

Expression of *RASSF1A* in epithelial ovarian cancers

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Abstract. – **OBJECTIVE:** Ovarian cancer is the third most common cancer in female reproductive system. But ovarian cancer is hard to detect at early phase. It is very urgent to develop effective early diagnosis method for ovarian cancer. *RASSF1A* (Ras association domain family 1 isoform A) is a tumor suppressor, which modulates multiple apoptotic and cell cycle checkpoint pathways. We aimed to find out the relationship between *RASSF1A* and ovarian cancer.

METHODS: We compared the expressions of *RASSF1A* gene in different ovarian cancer cell lines, and also in epithelial ovarian cancer tissues and normal ovarian tissues through RT-PCR (reverse transcription polymerase chain reaction) technique.

RESULTS: *RASSF1A* was expressed in SKOV-3 and HO8910PM cells, while *RASSF1A* mRNA was absent in SKOV-3 and OVCAR-3 cells. *RASSF1A* was expressed in 10 normal ovarian tissue samples (10/10, 100%), while *RASSF1A* was only expressed in 2 ovarian cancer tissue samples (2/47, 4.3%). The difference in the frequency was significant in tissue samples (100% vs 4.3%, $p < 0.05$).

CONCLUSIONS: *RASSF1A* could be a potential molecular marker for diagnosing ovarian cancer at early phase.

Key Words:

Ovarian cancer, *RASSF1A*, RT-PCR.

Introduction

Major ovarian tumor is one of the most malignant tumors in female reproductive system. It is a hidden killer with rapid development as clinical and biological behavior features, 70% of ovarian cancer cases were diagnosed as terminal types¹. With a survival rate around 20% within five years, ovarian cancer is one of female malignant tumors with the highest lethality rate. There is no effective diagnostic method at early phase for ovarian cancer so far². Although the developing

surgical techniques could remove most cancer cells and the clinical application of platinum, paclitaxel and other secondary chemical drugs bring the hopes of return to patients^{3,4}, a considerable part of the patients are still undergoing further deterioration or death after surgical and chemical treatments.

Recently, with the development of molecular biological techniques and methodologies, gene therapy is emerging as an effective new therapeutic method in genetic disease caused by single gene mutation and gaining worldwide attentions from experts of different fields⁵. In order to provide much more precise and effective diagnostic, prognostic, and precaution methods, medical scientists are trying to reveal the relationship between expression level of a certain gene and clinical biological behaviors of ovarian cancer.

As a new member of *RAS* (rat sarcoma) gene family, tumor repressor gene *RASSF1A* is regarded to be involved in the regulation of cell proliferation and apoptosis⁶. Some reports showed that *RASSF1A* functions as a micro-tubule binding protein and regulates mitosis proceeding⁶⁻¹⁰. *RASSF1A* is localized on the cytoplasmic micro-tubule of interphase cells, especially on the spindle body and centrosome during mitosis. The bind of *RASSF1A* to microtubule is supposed to regulate mitosis by stabilizing the microtubule structure. Overexpression of *RASSF1A* could retain the cell at interphase. The mutation of *RASSF1A* could destabilize the microtubule structure, influence the spindle configuration, and impair the attachment of chromosome to spindle, which could easily lead to gene instability and cell transformation under influential factors. This could be further deteriorated into abnormal cell proliferation and tumor formation by the loss of cell cycle brake and reduced apoptosis by *RASSF1A*⁶.

Some scientists also found that *RASSF1A* could regulate cell cycle directly, repress cell

growth *in vitro* and *in vivo*, and also induce apoptosis^{11,12}. Shivakumai et al¹³ found that cells transformed with *RASSF1A* could repress the accumulation of cyclinD1 and further prevent cell proliferation by hindering the cells at G1/S. STE20 (sterile twenty) is a serine/threonine kinase, which was firstly cloned from yeast. STE20 family members are the upstream kinases of MAPK (mitogen-activated protein kinase) cascade. Mst-1 (mammalian sterile 20-like kinase 1) is the homolog of STE20 in mammalian cells. Acting as the apoptosis inducer, Mst-1 induces the cell apoptosis through many pathways^{14,15}. Many evidences have demonstrated that Mst-1 and *RASSF1A* can form a complex called *RASSF1A/Mst-1*, which could maintain Mst-1 activity, help Mst-1 to be correctly localized inside cell, and further synergistically induce cell apoptosis^{14,16}. After being successively cloned through yeast two hybrid screening in 2000¹⁷, many reports showed that the *RASSF1* mRNA is absent or reduced in many types of cancer cells or tumor tissues, which is also accompanied by the abnormal hyper-methylation at the *RASSF1* promoter region¹⁷⁻¹⁹. All the results indicated that *RASSF1A* plays an important role in the tumorigenesis of many tumor types.

In this study, we compared the expression of *RASSF1A* gene between ovarian cancer tissues and normal ovarian tissues, and also in different ovarian cancer cell lines through RT-PCR (reverse transcription polymerase chain reaction) technique. In addition, we discussed the significant role of *RASSF1A* gene in tumor progression of ovarian cancer.

Materials and Methods

Ovarian Tumor Tissues and Cell Line Collection

Forty-seven malignant ovarian epithelial tumor patients (forty-three serous cystadenocarcinoma cases and four borderline cases), who received one time treatment of surgical operation at the hospital from September 2005 to January 2006, were selected for sample collection. Among these 47 cases, there were 5 cases at clinical stage I, 4 cases at stage II, 37 cases at stage III, and 1 case at stage IV. Ovarian samples from 47 patients who underwent ovarian anatomy or laparoscopic cystectomy were collected as control group. All the ovarian samples were collected under sterile condition and pathological vali-

dated. After being excised from human body, the ovarian samples were quickly frozen in liquid nitrogen and transferred into -80°C freezer. The cell lines of ovarian epithelial tumor (HO8910, HO8910PM, SKOV-3, and OVCAR3) were purchased from Cell Bank of Chinese Academy of Sciences. The ovarian samples were collected for this study upon the agreements of all the included patients.

Total RNA Extraction

After being sheared into small pieces, the ovarian samples were placed in 1.5 ml EP (Eppendorf) tube, 200 mg ovarian tissues were fractionated under 30 min homogenization and centrifuged at 12000 g, 4°C for 10 min. The supernatant was transferred into the 1.5 ml EP tube containing 200 μl chloroform and mixed by vortex for 15 s. The mixture was placed under room temperature for 3 min. After centrifugation under 12000 g, 4°C for 15 min, colorless supernatant (about 500 μl) was transferred into a new EP tube containing 500 μl isopropanol and placed under room temperature for 10 min for RNA precipitation. After centrifugation at 12000 g, 4°C for 10 min, white RNA pellet was recovered and washed with 1 ml 70% ethanol. After centrifugation at 12000 g, 4°C for 5 min, supernatant was discarded and pellet was dried under room temperature for 10-20 min. The dry RNA sample was dissolved in 20 μl diethylpytocarbonate (DEPC) water. After diluting RNA samples 100 times, RNA concentration and purity were determined by measuring OD260 value and OD260/OD280 ratio. The RNA was stored under -80°C . For RNA concentration determination:

RNA concentration ($\mu\text{g}/\mu\text{l}$) = OD260 \times 40 \times Dilution ratio/1000.

Reverse Transcription of cDNA

Total 2 μg RNA was used as template for cDNA reverse transcription. RT-PCR Kit (RNA PCR Kit AMV ver3.00) was used in the process (Takara, Tokyo, Japan). The reaction was performed in a 10 μl reaction system containing 2 μl MgCl_2 , 1 μl 10 \times RT buffer (reverse transcriptase buffer), 3.75 μl RNase free H_2O , 1 μl dNTP mixture (10 mM), 0.25 μl RNase inhibitor, 0.5 μl AMV (avian myeloblastosis virus) reverse transcriptase, 0.5 μl random 9-mers, and 1 μl RNA. The reaction mixture underwent the program of 10 min at 30°C , 30 min at 42°C , 5 min at 99°C , and 5 min at 5°C . The cDNA products were stored in -20°C freezer.

PCR Reaction

The PCR reaction was conducted in a 20 µl reaction system containing 4 µl cDNA, 4 µl 5×PCR buffer, 7.9 µl distilled water, 0.1 µl Ex Taq HS, 2 µl forward primer and reverse primer 2 µl. The reaction mixture underwent the program of 2 min 94°C, 30 sec at 94°C, 30 sec at 57°C, and 40 sec at 72°C for 30 cycles. The PCR products were stored at -20°C. Specific primers of *RASSF1A* was: forward, 5'-CTTCATCTGGGGCGTCGTG-3'; reverse, 5'-GCATCCTTGGGCAGGTAAAA-3'. Target fragment length for *RASSF1A* is 420 bp. Specific primers of β-actin was: forward, 5'-TGCGTGACATTAAGGAGAAGC-3'; reverse, 5'-GAAGGTGGACAGCGAGGC-3'. Primers were synthesized at Saibasheng Biotechnology. Target fragment length for β-actin is 431 bp. Amplification was run on Biometra GmbH (Gottingen, Germany).

PCR Products Detection

Total 4 µl PCR products were mixed with 1 µl Loading Buffer and loaded onto 1.5% agarose gel. After running at 150 V, 100 mA for 30 min, the DNA bands were detected via electrophoresis and gel imaging system (Chemizmager 5500 Alpha Inno Tec Schweiz AG, Altishofen, Switzerland). The 100 bp DNA ladder markers were from GeneBio Biology Company, Dalian, China and GeneFinder™ dye was purchased from

Statistical Analysis

The statistical analysis was carried out using SPSS12.0 software (SPSS Inc, Chicago, IL, USA). When $p < 0.05$, data was considered statistically significant.

Results

The Expression of *RASSF1A* in Ovarian Cancer Cell Lines

RASSF1A was expressed in HO8910 and HO8910PM cells and absent in SKOV-3 A and OVCAR-3 cells (Figure 1).

The Expression of *RASSF1A* in Normal Ovarian and Ovarian Tumor Tissues

The expression of *RASSF1A* was detected in 10 of 10 normal ovarian tissues (100%, 10/10), while it was detected in 2 cases among 47 ovarian tumor samples (4.3%, 2/47). Figure 2 listed PCR results of some ovarian normal and cancer tissue



Figure 1. The expression of *RASSF1A* in different ovarian cancer cell lines. Lane 1 was the DNA marker; lane 2, 4, 6, 8 represent *RASSF1A* band, while lane 3, 5, 7, 9 represent β-actin band.

samples. There was significant difference ($p < 0.05$) for frequency (100% vs. 4.3%). The two *RASSF1A* positive ovarian tissues were pathologically diagnosed as serous cystadenocarcinoma. One of which was clinical stage I and the other was stage III, which indicated that the phenomenon is not connected with cancer staging.

Discussion

The anti-tumor roles of *RASSF1A* haven't been fully revealed so far. Some reports have shown that *RASSF1A* is a micro-tubule binding protein and involved in regulation of mitosis pro-

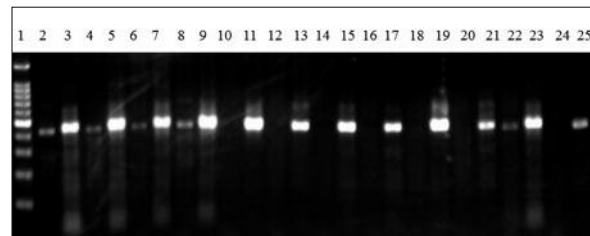


Figure 2. The expression of *RASSF1A* in normal ovarian and ovarian tumor tissues. Lane 1 was the DNA marker; The even lanes represented *RASSF1A* band, while the odd lanes represented β-actin band. Lane 2-9 were samples from normal ovarian tissues, while lane 10-25 were samples from ovarian tumor tissues.

ceeding⁶⁻¹⁰. *RASSF1A* could regulate cell cycle directly, repress cell growth *in vitro* and *in vivo*, and also induce apoptosis^{11,13,20}. Previous results showed that cells transformed with *RASSF1A* could repress the accumulation of cyclin D1 and further prevent cell proliferation by hindering the cells at G1/S¹³. Many evidences *RASSF1A*/Mst-1 complex could maintain high Mst-1 activity and assist Mst-1 to be correctly localized inside cell, and further synergistically induce cell apoptosis²¹.

Previous results from breast cancer²²⁻²⁶, lung cancer¹⁷, liver cancer²⁷⁻³⁰, gastric cancer³¹⁻³³ have discovered the absence of *RASSF1A* expression is connected with tumor development. In this study, we found that *RASSF1A* expression was absent from ovarian epithelial tumor tissues, which is inconsistent with previous report³⁴ which stated that *RASSF1A* was overexpressed in the ovarian tumor tissues. But our results are consistent with *RASSF1A* as tumor suppressor as previously reported^{35,36}. However, small number of samples may be the reason why these differences appeared. Thus, large number of ovarian cancer tissues and normal samples is needed to confirm our results in the future and further studies are needed to find out whether *RASSF1A* functions as a tumor suppressor through repressing cell cycle and apoptosis in ovarian tumor and other cancer types.

Our findings also provide important clues for developing new prognostic methods for ovarian cancer. As we all know, there is no effective diagnostic method at early phase for ovarian cancer so far because of its hidden and rapid development as clinical biological behavior features. For example, the serum Beta human chorionic gonadotropin level could be measured in women whom pregnancy is a possibility. In addition, serum alpha-fetoprotein (AFP) and lactate dehydrogenase (LDH) should be measured in young girl and adolescents with suspected ovarian tumors because the younger the age, the greater the likelihood of a malignant germ cell tumor. But these indicators are non-specific and the value of them is little in diagnosis³⁷. Our results show that *RASSF1A* was expressed in all tested normal ovarian tissues, while among the 47 ovarian tumor tissues, only two tissues had *RASSF1A* expression. And the absence of *RASSF1A* mRNA happened at each clinical stages. So *RASSF1A* could be served as a potential molecular marker for diagnosing ovarian cancer at early phase.

Conclusions

The expressions of *RASSF1A* genes are absent from ovarian cancer tissues, while there is considerable mRNA level of *RASSF1A* in normal ovarian tissues. These findings suggest that *RASSF1A*, as a molecular marker, could be instrumental in developing new effective diagnostic methods for ovarian cancer at early phase.

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Conflict of Interest

The Authors declare that they have no conflicts of interest.

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