by two-way ANOVA with the Bonferroni correction performed post hoc to correct for multiple comparisons. Differences were considered to be statistically significant when **P*<0.05.

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