

# Expression and significance of proapoptotic gene *Bax* in gastric carcinoma \*

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**Subject headings** stomach neoplasms/ pathology; *Bax* gene; gene expression; immunohistochemistry

## Abstract

**AIM** To study the expression of proapoptotic gene *Bax* in human gastric carcinoma and its significance.

**METHODS** Using immunohistochemistry methods, the *Bax* protein expression in 57 specimens of gastric carcinoma and its relationship with clinical status and pathomorphological parameters were observed.

**RESULTS** Thirty-three (57.9%) cases were positive for *Bax* protein staining which was mainly located in the cytoplasm of tumor cells. The rate of *Bax* protein expression was not correlated with the tumor size, lymph node metastasis, depth of invasion, clinical stages of tumors and age and sex of patients ( $P < 0.05$ ), but strongly associated with the morphological type and differentiation degree of tumors. It was significantly higher in intestinal type and well or moderately differentiated gastric carcinoma than in diffuse type and poorly differentiated gastric carcinoma ( $P < 0.05$  and  $P < 0.01$ ).

**CONCLUSION** The proapoptotic gene *Bax* is differently expressed in most of gastric carcinoma and may take part in the modulation of apoptosis in gastric carcinoma. The expression of *Bax* might be associated with the occurrence of intestinal type gastric carcinoma and the differentiation of gastric carcinoma.

## INTRODUCTION

Recent investigations have demonstrated that apoptosis plays a significant role in the pathogenesis of tumors<sup>[1,2]</sup>. Emphasis has been laid on the mechanisms that regulate apoptosis pathways. Bcl-2 associated X protein (*Bax*), which has extensive amino acid homology with Bcl-2, can form heterodimers with Bcl-2 *in vivo*. Overexpressed *Bax* can counter the death repressor activity of Bcl-2, and accelerate apoptotic cell death<sup>[3]</sup>. To determine whether proapoptotic gene *Bax* plays a role in the regulation of apoptosis in gastric carcinoma, an immunohistochemical study of *Bax* protein expression in gastric carcinoma and its relation to clinical status, pathomorphological parameters were carried out.

## MATERIALS AND METHODS

### *Histological specimens*

Fifty-seven cases of surgically resected gastric carcinomas (male 39, female 16; mean age 58.6 years) were collected from the files of the Department of Pathology of our hospital. All blocks were fixed in 10% formalin and embedded in paraffin. Serial sections were cut from each block in 4 $\mu$ m, stained with hematoxylin and eosin and confirmed pathologically.

### *Immunohistochemical methods*

Immunohistochemical staining for *Bax* protein was performed using SP technique with the following procedure: ① slides were deparaffinized in xylene for 10 minutes each and then were hydrated in decreasing concentrations of ethanol and rinsed in phosphate-buffered saline. Endogenous peroxidase was blocked by 30 mL/L H<sub>2</sub>O<sub>2</sub> in methanol for 5 minutes, and then incubated for 10 minutes at room temperature in normal goat serum (1:20). ② Slides were incubated with a 1:50 dilution of the primary rabbit antihuman *Bax* polyclonal antibody (Santa Cruz, USA) for 30 minutes at 37°C. A biotin-streptavidin detection system was employed with diaminobenzidine as the chromogen. ③ Slides were washed twice with phosphate-buffered saline and incubated with the linking reagent (biotinylated anti-immunoglobulin) for 10 minutes at 37°C. After rinsing in phosphate-buffered saline, the slides were incubated with the peroxidase-conjugated streptavidin

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\*Key project of the 9th 5-year plan for Medicine and Health of Army, No.96Z047.

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Received 1998-10-08

label for 10 minutes at 37°C, and incubated with diaminobenzidine and H<sub>2</sub>O<sub>2</sub> for 10 minutes in the dark, the sections were then counterstained with hematoxylin. With each batch of test samples, a positive control consisting of a tissue section from tonsil was evaluated. In addition, a negative control was prepared for each sample using an irrelevant antibody of the same isotype as the primary antibody.

The immunostaining of Bax protein was visually classified into negative and positive groups by observing 1000 tumor cells in the areas of the sections: no staining present in any of tumor cells or less than 10% tumor cells with staining (-); more than 10% tumor cells with positive staining. The classification was done by two senior pathologists who did not know the clinicopathological data.

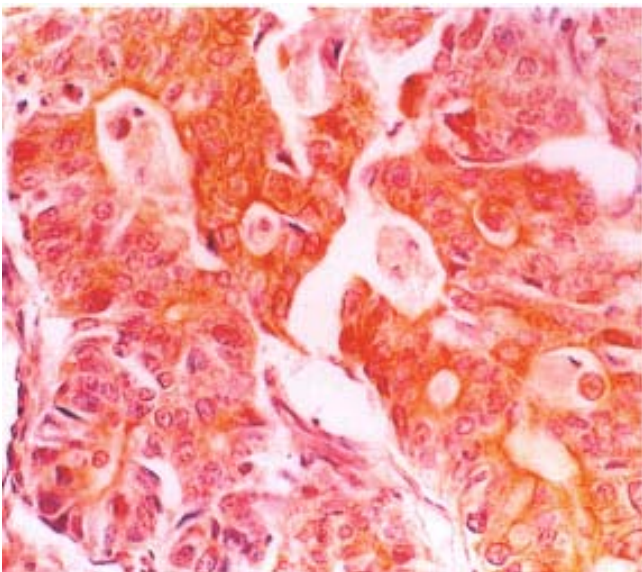
### Statistics

Analysis of data was accomplished using Chi-square test. *P* values less than 0.05 were considered to be statistically significant.

## RESULTS

### Expression of Bax protein in gastric carcinoma

Thirty-three (57.89%) of the fifty-seven gastric carcinomas showed immunoreactivity for Bax protein in gastric carcinoma cells. The Bax protein immunoreactivity appeared brown or dark brown, which was mainly located in the cytoplasm (Figure 1), and a few specimens simultaneously expressed Bax protein in the cell nuclear of tumor cells. Some of the mature lymphocytes infiltrating in the stroma of gastric carcinomas also had Bax protein expression.



**Figure 1** Bax immunoreactivity was detected in cytoplasm of gastric carcinoma cells. SP×200

### Correlation between Bax protein expression and clinicopathological parameters of gastric carcinomas

Correlation between Bax protein expression and clinical pathological data of gastric carcinoma is illustrated in Table 1. The rate of Bax protein expression was not correlated with patient age, sex, tumor size, lymph node metastasis, depth of invasion and clinical stages (*P*>0.05). The immunoreactivity of Bax was significantly associated with morphologic phenotype and grades of differentiation of gastric carcinoma. 20 (73.3%) of 30 gastric carcinomas of intestinal morphologic phenotype were immunoreactive versus 11 (40.7%) of 27 diffuse gastric carcinomas (*P*<0.05). 17 (81.0%) of 21 well and moderately differentiated gastric carcinomas were immunoreactive versus 10 (38.5%) of 26 poorly differentiated gastric carcinomas (*P*<0.01).

**Table 1** Correlation between Bax protein expression and clinicopathological parameters of gastric carcinomas

Parameters	<i>n</i>	Bax protein expression		Positive rate (%)
		-	+	
Age (year)				
≤59	39	22	17	56.41
≥60	18	11	7	61.11
Sex				
M	39	24	15	61.54
F	18	9	9	50.00
Type				
Intestinal	30	22	8	73.33 <sup>a</sup>
Diffuse	27	11	16	40.74
Grade of differentiation				
Well/moderate	21	17	4	80.95 <sup>b</sup>
Poor	26	10	16	38.46
Mucoid	10	6	4	60.00
Tumor size				
<5cm	35	21	14	60.00
≥5cm	22	12	10	54.55
Lymph-node metastasis				
Negative	23	13	10	56.52
Positive	34	20	14	58.82
Serosal invasion				
Absent	27	14	13	51.85
Present	30	19	11	56.67
Clinical stages				
I and II	34	20	14	58.82
III and IV	23	13	10	56.52

<sup>a</sup>*P* < 0.05,  $\chi^2 = 6.193$ , vs diffuse-type gastric carcinoma, <sup>b</sup>*P* < 0.01,  $\chi^2 = 8.580$ , vs poorly differentiated gastric carcinoma.

## DISCUSSION

Apoptosis is a highly regulated form of programmed cell death defined by distinct morphological and biochemical features. Apoptosis plays a major role in development, embryogenesis, regulation of the immune system, and carcinogenesis, as well as in the

maintenance of tissue homeostasis. Various protein molecules or oncogenes and suppressor genes are involved in the process of apoptosis, including *p53*, *myc*, *ras*, *Bcl-2*, *Bax* and the Fas/Fas ligand system<sup>[4]</sup>. In recent studies, *Bax* protein expression has been identified in various human malignant tissues, including the prostate, colon, breast, testis and ovary<sup>[5-8]</sup>. But, little is known about *Bax* protein expression and its relationship with the biological behavior of human gastric carcinoma.

In this study, we found that the positive rate of *Bax* protein staining in gastric carcinoma was 57.9%. The proapoptotic gene *Bax* can express to various degrees in most kinds of the gastric carcinoma and may take part in the regulation of apoptosis of gastric carcinoma. Our findings concerning the relationship between *Bax* protein expression and the pathological characteristics of gastric carcinoma showed that *Bax* expression was associated with morphologic phenotype and grades of differentiation of gastric carcinomas. The difference in the *Bax* protein expression in the intestinal and diffuse types demonstrated that aberrant *Bax* protein expression was preferentially associated with development of intestinal type gastric carcinoma, indicating once more the different biologic mechanisms involved in the development of these two histologic subtypes. The difference in the *Bax* protein expres-

sion between poorly differentiated and well/moderately-differentiated gastric carcinomas demonstrated that aberrant *Bax* protein expression was associated with differentiation or growth speed of gastric carcinomas. There was no significant relationship between *Bax* protein expression and tumor size, lymph node metastasis, serosal invasion or clinical stages. Therefore, *Bax* protein expression might play an important role in the early development and phenotypic differentiation of gastric carcinomas, but not in tumor progression.

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Edited by MA Jing-Yun