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Expression of CDC20, TOP2A in Esophageal Phosphorus Carcinoma and Its Relationship with Survival of Esophageal Carcinoma

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ABSTRACT

Objective: To study the expression of CDC20, TOP2A in esophageal squamous cell carcinoma and its relationship with survival of esophageal carcinoma. Methods: 65 patients with esophageal squamous cell carcinoma from January 2016 to June 2018 were selected by computer random selection. All patients were treated with radical operation. The CDC20, TOP2A expression of the patients was examined. At the same time, the relationship between 3-year survival rate and CDC20, TOP2A was analyzed by follow-up investigation. Results: the CDC20, TOP2A expression level of cancer tissue group was higher than that of adjacent tissue group and normal tissue group (P <0.05), and the CDC20, TOP2A expression level of adjacent tissue group was higher than that of normal tissue group (P <0.05). There was no significant difference in sex, age, tumor size, tumor location and CDC20, TOP2A expression level in patients with esophageal squamous cell carcinoma, P >0.05; there were differences between groups (P <0.05), and showed inverse proportion relationship. Conclusion: metastasis, recurrence and prognosis of esophageal squamous cell carcinoma are related to the level of CDC20, TOP2A expression. These two indexes can effectively evaluate the pathological situation of esophageal cancer and provide an important reference for the prognosis of esophageal squamous cell carcinoma patients.

1. Introduction

As the level of medical science continues to improve, the biological mechanism and analysis of esophageal squamous cell carcinoma are also more in-depth. TOP2A expression and tumor cell death are related to the mechanism of gene and protein formation of esophageal squamous cell carcinoma. It is also found that cell division cycle protein 20 plays a role in promoting tumor cell infiltration. Based on this, this paper will analyze the causes of esophageal squamous cell carcinoma from the aspects of tumor cell proliferation and tumor cell division, and study the expression and survival relationship between CDC20, TOP2A and esophageal squamous cell carcinoma tissue, in order to provide new research ideas and methods for the industry.

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2. Clinical Data and Methods

2.1 Clinical Information
Random selection by computer, From January 2019 to June 2020, 65 patients with esophageal squamous cell carcinoma, All patients underwent radical surgery, Pathological specimens during surgery, All patients were diagnosed as esophageal squamous cell carcinoma. In radical surgery for esophageal cancer, Fresh tissue samples, It was divided into cancer tissue group, adjacent tissue group and normal tissue group. Of the 65 patients, 45 males, Twenty women, Forty patients aged under 60, 25 patients over 60 years of age; According to the size of the tumor, 39 cases less than 5 cm, 26 cases greater than 5 cm; According to the tumor focus, In the last 35 cases, 30 cases in the lower section; According to TNM staging criteria, Eight cases in the first phase, 29 cases in phase II, There were 16 cases in phase III, The fourth stage was 12 cases; Depending on the tumor, In 36 cases, Low differentiation into 29 cases; Based on lymphatic metastasis, Lymphatic metastasis, 27 cases, No lymphatic metastasis in 38 cases; According to the vein infiltration, In 26 cases, No venous infiltration in 39 cases; Based on survival, More than three years, 34 cases, Less than three years was 31 cases.

2.2 Inspection Methods
The specimens were fixed for 4-6 hours according to the basic formaldehyde (10% concentration), treated with gradient dehydration, waxed tissue, paraffin embedded treatment, expanded sections, stained with immunohistochemical S-P method, and read films with microscope. The gray value of CDC20, TOP2A expression in esophageal squamous cell carcinoma was observed by using image processing system. The results were determined by two experienced pathologists in the case of double-blind method, with the help of high power microscope to observe the tumor cells, the nucleus or cytoplasm produced yellow or brown granules, which were incorporated into the positive cells. Five visual fields were randomly selected for each specimen, 100 tumor cells were counted in each field, and a total of 500 tumor cells were counted. The positive cell rate of more than 10% is positive, and the positive cell rate of less than 10% is negative. Meanwhile, using semi-quantitative reverse transcription polymerase chain reaction, the expression of CDC20, TOP2A in pathological tissue was tested, gene RNA was extracted according to the standard of Trizol RNA kit, DEPC preparation was carried out, and then the whole study of agarose gel electrophoresis identification mRNA was carried out. Through the use of real-time quantitative PCR equipment for standard gene amplification processing, with the help of ultraviolet gel imaging equipment and analysis equipment in the observation function, scanning function, photo-taking function, the CDC20, TOP2A and β-actin expression intensity was calculated and studied.

2.3 Statistical Treatment
This clinical basic data all uses the statistics processing way, the statistics software system SPSS 21.0 version, the count data is expressed in the percentage, uses the x² Test, when the result is P <0.05, prove that there is statistical difference between groups.

3. Results

3.1 CDC20, TOP2A Expression in Esophageal Squamous Cell Carcinoma
By means of immunohistochemical S-P, it was found that the tumor cells showed a nest-like distribution pattern, accompanied by irregular cell series, mainly cell heteromorphism and nuclear mitosis.

3.2 Analysis of CDC20, TOP2A Expression in Different Esophageal Squamous Cell Carcinoma Specimens
The CDC20, TOP2A expression level of cancer tissue group was higher than that of adjacent tissue group and normal tissue group (P <0.05), and the CDC20, TOP2A expression level of adjacent tissue group was significantly higher than that of normal tissue group (P <0.05), as shown in Table 1.

Table 1. Analysis of CDC20, TOP2A expression in different esophageal squamous cell carcinoma specimens

| Group               | CDC20 mRNA Relative Expression Coefficient | CDC20 The gray level of protein expression | TOP2A mRNA Relative Expression Coefficient | TOP2A The gray level of protein expression |
|---------------------|-------------------------------------------|-------------------------------------------|-------------------------------------------|-------------------------------------------|
| Cancer Tissue Group | 1.246±0.233**                          | 15.245±5.145**                            | 0.655±0.105**                            | 53.779±1.863**                           |
| Paracancerous Tissue group | 0.976±0.177**                        | 10.178±4.333**                           | 0.525±0.093**                            | 42.882±1.726**                           |
| Normal Organization Group | 0.756±0.153                            | 7.356±3.174**                            | 0.410±0.084**                            | 37.081±1.750**                           |

Note: Compared with normal tissue groups, *P <0.05; paracancerous tissue compared to normal tissue, **P <0.05

3.3 Relationship between CDC20, TOP2A Expression and Esophageal Squamous Cell Carcinoma
There was no significant difference in gender, age, tumor
size, tumor location and CDC20, TOP2A expression in patients with esophageal squamous cell carcinoma, \( P > 0.05 \). There were differences \( (P > 0.05) \) and positive proportional relationship between groups in TNM stage, lymphatic metastasis and invasion factors and CDC20, TOP2A expression level, as shown in Table 2.

**Table 2.** Analysis of the relationship between CDC20, TOP2A expression and clinical characteristics of esophageal squamous cell carcinoma

| General information       | Number of cases | CDC20 positive | X² | P    | TOP2A positive | X² | P    |
|---------------------------|-----------------|----------------|----|------|----------------|----|------|
| Gender                    |                 |                |    |      |                |    |      |
| Male                      | 45              | 29             | 0.1909 | 0.6622 | 30             | 0.0172 | 0.8957 |
| Female                    | 20              | 14             | 0.8739 | 0.3498 | 13             | 2.3029 | 0.1291 |
| Age (years)               |                 |                |    |      |                |    |      |
| Less than 60              | 40              | 26             | 0.0469 | 0.8285 | 23             | 0.1794 | 0.6718 |
| >60                       | 25              | 19             | 1.5043 | 0.2200 | 19             | 0.0076 | 0.9305 |
| Tumor size (cm)           |                 |                |    |      |                |    |      |
| Less than 5               | 39              | 26             | 2.8715 | 0.0004 | 26             | 1.2544 | 0.0006 |
| greater than 5            | 26              | 18             | 6.3819 | 0.0115 | 16             | 15.4601 | 0.0000 |
| Tumor location            |                 |                |    |      |                |    |      |
| Upper paragraph           | 35              | 29             | 4.5772 | 0.0194 | 22             | 7.0172 | 0.0080 |
| Medium, next paragraph    | 30              | 21             | 5.5093 | 0.0152 | 22             | 10.1703 | 0.0012 |
| TNM analysis              |                 |                |    |      |                |    |      |
| I                         | 8               | 3              | 6.3819 | 0.0115 | 3              | 15.4601 | 0.0000 |
| II                        | 29              | 19             | 36.9789 | 0.0000 | 17             | 36.9789 | 0.0000 |
| III                       | 16              | 13             | 36.9789 | 0.0000 | 13             | 36.9789 | 0.0000 |
| IV                        | 12              | 11             | 36.9789 | 0.0000 | 11             | 36.9789 | 0.0000 |
| Tumor differentiation     |                 |                |    |      |                |    |      |
| Medium High Differentiation| 36              | 18             | 10.1703 | 0.0012 | 17             | 10.1703 | 0.0012 |
| Low differentiation       |                 |                |    |      |                |    |      |
| lymphatic metastasis      |                 |                |    |      |                |    |      |
| Yes                       | 27              | 25             | 5.4572 | 0.0194 | 25             | 4.5772 | 0.0323 |
| No                        | 38              | 26             | 5.4572 | 0.0194 | 27             | 4.5772 | 0.0323 |
| Venous infiltration       |                 |                |    |      |                |    |      |
| Yes                       | 26              | 24             | 5.7778 | 0.0162 | 25             | 8.0264 | 0.0046 |
| No                        | 39              | 26             | 5.7778 | 0.0162 | 26             | 8.0264 | 0.0046 |
| Survival                  |                 |                |    |      |                |    |      |
| Less than 3 years         | 31              | 28             | 5.0679 | 0.0243 | 29             | 7.0172 | 0.0080 |
| More than 3 years         | 34              | 26             | 5.0679 | 0.0243 | 26             | 7.0172 | 0.0080 |

**4. Discussion**

The pathogenesis of esophageal squamous cell carcinoma is caused by many factors, many processes and many gene changes. However, abnormal cell cycle regulation and imbalance of cell growth are also the main mechanisms of esophageal squamous cell carcinoma tumor formation. Based on this, most researchers believe that according to the mechanism of esophageal squamous cell carcinoma tumor proliferation and invasion analysis, the sensitivity and specific diagnostic criteria to meet the treatment of esophageal squamous cell carcinoma are analyzed to evaluate the metastasis, recurrence and prognosis of esophageal squamous cell carcinoma.

CDC20, as a cyclin, is also the core protein to ensure the routine implementation of cell mitosis. It regulates the S and G2/M stages of cell mitosis, promotes the DNA of cell chromosomes to complete mitosis replication, and is also a whole regulator. It can promote the APC/C of late complex / periodic body. Clinical studies have shown that CDC20 abnormal expression can cause mitosis errors and induce mutations in tumor suppressor genes. At present, clinical studies have found that there is some correlation between the activation of esophageal squamous cell carcinoma and proto-oncogene, the inactivation of tumor suppressor gene, and the dysfunction of regulatory proteins that promote DNA repair and maintain gene stability.

The results showed that the expression level of esophageal squamous cell carcinoma was high, and the CDC20, TOP2A expression level was higher, compared with the adjacent tissue and normal tissue, and the difference between CDC20, TOP2A groups was significant. At the same time, there was a proportional relationship with TNM analysis, tumor differentiation, lymphatic metastasis and tumor invasion. Hence, there is a certain correlation between CDC20, TOP2A and esophageal squamous cell carcinoma. Moreover, the results also demonstrated that the main factors affecting the prognosis survival of patients with esophageal squamous cell carcinoma were TBN stage iii-phase iv, highly differentiated tumors, lymphatic metastasis, and venous infiltration, especially when the TNM stage was more severe, the index expression was further increased.

However, the metastasis, recurrence and prognosis of esophageal squamous cell carcinoma are related to the level of CDC20, TOP2A expression. These two indexes can effectively evaluate the pathological situation of esophageal cancer and provide an important reference for the prognosis of esophageal squamous cell carcinoma patients.
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