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Molecular Mechanism Study on the Expression of TF-MPs in Cervical Cancer Patients and Deep Venous Thrombosis

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Abstract: *Objective:* To explore the molecular mechanism of tissue factor-positive microparticles (TF-MPs) expression and deep venous thrombosis (DVT) in patients with cervical cancer. *Methods:* A total of 200 patients with cervical cancer and benign cervical diseases who were hospitalized in the First Department of Gynecologic Oncology of Gansu Provincial Cancer Hospital from January 2024 to December 2025 were selected, including 100 patients with benign cervical diseases as the control group and 100 patients with cervical cancer as the experimental group. Enzyme-linked immunosorbent assay (ELISA) was used to detect the expression level of TF-MPs in peripheral blood samples from patients with cervical cancer and healthy controls. At the same time, real-time quantitative PCR was used to explore the molecular mechanism of TF-MPs promoting DVT formation. Finally, the formation of DVT in the two groups was observed and recorded, and the incidence of DVT was counted. *Results:* Experimental measurements showed that the expression levels of TF-MPs, coagulation factors FVII, FX, PT, and inflammatory factors IL-6 and TNF-a in the experimental group were significantly higher than those in the control group ($P < 0.01$); the incidence of DVT in the experimental group was up to 38%, far exceeding the 6% in the control group ($P < 0.001$). *Conclusion:* Abnormal expression of TF-MPs in patients with cervical cancer is an important risk factor for DVT. Through in-depth analysis of the molecular mechanism of TF-MPs promoting DVT formation, it provides a new perspective and theoretical basis for the prevention and treatment of DVT in patients with cervical cancer. In the future, intervention strategies targeting TF-MPs and their related molecular pathways are expected to become effective ways to reduce the incidence of DVT in patients with cervical cancer.

Keywords: Cervical cancer; TF-MPs; Deep venous thrombosis; Molecular mechanism

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1. Introduction

Cervical cancer is a common gynecological malignancy and its development is closely related to various molecular mechanisms. In recent years, studies have found that tissue factor microparticles (TF-MPs) play an important

role in tumor-associated thrombosis. As a combination of tissue factor (TF) and microparticles (MPs), TF-MPs have strong procoagulant activity, which can activate the extrinsic coagulation pathway and promote thrombosis [1]. In patients with cervical cancer, the expression level of TF-MPs is prone to changes, which in turn affects the formation of deep vein thrombosis (DVT) [2]. Therefore, to explore the gene expression and molecular mechanisms of DVT formation in cervical cancer patients, this study observes and records changes in TF-MPs expression in cervical cancer patients, analyzes the correlation between TF-MPs expression and DVT formation, and aims to reveal the intrinsic relationship between cervical cancer and DVT formation. This provides a new target for anticoagulation therapy in cervical cancer patients, explores more innovative treatment options, clarifies the expression of TF-MPs in cervical cancer patients, elucidates its role in DVT formation, and provides a scientific basis for comprehensive treatment of cervical cancer.

2. Subjects and methods

2.1. Study subjects

The study selected 200 patients with cervical cancer and benign cervical diseases who were hospitalized in the First Department of Gynecologic Oncology of Gansu Provincial Cancer Hospital from January 2024 to December 2025. Among them, 100 patients with benign cervical diseases were included in the control group, and 100 patients with cervical cancer were included in the experimental group. The experimental group had an age range of 35–70 years, with an average age of (57.32 ± 11.68) years, a heart rate of (75.42 ± 5.47) beats/min, and a blood pressure of (118.64 ± 75.40) mmHg. The control group had an age range of 36-71 years, with an average age of (56.73 ± 11.16) years, a heart rate of (74.93 ± 5.25) beats/min, and a blood pressure of (119.35 ± 75.69) mmHg. There were no significant differences in general information between the two groups, and the study was comparable ($P > 0.05$).

The inclusion criteria consisted of: (1) Pathologically confirmed diagnosis of cervical squamous cell carcinoma, cervical adenocarcinoma, or other types of cervical cancer; (2) No chemotherapy, radiotherapy, surgery, immunotherapy, or other treatments received in the past month; (3) No psychiatric disorders, no language communication barriers, and clear consciousness; (4) Healthy individuals with no family history of cervical cancer, high-risk HPV infection, or other risk factors; (5) All subjects and their families were informed of the study details and signed informed consent forms.

However, the exclusion criteria were: (1) Pregnant or lactating women; (2) Presence of severe cardiovascular and cerebrovascular diseases, hepatorenal dysfunction, autoimmune diseases, or other complications or comorbidities; (3) Concomitant with other malignancies; (4) Incomplete clinical data or withdrawal from the study.

2.2. Research methods

2.2.1. Detection of TF-MPs expression levels

Peripheral blood samples were collected from both groups and processed rapidly to avoid degradation of TF-MPs. The ELISA kit was used to detect the samples according to the manufacturer's instructions. During the detection process, experimental conditions were strictly controlled. The incubation temperature for both the samples and enzyme-labeled antibodies was maintained at 37°C to ensure sufficient binding of antibodies to TF-MPs. The chromogenic reaction temperature of the substrate was 25°C. The incubation time for samples was 60 minutes and the incubation time for enzyme-labeled antibodies was 30 minutes. The chromogenic reaction time of the substrate was 15 minutes, during which the enzyme-catalyzed the substrate to produce a significant color change.

After each incubation, washing was performed three times to remove unbound antibodies and impurities, ensuring the accuracy of the detection results. After completing the above steps, an enzyme labeler was used to measure the absorbance value of each well at a wavelength of 450nm. Based on this, the concentration of TF-MPs in the sample was calculated. The most reliable sample absorbance values ranged from 0.2 to 1.8.

2.2.2. Detection of coagulation and inflammation-related genes

Peripheral blood samples were collected from all subjects, and high-quality RNA was extracted to ensure RNA integrity. Subsequently, specific primers were designed based on the target gene sequence, and reverse transcriptase was used to reverse transcribe RNA into cDNA. In the qPCR reaction, the SYBR Green I dye method or TaqMan probe method was used to mix cDNA with specific primers and fluorescent substances for PCR amplification. By monitoring the fluorescence signal intensity in real-time, the cycle threshold (Ct) value was calculated, reflecting the initial copy number of the target gene. Through qPCR technology, the gene expression differences of coagulation factors and inflammatory factors between cervical cancer patients and healthy individuals were accurately measured. The coagulation factors included Factor VII (FVII), Factor X (FX), and Prothrombin (PT), while the inflammatory factors included Interleukin-6 (IL-6) and Tumor Necrosis Factor-alpha (TNF-α).

2.3. Observation indicators

2.3.1. Laboratory indicators

Coagulation factors FVII and FX play critical roles in the coagulation process, and their activity levels affect coagulation efficiency. The normal value of PT is generally 10-4s. Prolongation of PT suggests a deficiency of coagulation factors such as FVII and FX, increasing the risk of DVT. High expressions of inflammatory factors IL-6 and TNF-α, such as IL-6 exceeding 348.92 pg/mL, indicate septic shock and a hypercoagulable state, increasing the risk of DVT. TNF-α increases with the progression of sepsis and its high level also suggests poor prognosis and a tendency for thrombosis. In cases of high TF-MPs expression, the activity of coagulation factors FVII and FX is abnormally enhanced, leading to a shortened prothrombin time (PT). This results in a hypercoagulable state, significantly increasing the risk of deep venous thrombosis (DVT). Conversely, when TF-MPs expression is low, coagulation factor activity is normal, PT maintains a normal range, and the risk of DVT is relatively low.

2.3.2. Incidence of DVT

The formation of DVT cases in both groups was observed and recorded, and the incidence of DVT was calculated. The formula for DVT incidence is:

$$\text{DVT incidence} = \text{number of DCT formation cases} / \text{total number of cases} \times 100\%.$$

2.4. Statistical analysis

Statistical software SPSS 21.0 was used to organize and statistically analyze relevant data. Measurement data were expressed as mean ± standard deviation ($\bar{x} \pm s$), and the t-test was performed. Count data were expressed as percentages (%), and the chi-square test was performed. Differences between groups were considered statistically significant if $P < 0.05$.

3. Results

3.1. Comparison of TF-MPs expression levels between the two groups

According to clinical experiments, the expression level of TF-MPs in the experimental group was significantly higher than that in the control group, with a significant difference ($P < 0.01$), as shown in **Table 1**.

Table 1. Comparison of TF-MPs levels between the two groups($\overline{x} \pm s$)

Grouping	*n*	TF-MPs(pg/mL)
Experimental group	100	125.73 ± 34.54
Control group	100	82.30 ± 21.68
t	-	4.896
P	-	＜ 0.001

3.2. Comparison of coagulation and inflammatory gene expression levels between the two groups

Comparing coagulation factors between the two groups, the levels of FVII, FX, and PT in the experimental group were significantly higher than those in the control group, with statistically significant differences ($P < 0.05$). Comparing inflammatory factors between the two groups, the levels of IL-6 and TNF-α in the experimental group were significantly higher than those in the control group, with significant differences ($P < 0.05$), as shown in **Table 2**.

Table 2. Comparison of FVII, FX, PT, IL-6, and TNF-a factor levels between the two groups($\overline{x} \pm s$)

Grouping	FVII	FX	PT	IL-6	TNF-a
Experimental group (n = 100)	2.87 ± 0.34	3.46 ± 0.51	2.23 ± 0.27	2.69 ± 0.52	3.04 ± 0.62
Control group (n = 100)	1.13 ± 0.15	1.37 ± 0.20	1.05 ± 0.14	1.24 ± 0.23	1.53 ± 0.28
t	4.566	5.120	4.215	2.783	3.146
P	＜ 0.01	＜ 0.01	＜ 0.01	＜ 0.05	＜ 0.05

3.3. Comparison of DVT incidence between the two groups

In the experimental group, there were 38 cases of DVT, while in the control group, there were 6 cases of DVT. The incidence of DVT in the experimental group was 38%, which was significantly higher than the 6% in the control group ($P < 0.01$). The details are shown in **Table 3**.

Table 3. Comparison of DCT incidence between the two groups (n,%)

Grouping	*n*	Incidence of DVT
Experimental group	100	38(38.00)
Control group	100	6(6.00)
t	-	7.504
P	-	＜ 0.001

4. Discussion

The study of TF-MPs expression in cervical cancer patients and its association with deep vein thrombosis (DVT) formation has profound significance [3]. Based on the clinical manifestations of cervical cancer patients, coagulation abnormalities are often observed and TF-MPs serve as key coagulation regulatory factors. Changes in their expression levels have a significant impact on DVT formation. This study delves into the molecular mechanisms underlying TF-MPs expression and DVT in cervical cancer patients, aiming to uncover the intrinsic relationship between the two and enrich our understanding of the pathology and physiology of cervical cancer complications. It provides a new perspective for clinical prevention and treatment of DVT, carrying important clinical value in improving patient prognosis and quality of life [4].

Through clinical experiments, our study results showed that the expression level of TF-MPs in the experimental group was significantly higher than that in the control group, with a statistically significant difference ($P < 0.001$). As an important regulatory factor in the coagulation system, the high expression of TF-MPs can promote abnormal activation of the coagulation process, providing favorable conditions for DVT formation [5,6]. Further analysis of coagulation and inflammatory gene expression levels revealed that the levels of coagulation factors such as FVII, FX, and PT in the experimental group were significantly higher than those in the control group ($P < 0.01$). Simultaneously, the levels of inflammatory factors IL-6 and TNF-a were also significantly higher than those in the control group ($P < 0.05$). These results suggest that there is abnormal activation of coagulation and inflammatory responses in cervical cancer patients, which interact with each other to jointly promote the formation of DVT [7, 8]. In addition, by comparing the incidence of DVT between the two groups, this study showed that the incidence of DVT in the cervical cancer patient group was as high as 38%, significantly exceeding the 6% in the control group ($P < 0.01$), further confirming the higher risk of DVT in cervical cancer patients [9].

5. Conclusion

In summary, this study uncovers the close relationship between high TF-MPs expression in cervical cancer patients and abnormal activation of coagulation and inflammatory responses, as well as DVT formation. Future research should further explore the role of TF-MPs in DVT formation in cervical cancer patients and investigate new targets and strategies for preventing DVT formation in cervical cancer treatment [10].

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Disclosure statement

The authors declare no conflict of interest.

References

[1] Lan S, Sun X, Mao J, 2024, Study on the Expression of SHCBP1 Gene and Its Effect on the Biological Behavior of Cervical Cancer Cells. Chinese Journal of Maternal and Child Health, 39(22): 4494–4499.

[2] Zhang X, Ma H, Song F, et al., 2024, Changes in Proliferation, Migration, and Invasion of Human Cervical Cancer Cell Line HeLa with Overexpression of miR-216a and CAPN6 Genes and Their Targeting Relationship. Shandong Medical Journal, 64(18): 21–25.

[3] Dan X, He Y, Tian Y, et al., 2024, Relationship Between Mitochondrial-Related Gene Expression Changes and Cancer-Related Fatigue in Patients with Cervical Cancer Undergoing Concurrent Chemoradiotherapy. Guangdong Medical Journal, 45(6): 782–788.

[4] Tuo J, Cheng H, Zhao X, et al., 2024, Effects of CDH18 Gene on Proliferation and Migration of Cervical Cancer Cells. Journal of Shihezi University (Natural Science Edition), 42(3): 349–357.

[5] Zhu L, Li H, Ren W, 2024, Expression of MAPK6 Gene in Cervical Cancer Tissue and Its Clinical Significance. Chinese Journal of Birth Health and Heredity, 32(4): 741–744.

[6] Cao M, Feng G, Zhou D, 2024, Changes in Prothrombin Time International Normalized Ratio in Patients with Early-Stage Cervical Cancer and Its Predictive Value for Postoperative Lower Extremity Deep Venous Thrombosis. Chinese Journal of Human Sexuality, 33(1): 70–74.

[7] Zhou L, Wang X, 2024, Evaluation of the Effect of Cluster Nursing on Preventing Lower Extremity Deep Venous Thrombosis after Cervical Cancer Surgery. Hebei Medical Journal, 46(1): 158–160.

[8] Xiao B, Sun H, Meng S, et al., 2023, Analysis of PVR Gene Expression in Cervical Cancer and Its Effect on Tumor Immune Microenvironment Based on TCGA Data. Journal of Cancer Prevention and Treatment, 36(3): 214–228.

[9] Zhang L, Wang Y, Luo S, et al., 2023, Preventive Effect of Graded Psychological Intervention Combined with Pneumatic Pump Therapy on Lower Extremity Deep Venous Thrombosis after Cervical Cancer Surgery. Oncology Progress, 21(6): 652–655.

[10] Xia N, Yang A, Yu M, 2023, Screening of Cisplatin Resistance-Related Genes in Cervical Cancer and the Effect of KRT6A Expression on the Biological Behavior of Cisplatin-Resistant Cervical Cancer SiHa Cells. Chinese Journal of Practical Diagnosis and Therapy, 37(3): 252–260.