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Progress in Epigenetic Research of Transparent Cell Kidney Cell Cancer

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Abstract: With the rapid development of society and economy in recent years, the development of the medical industry is increasingly rapid. Therefore, medical researchers have increased the research and analysis of various malignant diseases, including transparent cell kidney cell cancer, which ranks third and the patients account for 3%. About 90,000 patients die from disease every year, mainly distributed from 50 to 70 years old. As the number of patients with this disease has risen in recent years, scholars from various countries have increased the research and analysis of the disease, among which it attracts the most attention It is the epigenetics. Then the epigenetic study of transparent cell renal cell carcinoma is reviewed.

Keywords: Transparent Cell Renal Cell Carcinoma; Epigenetics; Research Progress

Introduction

Through summary analysis of the clear cell renal cell carcinoma of the disease can be learned that this disease at the beginning of the illness does not appear obvious symptoms, and twenty percent to thirty percent of the patients to find the condition at has developed to the period, so the effect of disease prognosis is poor, and even some patients after the disease or disorder show has missed the best treatment time. As the mechanism and mechanism of this disease are still unclear, some scholars have increased the research on the etiology and pathogenesis of this disease. Through the final summary, it is understood that most patients will have epigenetic changes. Therefore, in the process of in-depth exploration and research, the diagnosis, treatment and prognosis of clear cell renal cell carcinoma were explored.

Through the summary analysis of clear cell kidney cell cancer disease can be learned that the disease does not appear in the early stage of the disease, and 20 to 30 percent of the patients have developed to the disease, so the prognosis is very poor, even some patients in the disease or performance has missed the optimal treatment time. Because the mechanism and mechanism of this disease are not clear, some scholars have increased the research of the cause and pathogenesis of this disease, and through the final summary, we have learned that most patients will have epigenetic changes. So, exploring deeply During the study, the diagnosis, treatment and prognosis of transparent cell renal cell cancer.

1. Abnormal DNA methylation in clear cell renal cell carcinoma

Disease in clear cell renal cell carcinoma after an analysis of epigenetics can realize, DNA methylation belong to disease of the main epigenetic modifications, and in the operation process of the human body needs to be done to synthetic DNMTs, phosphorylation will appear in the process of transition performance, the performance belongs to the function of DNA methylation from the start control model. In the process of in-depth summary and exploration, it is found that the probability of cancer in various organs of the human body is related to the probability of abnormal DNA methylation. The fundamental reason is that hypermethylation inactivates tumor gene promoters, which silenced gene expression during the body's operation. In a study conducted by the researchers, abnormal DNA methylation is one of the mechanisms involved in the

pathogenesis of clear cell renal cell carcinoma. In the data, 15 percent of patients with clear cell renal cell carcinoma were diagnosed with inactivation of tumor suppressor gene promoter methylation. Hypermethylation corresponds to hypomethylation. DNA hypomethylation refers to DNA, such as satellite DNA, which leads to reduced methylation through repeated sequences, resulting in reduced chromosome stability and rearrangement, or transcriptional activation and increased oncogene expression. So, the CpG island locus was used to regulate genes in this way. At the same time, it has also been learned in recent years through high-resolution determination that the regulation of body methylation is more important than promoter methylation [1].

2. Abnormal DNA methylation of tumor suppressor genes in clear cell renal cell carcinoma

It can be learned from relevant studies that abnormal DNA methylation plays a very important regulatory role in clear cell renal cell carcinoma, and the down-regulation and silenced expression of tumor suppressor genes such as RASSFIA, VHL and P16 can lead to abnormal cyclin accumulation, which can lead to renal cancer after long-term accumulation. Therefore, tumor suppressor genes have a strong regulatory effect in human operation, and their changes are very common in clear cell renal cell carcinoma, which proves that the methylation of the seed region of tumor suppressor genes directly affects the promoter activity.

2.1 Tumor suppressor gene RASSFIA

In the study of RASSFIA, it was learned that the inactivation of RASSFIA after the emergence of tumor would directly affect the methylation of promoter region and chromosome deletion, and the level of RASSFIA methylation would also have a certain connection with the future of clear cell renal cell carcinoma. In conclusion, we analyzed 179 patients who had undergone radical partial nephrectomy. CpG island methylation levels in RASSFIA were assessed using restriction analysis and nitrite sequencing. The final results showed that CpG island methylation levels in RASSFIA were higher than those in grade I and GRADE II tumors. The methylation level of RASSFIA promoter in grade III tumors was significantly increased, and methylation was also more frequent. The methylation level of patients in different stages also has certain differences. For example, the methylation level of patients in stage iii and stage iv is higher than that of patients in stage ii . At the same time, the higher the methylation level of patients, the worse the subsequent effect, so the methylation level of patients is directly related to the adverse prognosis of patients. Therefore, RASSFIA gene promoter methylation level was analyzed as a prognostic marker for clear cell renal cell carcinoma.

2.2 Tumor suppressor gene VHL

It can be learned from relevant studies that most of the VHL gene inactivation will occur in the early stage of human tumors. The inactivation of the VHL gene in the short arm 3P25 of chromosome 3 is usually associated with the occurrence of clear cell renal cell carcinoma. In summary also learned VHL syndrome caused by clear cell renal cell carcinoma usually appear VHL gene mutation, through data can understand that there are eighty-three point percent to ninety percent of sporadic clear cell renal cell carcinoma patients can appear VHL gene mutation, eight point three percent to fifteen percent will be mutated gene promoter methylation, In 90 percent of cases, the short arm of chromosome 3 is missing, resulting in a biallele inactivation of the VHL gene. Some studies have shown that the dysfunction of VHL gene is related to the accumulation of hypoxia-inducible factor and the angiogenesis and pathogenesis of clear cell renal cell carcinoma. Therefore, after summary and analysis, it was determined that VHL gene has a certain influence in clear cell renal cell carcinoma [2].

3. Histone modification and clear cell renal cell carcinoma

It is known in medical research that because DNA methylation is related to histone modification, histone deacetylase may play a role in maintaining tumor suppressor gene silencing together with DNMTs in the action process. In the process of in-depth summary and exploration, it can be learned that acetylation and deacetylation should generally be in a state of

balance. Once there is an imbalance between the two sides, there is a high probability of tumors in the human body. Enzymes that can affect the regulation of human cells include HDACs, histone methyltransferase, histone acetyltransferase, etc., which can directly affect cell proliferation and angiogenesis. In experiments with these enzymes, it is known that the reversal of epigenetic modification of these enzymes can activate the potential of tumor suppressor genes or oncogene suppressors. Therefore, histone protease modification is important in the changes of clear cell renal cell carcinoma. Epithelial-mesenchymal transformation is also a process of tumor activity and in the medical community is a major factor in the progression of clear cell renal cell carcinoma and other cancers. HDACs inhibitors inhibit epithelial-mesenchymal transition in proximal tubule epithelial cells produced under the action of transformation factor β. In this study, we demonstrated that HDACs inhibitors can reverse epithelial-mesenchymal transition in the development of clear cell renal cell carcinoma.

4. Micrornas and clear cell renal cell carcinoma

In the summary of epigenetics of clear cell renal cell carcinoma, it was learned that the abnormal expression of microrNAS was related to the onset and metastasis of clear cell renal cell carcinoma. Micrornas (224, 200 family, 21, 221, 199a, 214) were associated with the onset of clear cell renal cell carcinoma. Among them, microrNA-21 can help clear cell renal cell carcinoma invasion and metastasis. Because micrornas can pass through the quadrilateral of damaged or apoptotic cells and enter the blood, and are abundant in plasma, serum, and other fluids, peripheral microrNas can be used for noninvasive detection. In a further summary of the study, it was also known that patients with renal cell tumor had increased mir-378 and decreased Mir-451 in their serum, so the two microrNAS were identified together during the study, which ultimately showed 81% sensitivity and 83% specificity. Some researchers also summarized and analyzed the relationship between microrNAS and the prognosis of clear cell renal cell carcinoma in the exploration process, and finally learned that the change of microrNA-126 was related to the survival rate of patients. In the study, we also learned that the survival cycle of patients with high levels of microrNA-221 was significantly lower than that of patients with standard levels of microrNA-221, which indicates that microrNAS are independent prognostic factors in clear cell renal cell carcinoma [3].

Conclusion

In summary, the pathogenesis of clear cell renal cell carcinoma is very complex and there are many etiologies, so epigenetic changes are needed to control the development of clear cell renal cell carcinoma. So in the current medical enterprise development under the background of modernization, the researchers will need to rely on HDACs and reverse promoter methylation clear cell renal cell carcinoma tumor suppressor genes, further summarizes the research, and continuously explore new diagnosis and prognosis in the process of study way, to ensure that can further improve the efficiency of disease diagnosis and treatment, Ensure the rationality of diagnosis and treatment of clear cell renal cell carcinoma, and promote the development of China's medical industry.

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