and the activities of SOD decreased significantly in cavernous tissue of the diabetes group. The degeneration of mitochondria in the endothelia and smooth muscle cells of penis was observed, following with the reduction of mitochondria, and mitochondria transmembrane potential was decreased. A remarkable decrease in MDA and increase in SOD was observed in GSH treatment group. Meanwhile, the morphology changes of mitochondria were ameliorated and the decrease of mitochondria transmembrane potential was inhibited, in diabetic rats with GSH treatment.

Conclusions: Hyperglycemia could cause oxidative stress in the cavernous tissue of diabetic rats and this impairment could contribute to diabetic erectile dysfunction (DMED); oxidant treatment could attenuate oxidative stress by improving the function of mitochondria in cavernous tissue. Oxidative stress plays an important role in DMED and our study might provide a new insight for the prevention and treatment of DMED.

Keywords: Oxidative stress; erectile function

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AB162. Prognostic and predictive value of epigenetic biomarkers and clinical factors in upper tract urothelial carcinoma

Gengyan Xiong, Jin Liu, Qi Tang, Dong Fang, Lei Zhang, Yanqing Gong, Qun He, Kan Gong, Zhisong He, Gang Wang, Xuesong Li, Yinglu Guo, Liqun Zhou

Peking University First Hospital, Beijing 100034, China

Objective: Prognostic epigenetic biomarkers and clinical factors in upper tract urothelial carcinoma (UTUC) are inconclusive. We conducted this study to identify gene

promoter (ABCC6, BRCA1, CDH1, GDF15, HSPA2, RASSF1A, SALL3, THBS1, TMEFF2 and VIM) methylation status and clinical predictors for UTUC patients (N=687).

Methods: Using methylation-sensitive polymerase (MSP) chain reaction, we examined 10-gene promoter methylation status in 687 UTUC patients. The log-rank test and Cox regression were applied, and two nomograms were utilized to construct the prognostic model for cancer specific survival (CSS) and bladder recurrence free survival (BRFS), respectively.

Results: Methylation in tumor tissue was detected in 14.3% for ABCC6, 17.3% for BRCA1, 14.3% for CDH1, 49.9% for GDF15, 41.2% for HSPA2, 26.6% for RASSF1A, 34.4% for SALL3, 25.2% for THBS1, 43.2% for TMEFF2 and 63.2% for VIM. A methylated promoter of CDH1 (P=0.045), HSPA2 (P<0.001) and RASSF1A (P=0.037) was significantly associated with a higher tumor stage (T3 and T4). A methylated promoter of BRCA1 (P=0.013), HSPA2 (P=0.030), RASSF1A (P=0.031) and THBS1 (P=0.001); and an unmethylated promoter of GDF15 (P<0.001) were significantly associated with tumor grade 3. A methylated promoter of RASSF1A (P=0.005) was associated with pN+. Older age (P<0.001), male sex (P=0.033), tumor multifocality (P=0.008), ipsilateral hydronephrosis (P<0.001), larger main tumor diameter (5 cm, P<0.001), higher tumor stage (P<0.001), positive N status (P=0.018), methylated TMEFF2 promoter (P=0.002) and unmethylated BRCA1 promoter (P=0.004) were significantly associated with poor CSS. Tumor multifocality (P=0.002), ureteroscopy history (P=0.001), lower tumor grade (P=0.046), unmethylated promoter of GDF15 (P=0.030) and RASSF1A (P=0.001) were considered as predictors to develop bladder recurrence after surgery.

Conclusions: Methylation occurs commonly in UTUCs, may affect carcinogenic mechanisms, and is a well predictive factor for CSS and BR in UTUCs.

Keywords: Upper tract urothelial carcinoma (UTUC); predictive factor; epigenetic markers

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