Research Article

Effect of t (11;19 (q23; p13.1) Gene on SGC 7901 Gastric Cancer Cell Line

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Abstract

Objective: To investigate the effect of t (11; 19) (q23; p13.1) gene on proliferation and apoptosis 0f SGC 7901 gastric cancer cell line.

Methods: Gastric cancer cell line SGC 7901 cells were selected to transfect t (11; 19) (q23; p13.1) gene. MRNA levels of t (11; 19) (q23; p13.1) in each group were regulated after 24, 48 and 72h by RT-PCR. Cell proliferation was determined MTT assay. The apoptosis status of the SGC 7901 cells was detected TUNEL method.

Results: The MTT assay showed that t (11; 19) (q23; p13.1) decreased the proliferation of SGC 7901 cells. TUNEL method detected t (11; 19) (q23; p13.1) could improve apoptosis of SGC 7901 cells.

Conclusion: T (11; 19) (q23; p13.1) gene can inhibit gastric cancer cell proliferation and improve apoptosis of gastric cancer cell.

Introduction

Gastric Cancer (GC) is the fourth most common malignancy and the second most common cause of cancer-related mortality [1]. Gastric cancer is a multi-factorial disease and causes continuous cell damage due to a lifetime of exposure to different carcinogens. Gene therapy as a novel treatment method has achieved improvements over past decades, particularly for treating malignant cancer [2-6]. However, there are still some unsolved problems, limiting the further development of gene therapy for malignant cancer. Recently, several preliminary studies of targeted genes in gastric cancer have been performed [7-11].

The translocation t (11;19) (q23; p13.1) is a recurring abnormality in gastric cancer. In the study, to investigate the effect of t (11; 19) (q23; p13.1) gene silence on proliferation and apoptosis 0f SGC 7901 gastric cancer cell line.

Material and Methods

Designing and Constructing Expression Plasmid

To find the gene sequence of chromosome t (11; 19) (q23; p13.1) from NCBI Gen Bank, using siRNA design software to find the target sequence with characteristics in the downstream of the starting codon, and manually designing and synthesizing the siRNA oligonucleotide sequence, End plus corresponding enzyme cut point and protection base, PCR amplification, reaction conditions: 94℃ pre-degeneration 5 min,94℃ degeneration 30s, 65℃ annealing 30s, 70℃ extended 110s, 25 cycles, 70℃ extended 7 min after the end amplification reaction, the product was recycled and purified by glue. Negative control siRNA is a universal unrighteous sequence, and all siRNA chains are purified by high performance liquid phase to remove unpaired single chains.

Cell Culture and Cell Gene Transfection

SGC-7901 cells were cultured continuously under the condition of RBMI1640 culture solution containing 10% fetal bovine serum, 37cc, 5%CO and saturated humidity environment. 1days before transfection, select logarithmic growth SGC-7901 cells. Inoculation of appropriate density cell suspension in cultured utensils (24-hole culture Plate: 2.5x10 cell/fl; 96 Hole culture Plate: 0.4xl0 cell/fl; 6 Hole culture Plate: 1.2x10 cell/fl; 6cm Petri dish: 2.5x10; 10cm petri dish: 7x10), culture overnight up to 40%~50% Fusion, the next day for instantaneous transfection. The basic operation refers to the cationic liposome Meta fectenetm (Biontex Company) Manual. Experimental group:

① negative control group: only inoculated cells, not transfected plasmid;

② Air Carrier control group: transfection Pegfp-c1;

③ Experimental Group: Transfection pegfp-c1-t (one;) (q23; p13.1). Continue to be cultured to 24, 48, 72h, respectively.

RT PCR Detects mRNA Expression

After transfection, collected each group of cells from the 6-hole culture plate at 24, 48 and 72h, extracted the total RNA, ultraviolet spectrophotometry and agarose gel electrophoresis to detect its purity and concentration in accordance with the Trizol reagent (Invitrogen Company) manual, according to reverse transcription System Kit Fpromega Company operated synthetic cDNA for PCR amplification. Reaction conditions: 94℃ Pre-degeneration 5 Min,94℃ degeneration S, 65℃ annealing 3O S, 70℃extended S, 25 cycles, 70℃ extended 7 rain after the end amplification reaction, amplification products by 1.5% agarose gel electrophoresis detection.

MTT Assay for Cell Proliferation

After transfection, MTT assay was applied to evaluate the proliferation of both introduced MGC-803, AGS, and SGC-7901 cells and normal GES-1 cells. A total of 2×10^4 cells per well were plated in 96-well plates that were cultured for 24, 48, and 72 h. Before removal from incubation, the cells were incubated with 200 μl of 0.5 mg/ml MTT (Sigma, Guangzhou, China) for an additional 4 h. The medium was then replaced with 200 μl of dimethyl sulfoxide (Sigma-Aldrich, Guangzhou, China) to resolve the crystals. The absorbance at 490 nm was then measured for each well.

TUNEL Assay

Apoptosis cells were detected in a MEBSTAIN Apoptosis Kit Direct (MBL International, Woburn, MA, USA) for Tunel assay. After transfection for 24 to 72h, POD-horseradish peroxidase was added. Then cells were incubated with TdT buffer for 1h. The apoptosis cells were counted under an Olympus fluorescent microscope (Olympus Corp). The Apoptotic Index (AI) was (number of apoptotic cells/total number) × 100%.

Statistical Analysis

The paired two-tailed Student t test was used to analyze the results by Clinical Physician Statistics Assistant 5.0 (Book Sword Software Online, hangzhou, china) and significance was assumed at $P < 0.05$.

Results

Expression of Transfection Cell mRNA

The cells of transfection t (11; 19) (q23; p13.1) siRNA group and other groups of cells were collected at 24,48 and 72h respectively. The total RNA were extracted. RT-PCR test results showed the relative expression of t (11; 19) (q23; p13.1) mRNA was lower than that of the control group, respectively, the difference was statistically significant (P<0.05); In the transfection siRNA group, the relative expression of mRNA at different points of time was also statistically significant, and the expression of mRNA decreased with the prolongation of transfection time (P<0.05). There was no statistically significant difference in the expression of mRNA between control groups at each point in time (P>0.05). This showed that the role of siRNA is specific and time-dependent (Table 1).

Group	24h	48h	72h
Blank control	0.883±0.055	0.866±0.043	0.872±0.057
Blank liposomes	0.875±0.035	0.869±0.036	0.851±0.037
Negative control	0.869±0.025	0.871±0.052	0.863±0.029
Transfection	0.623±0.014[1]	0.553±0.031[1,2]	0.269±0.024[1,2,3]
Comparing the transfected siRNA group with other control groups, 1) P<0.05; compared with the same group of H, 2) P<0.05; compared with the same group, 3) P<O.05			

Table 1: Expression of t (11;19) (q23; p13.1) mRNA in each group of cells.

Expression of t (11; 19) (q23; p13.1) gene inhibits SGC -7,901 Cell Proliferation

T (11; 19) (q23; p13.1) after transfection into SGC-7901 cells for 24, 48and 72h, the proliferative ability of cells decreased significantly compared with the control group (P<0.05), and the growth inhibition rate increased with the prolongation of transfection time. There was no statistically significant difference in cell growth rate between points in the control group (P>0.05), which suggested that siRNA might have the ability to inhibit cell proliferation (Table 2).

Group rate	24h		48h		72h	
	OD	Inhibitive % Rate	OD	Inhibitive % Rate	OD	Inhibitive % Rate
Blank control	0.516±0.021	0. .0	0.523±0.037	0. .0	0.528±0.023	0. 0
Blank liposomes	0.502±0.016	2.4	0.517±0.018	3.2	0.519±0.014	2.6
Negative control	0.508±0.018	0.6	0.509±0.028	0.8	0.515±0.018	0.7
Transfection	$0.356±0.016^{1)}$	5.8	$0.286±0.023^{1)2)}$	27.3	$0.201±0.012^{1) \ 2) \ 3)}$	47.9
Comparing the transfected siRNA group with other control groups, 1) $P<0.05$; compared with the same group of H, 2) $P<0.05$; compared with the same group, 3) $P<O.05$.						

Table 2 Inhibitory effect of siRNA on cell proliferation.

Detection of Apoptosis by Tunel Method

Positive staining was in the nucleus (Figure 1). After transfection of 24,48 and 72 the number of apoptosis of SGC-7901 cells increased significantly with time. The apoptosis index of 24h group was 4.95±0.29%. The apoptosis index of 48h group was 16.97±0.34%. The apoptosis index of 72h Group was 27.56±0.39%, and the difference was significant (P<0.05) after examination.
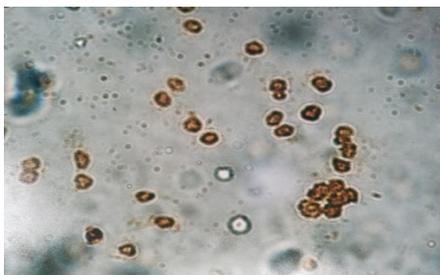

Figure 1: Apoptotic cells as shown by the TUNEL assay. Positive staining located in the nucleus. Magnification × 200.

Discussion

Gastric Cancer (GC) is the fourth most common malignancy and the second most common cause of cancer-related mortality. Gastric cancer is a multi-factorial disease and causes continuous cell damage due to a lifetime of exposure to different carcinogens. Gene therapy as a novel treatment method has achieved improvements over past decades, particularly for treating malignant cancer.

However, there are still some unsolved problems, limiting the further development of gene therapy for malignant cancer. Recently, several preliminary studies of targeted genes in gastric cancer have been performed. Some studies that the t (11;19) (q23; p13.1) translocation results in many cancers [12-13]. The translocation t (11;19) (q23; p13.1) is a recurring abnormality in gastric cancer. In the study, to investigate the effect of t (11; 19) (q23; p13.1) gene silence on proliferation and apoptosis 0f SGC 7901 gastric cancer cell line.

This study showed the relative expression of t (11; 19) (q23; p13.1) mRNA transfection t (11; 19) (q23; p13.1) siRNA group was lower than that of the control group, respectively, In the transfection siRNA group, the relative expression of mRNA at different points of time was also statistically significant, and the expression of mRNA decreased with the prolongation of transfection time. This showed that the role of siRNA is specific and time-dependent.

This study showed after transfection into SGC-7901 cells for 24, 48and 72h, the proliferative ability of cells decreased significantly compared with the control group, and the growth inhibition rate increased with the prolongation of transfection time. I t suggested that siRNA might have the ability to inhibit cell proliferation. After transfection into SGC-7901 cells for 24, 48and 72h, the AIs decreased with the prolongation of treatment time.

Conclusion

We found that t (11;19) (q23; p13.1) gene can inhibit gastric cancer cell proliferation and improve apoptosis of gastric cancer cell.

Acknowledgments

References

1. Zhu YL, Yang L, Sui ZQ, Liu L, Du JF (2016) Clinicopathological features and prognosis of Borrmann type IV gastric cancer. J BUON 21: 1471-1475.

2. Buechler SA, Gökmen-Polar Y, Badve SS (2018) EarlyR signature predicts response to neoadjuvant chemotherapy in breast cancer. Breast 43: 74-80.

3. Abedi-Gaballu F, Dehghan G, Ghaffari M, Yekta R, Abbaspour-Ravasjani S, et al. (2018) PAMAM dendrimers as efficient drug and gene delivery nanosystems for cancer therapy. Appl Mater Today 12: 177-190.

4. Okazaki S, Shintani S, Hirata Y, Suina K, Semba T (2018) Synthetic lethality of the ALDH3A1 inhibitor dyclonine and xCT inhibitors in glutathione deficiency-resistant cancer cells. Oncotarget 9: 33832-33843.

5.   Cao H, Huang S, Liu A, Chen Z (2018) Up-regulated expression of miR-155 in human colonic cancer. J Cancer Res Ther 14: 604-607.

6.   Kurtanich T, Roos N, Wang G, Yang J, Wang A, et al. (2018) Pancreatic Cancer Gene Therapy Delivered by Nanoparticles. SLAS Technol 5: 2472630318811108.

7.   Wu X, Zheng Y, Han B, Dong X (2018) Long noncoding RNA BLACAT1 modulates ABCB1 to promote oxaliplatin resistance of gastric cancer via sponging miR-361. Biomed Pharmacother 99: 832-838.

8.   Kang M, Zhang Y, Jin X, Chen G, Huang Y, et al. (2018) Concurrent Treatment with Anti-DLL4 Enhances Antitumor and Proapoptotic Efficacy of a γ-Secretase Inhibitor in Gastric Cancer. Transl Oncol 11: 599-608.

9.   Zhao J, Geng L, Duan G, Xu W, Cheng Y, et al. (2018) REC8 inhibits EMT by downregulating EGR1 in gastric cancer cells. Oncol Rep Apr 39: 1583-1590.

10. Weren RDA, van der Post RS, Vogelaar IP, van Krieken JH, Spruijt L, et al. (2018) Role of germline aberrations affecting CTNNA1, MAP3K6 and MYD88 in gastric cancer susceptibility. J Med Genet Oct 55: 669-674.

11. Wang W, Li Z, Wang J, Du M, Li B, et al. (2018) A functional polymorphism in TFF1 promoter is associated with the risk and prognosis of gastric cancer. Int J Cancer May 142: 1805-1816.

12. By Kinuko Mitani, Yoshinobu Kanda, Seishi Ogawa, Tornoyuki Tanaka, Joji Inazawa, et al. (1995) Cloning of Several Species of MLL/MEN Chimeric cDNAs in Myeloid Leukemia With t(l1; 19)(q23; p13.1) Translocation Blood 85: 2017-2024.

13. Thirman MJ, Levitan DA, Kobayashi H, Simon MC, Rowley JD. (1994) Cloning of ELL, a gene that fuses to MLL in a t (11;19) (q23; p13.1) in acute myeloid leukemia. Proc Natl Acad Sci U S A 91: 12110-12114.