effective promoter component can help us overcome these limitations.

Methods: Here, we transfected the artificially hTERT promoter sequence into cancer cells and kept the specificity of the promoter. Then we used the Dual luciferase reporter gene system to prove the artificial hTERT promoter's specificity and efficacy. Last, we demonstrated its modularity by replacing the luciferase reporter gene with other cellular functional genes like hBAX.

Results: Using the Dual luciferase reporter gene system, we have shown that the aritificial hTERT promoter specifically detected bladder cancer cells and significantly enhanced luciferase expression in comparison to the WT-hTERT-renilla luciferase (Rluc) construct. The functional module of artificial hTERT promoter effectively inhibited bladder urothelial carcinoma cell growth and induced apoptosis by regulating the down-stream gene.

Conclusions: This functional module provides a synthetic biology platform for targeting and controlling bladder cancer.

Keywords: Htert; BAX; bladder cancer

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AB114. The expression and significance of W E E 1 in renal clear cell carcinoma

Wu Xu, Xianzhen Jiang

Department of Urology, the Third Xiangya Hospital of Central South University, Changsha 410013, China

Objective: To investigate the expression and significance of W E E 1 protein in renal clear cell carcinoma (RCCC), as well as the relationship between W E E 1 and biology behaviors (clinical stages, pathological grades and lymphatic metastases) of RCCC, providing evidence for diagnosis, therapy and prognosis of RCCC.

Methods: Immunohistochemical analysis (SP method), real time PCR and Western blot were used to determine the W E E 1 expression in 32 RCCCs and 25 normal renal tissues. Then the relationships between clinical stage, pathological grade, lymphatic metastases and W E E 1 expressions of RCCC were analyzed. All statistical analyses were carried out with SPSS 14.0 software. The probability of less than 5% was assumed to be statistically significant ($P<0.05$).

Results: The positive rate of W E E 1 expression in RCCC was 87.5% (28/32), compared with 8% (2/25) in normal tissues. W E E 1 expressions in RCCC were significantly higher than those in normal renal tissues ($P<0.01$). The CT value of W E E 1 mRNA expression in the renal cell carcinoma was 13.7±3.7, compared with 4.5±2.0 in normal tissues. There is significant difference between the two groups ($P<0.01$). Western Blot analysis indicates a significant higher expression of W E E 1 (5.2±1.5) in RCCC as compared with that (0.6±0.37) in normal tissues. In stage I, II and III-IV, the expressions of W E E 1 were 3.1±0.7, 4.7±0.9 and 6.7±0.9 respectively. The expressions of W E E 1 in stage II and III-IV were 1.5 times and 2.2 times compared with those in stage I ($P<0.05$). The W E E 1 expression was also closely related with pathological grade. The W E E 1 expressions in well differentiated group, moderately differentiated group and poorly differentiated group were 3.1±0.5, 4.4±0.5, and 6.4±0.9 respectively. The W E E 1 expression in moderately and poorly differentiated group were 1.75 times and 1.8 times compared with the other one ($P<0.05$). The W E E 1 expression was 4.3±1.1 in patients without lymph node metastasis while 6.8±0.6 in those with lymph node metastasis; The W E E 1 expression in metastasis group was 1.6 times as the other group ($P<0.05$). There was positive correlation between expression of W E E 1 protein and metastasis. The correlation coefficient is 0.805, ($P<0.01$).

Conclusions: W E E 1 expression in RCCCs higher than those in normal renal tissues, the expression of W E E 1 was much lower in the normal kidney tissue. WEE1 expression in RCCC was closely related to pathological grades, clinical stage and lymph node metastases. The W E E 1 expression in III, IV group was higher than the phase I and II. The expression in the differentiation of low and moderately differentiated groups was higher than the high group. In addition, the expression of lymph node metastasis group was higher than other groups. W E E 1 is expected to become an important biological index to evaluate RCCC metastasis and prognosis and may be a novel therapeutic target of RCCC.

Keywords: Renal clear cell carcinoma (RCCC); W E E 1; immunohistochemical; real time PCR; cell cycle; G2 arrest

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AB115. Preliminary study on the immune status of patients with prostate cancer

Jingliang He, Leye He

Department of Urology, the Third Xiangya Hospital of Central South University, Changsha 410013, China

Objective: To preliminarily assess the immune status of patients with prostate cancer through detecting various immune indexs and then analyse the relationship between immune status and clinical factors such as clinical stage, pathological classification and endocrine therapy.

Methods: Flow cytometry was used to detect the percentage of CD4, CD8and NK cells in peripheral blood lymphocyte (PBL) of 28 patients with PCa, 16 BPH patients and ten healthy men (HM). The expression of perforin and granzyme-B in PBL of 30 patients with PCa, 17 BPH patients and 7 HM were tested by fluorescence quantitative reverse transcription polymerase chain reaction. The results and evaluation of the relationship between these immune indexes and several clinical variables were analysed statistically.

Results: The percentage of CD4lymphocyte and the ratio of CD4/CD8 in PCa group were significantly lower than those in BPH group and HM group while the percentage of CD8lymphocytes in PCa group was statistically higher than that in BPH group and HM group (P<0.05). There are no statistical difference of percentage of NK cells between PCa group, BPH group and HM group (P>0.05). The percentage of CD4lymphocyte and the ratio of CD4/CD8in low pathological grade PCa patients were significantly higher than those in high pathological grade PCa patients while the percentage of CD8 lymphocyte in low pathological grade PCa patients was lower than that in high pathological grade PCa patients (P<0.05). The difference of percentage of NK cells between low pathological grade PCa patients and high pathological grade PCa patients has no statistical significant (P>0.05). The percentage of CD4lymphocyte and the ratio of CD4/CD8 in metastatic PCa group were significantly lower than those in non-metastatic PCa group while the percentage of CD8lymphocytes in metastatic cPCa was higher than that in non-metastatic PCa group (P<0.05). The difference of percentage of NK cells between metastatic PCa group and non-metastatic PCa group has no statistical significant (P>0.05). There is no statistically significant difference between lymphocyte subgroup percentage of T_3PCa group and T_4PCa group (P>0.05). There was no statistical difference of percentage of lymphocyte subgroup in PCa patients whether they received endocrine therapy or not (P>0.05).

The expression of perforin and granzyme-B inPBL was significantly lower in patients with PCa than that in patients with BPH and HM group (P<0.05). Furthermore, in low pathological grade PCa patients, the expression of perforin and granzyme-B in PBL was statistically higher than that in high pathological grade PCa patients (P<0.05). There is no statistical difference between expression of perforin and granzyme-Bin metastatic PCa group and those in non-metastatic PCa group (P>0.05). The difference between expression of perforin and granzyme-B in PCa patients who have not receive endocrine therapy and those in PCa patients who have received endocrine therapy for more than 4 weeks also have no statistical significance (P>0.05). The expression level of perforin and granzyme-B in T_3 PCa group were significantly higher than those inT_4PCa group (P<0.05).

Conclusions: Firstly, compared with BPH patients and healthy men, PCa patients have a lower immunity. Secondly, the degree of immuno-suppression in PCa patients may be related to the degree of tumor malignancy and clinical progress. High grade malignancy and late clinical stage may suggest heavy immunosuppression. Thirdly, Endocrine therapy seems to have no obvious influence on the immune function of PCa patients.

Keywords: Prostate cancer (PCa); lymphocytes; perforin; granzyme-B; CD4; CD8; NK cell

