Expression and clinicopathological significance of Mel-18 and Bmi-1 mRNA in gastric carcinoma

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Abstract

Background: The Polycomb group (PcG) genes are a class of regulators responsible for maintaining homeotic gene expression throughout cell division. PcG expression is deregulated in some types of human cancer. Both Bmi-1 and Mel-18 are of the key PcG proteins. We investigate the expression and clinicopathological roles of Mel-18 and Bmi-1 mRNA in gastric cancer.

Methods: The expression of Mel-18 and Bmi-1 in a series of 71 gastric cancer tissues and paired normal mucosal tissues distant from the tumorous lesion was assayed by quantitative real time RT-PCR. The correlation between Mel-18 and Bmi-1 mRNA expression, and between Mel-18 or Bmi-1 mRNA level and clinicopathological characteristics were analyzed.

Results: Expression of Mel-18 and Bmi-1 genes was variably detected, but overexpression of Bmi-1 mRNA and decreased expression of Mel-18 mRNA were the most frequent alteration. In addition, the expression of Bmi-1 and Mel-18 mRNA inversely correlates in gastric tumors. Moreover, a significant positive correlation between Bmi-1 overexpression and tumor size, depth of invasion, or lymph node metastasis, and a significant negative correlation between Mel-18 low-expression with lymph node metastasis or the clinical stage were observed.

Conclusion: Our data suggest that Mel-18 and Bmi-1 may play crucial but opposite roles in gastric cancer. Decreased Mel-18 and increased Bmi-1 mRNA expression was associated with the carcinogenesis and progression of gastric cancer. It is possible to list Bmi-1 and Mel-18 as biomarkers for predicting the prognosis of gastric cancer.

Background

The Polycomb group (PcG) genes were first identified in Drosophila as a class of regulators responsible for maintaining homeotic gene expression throughout cell division [1]. PcG genes are conserved from Drosophila to mammals, and the expression levels of mammalian PcG genes differ between different tissues and cell types [2]. PcG genes act as epigenetic silencers during embryo morphogenesis with a central role in the nervous system, heart, and skeleton development [3-7]. In addition, PcG members have been involved in the regulation of such adult processes as the cell cycle, X-inactivation, and hematopoiesis [8-14]. PcG expression is deregulated in some types of human cancer [15]. Moreover, several PcG genes may regulate the self-renewal of specific stem cell types, suggesting a link between the maintenance of cell homeostasis and carcinogenesis [16,17].

Bmi-1 is one of the key PcG proteins. It was initially identified as an oncogene that cooperated with c-Myc in the generation of mouse pre-B-cell lymphomas. It is also considered the first functional mammalian PcG protooncogene to be recognized, and it has been implicated in axial patterning, hematopoiesis, cell cycle regulation, and senescence [18-21]. Human Bmi-1 gene is located at the short arm of chromosome 10p13 [22]. The region is involved in chromosomal translocations in leukemia and is amplified in non-Hodgkin’s lymphoma as well as in solid tumors [23]. Bmi-1 induces S-phase entry by inhibiting Rb function via repression of the INK4a/ARF locus [24-26]. Moreover, overexpression of Bmi-1 in mammary epithelial cells may activate telomerase and lead to immortalization [27]. Overexpression of Bmi-1 has been found in several human malignancies including breast cancer, colorectal cancer, nasopharyngeal carcinoma, melanoma, gastric cancer, and bladder
cancer [28-33]. Overexpression of Bmi-1 often correlates with poorer prognosis and treatment failure [30,32-34]. Bmi-1 also plays an important role in self-renewal of hematopoietic stem cells, neural stem cells and mammary stem cells [35-37].

In addition to Bmi-1, mammalian cells also express a Bmi-1-related PcG protein Mel-18. The Mel-18 gene product is structurally highly similar to Bmi-1 protein. Interestingly, we have found that Bmi-1 is negatively regulated by Mel-18 and expression of Mel-18 negatively correlates with Bmi-1 in breast tumors, and Mel-18 overexpression in breast cancer cell line MCF7 results in downregulation of Bmi-1 and reduction of transformed phenotype [38]. Negative correlation between Bmi-1 and Mel-18 expression was also recently reported in hematopoietic stem cells [39]. Lee et al. also recently reported that overexpression of Mel-18 inhibits growth of breast cancer cells [40]. These data suggested that Mel-18 acts as a potential tumor suppressor. However, the function of Mel-18 is still debatable. In few other studies, it was found that similar to Bmi-1, Mel-18 can act as an oncogene [41,42]. So, the role of Mel-18 in cancers other than breast cancers and different pathological conditions is still not clear and need to be clarified.

Gastric cancer is one of the most common malignancies throughout the world. It has been reported that Bmi-1 is overexpressed in gastric cancer and is an independent prognosis factor [32]. We have also studied the expression of Mel-18 and Bmi-1 in gastric tumors by immunohistochemistry (IHC). We found that gastric tumor tissues expressed significantly higher Bmi-1 and lower Mel-18, and the expression of Mel-18 negatively correlated with Bmi-1; there was a significant positive correlation between Bmi-1 expression with lymph node metastasis, or clinical stage, but there was no obvious correlation between Mel-18 expression and clinicopathological factors; downregulation of Bmi-1 by Mel-18 overexpression or knockdown of Bmi-1 expression was accompanied by decreased transformed phenotype and migration ability in gastric cancer cell lines in vitro study [33]. So, the results of Bmi-1 expression correlated with lymph node metastasis or clinical stage in in vivo study was accordance with the results in in vitro study, while the results of no correlation was found between Mel-18 expression and clinicopathological factors in in vivo study was not accordance with the results in in vitro study, we suspected that one of the reason may due to the reliability of IHC method which was used to detect the expression of Bmi-1 and Mel-18 in tumor tissues in most paper of literature including our previous study. This method lacks standard procedure and evaluation criterion and its’ reliability depends on the specific of antibody. The results of quantitative Real time RT-PCR (QRT-PCR) with specific primer is more reliable than that of IHC to measure the gene expression level especially for Mel-18, which lacks specific mouse monoclonal antibody till now. Here, we examine the expression of Mel-18 and Bmi-1 at mRNA level by using QRT-PCR method in a series of gastric cancer, and evaluate the correlation between Mel-18 and Bmi-1 expression levels. Furthermore, a correlation study between expression levels of both the analyzed genes and several clinical pathologic variables of the tumors was designed. In this study, we characterized the expression profile of Mel-18 and Bmi-1, and their clinical significance in gastric cancer.

Materials and methods
Clinical samples
Human gastric cancer samples were obtained from patients who underwent surgery for gastric cancer in our hospital from 2007 to 2008. All of the patients didn’t receive prior chemotherapy or radiotherapy before surgery. A total of 71 fresh gastric tissues and paired normal mucosal tissues distant from the tumorous lesion were removed and frozen in liquid nitrogen and stored at -80°C until further use. After the diagnosis of gastric cancer was confirmed, RNA was extracted with Trizol reagent (Invitrogen) according to the manufacturer’s protocol from the cancerous and paired normal tissues for further RT-PCR analysis of Mel-18 and Bmi-1 expression. By pathological types, all cases of gastric cancer are adenocarcinomas.

The clinicopathologic variables were obtained from the medical records and the disease stages of the patients were classified according to the 2002 UICC gastric cancer TNM staging system. Prior patients’ consent and approval from the Institute Research Ethics Committee were obtained for the use of clinical materials described in the present study.

Quantitative real time RT-PCR (QRT-PCR) assays
The QRT-PCR was carried out as described using Brilliant SYBR Green QRT-PCR Master Mix, 2-Step kit (Stratagene, La Jolla, CA) [43]. cDNA was synthesized using reverse transcriptase, and the PCR amplification was carried out using PTC-200 Real Time PCR system (MJ Research Inc, USA). The primers for QRT-PCR were Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) forward (F)-5’ GCTGAACTGGAAGCTCACTG-3’; GAPDH reverse (R)-5’ GTGCTCACTGTGAGCCAGGA3’; Bmi-1 R 5’ GCTTCAAGATGCCCTGGCTGTG’; Bmi-1 R 5’-TTCTCGTGTGTTCAGATGAC-3’; and Mel-18 R 5’-ATGAGATGTGGCCCAAGT-3’, Mel-18 R 5’GGAGCTTGTGCGTGACTGTA-3’. All reactions were done in a 20-μl reaction volume in biplate. PCR amplification consisted of 10 min of an initial denaturation step at 95°C, followed by 40 cycles of PCR.
at 95°C for 30 sec, 58°C for 30 sec and 72°C for 30 sec. Standard curves were generated and the relative amount of target gene mRNA was normalized to GAPDH. Specificity was verified by melt curve analysis and agarose gel electrophoresis. Data normalization and analysis an endogenous control, GAPDH present on the PCR was used for normalization. Each replicate cycle threshold (CT) was normalized to the average CT of endogenous control on a sample basis. The comparative CT method was used to calculate the relative quantification of gene expression. The following formula was used to calculate the relative amount of the transcripts in the gastric cancer samples and the control group, both of which were normalized to the endogenous control. \( \Delta \Delta CT = \Delta CT \) (gastric cancer)- \( \Delta CT \) (control) for RNA samples. \( \Delta CT \) is the log2 difference in CT between the target genes and endogenous controls by subtracting the average CT of controls from each replicate. The fold change for each gastric cancer sample relative to the control sample = \( 2^{-\Delta \Delta CT} \). When the expression showed a 2-fold increase or decrease compared with normal counterpart tissue, it was considered as an altered expression.

Statistical analysis
All statistical analyses were done by SPSS 15.0 software package. Two-tailed P value less than 0.05 was considered statistically significant. In the set of RT-PCR analysis of fresh tumors and paired normal tissues, the ratio of Bmi-1 and Mel-18 mRNA expression was not normally distributed. Hence, the distribution was established by using Log10, and geometric averages. The correlation between Bmi-1 and Mel-18 expression levels was analyzed by the Pearson coefficient test. The correlation between Bmi-1 or Mel-18 expression and clinicopathologic characteristics was analyzed by ANOVA.

Results
Expression of Bmi-1 and Mel-18 at mRNA level inversely correlates in gastric tumors
Our previous data showed an inverse correlation between Bmi-1 and Mel-18 expression in breast cancer cells and breast cancer tissues. Based on these data, we hypothesized that gastric cancer may also express high Bmi-1 and low Mel-18. To probe this hypothesis, we studied the expression of Mel-18 and Bmi-1 in gastric tumors by QRT-PCR. QRT-PCR analysis showed that 35 of 71 (49.3%) fresh gastric tumor tissues overexpressed Bmi-1, and 46 of 71 (64.79%) expressed low levels of Mel-18, compared with paired normal gastric mucosal tissues. (Table 1, Figure 1).

The correlation between Bmi-1 and Mel-18 expression at mRNA level was further analyzed by the Pearson coefficient correlation analysis, which showed a strong negative correlation (\( r = -0.252, P = 0.034 \)).

The correlation between the expression of Mel-18 or Bmi-1 with clinicopathologic characteristics
We found a significant positive correlation between Bmi-1 overexpression and tumor size, depth of invasion (T classification), or lymph node metastasis (N classification). The expression of Bmi-1 was higher in the patients with bigger tumor, deeper invasion, or positive lymph node metastasis. We also found that there was a significant negative correlation between Mel-18 expression with lymph node metastasis or the clinical stage. Its expression was lower in the patients with lymph node metastasis, or late stage disease (Table 2).

Discussion
Mammalian PcG protein complexes are generally classified into two distinct types: Polycomb repressive complexes 1 and 2 (PRC1 and PRC2). Mel-18 protein product is a constituent of mammalian PRC1 together with M33, Bmi-1 or rae28/Mph-1, and Scmh1 [13,44-47]. It has been reported that solid tumors, such as lung cancers [53], medulloblastomas [3], liver [54], penis [55], breast [28,56], colon [57], and prostate carcinomas [58], also display disturbed PcG gene expression.

Bmi-1 is one of the most important PcG proteins that is known to regulate proliferation and senescence in mammalian cells, and plays an important role in self-renewal of stem cells. It can not only immortalize human mammary epithelial cells (HMECs) [27], but also can cooperate with H-Ras to transform HMECs and transform keratinocytes [59,60]. Abnormal expression of Bmi-1 has been found in several human cancers and its overexpression is often correlated with poor prognosis in many types of malignances [28-34]. Overexpression of Bmi-1 in gastric cancer has been previously reported [32,61]. It was found that Bmi-1 overexpression was highly correlated with tumor size, clinical stage, lymph node metastasis and T classification [32]. In another study, Bmi-1 expression was closely related with the Lauren’s and Borrmann’s classification and clinical stage in gastric cancer [61]. We also found that gastric tumor tissues expressed significantly higher Bmi-1, and Bmi-1 overexpression correlated with lymph node metastasis, or clinical stage, which was accordance with the results in in vitro study that knockdown of Bmi-1 expression was accompanied by decreased transformed phenotype and migration ability in gastric cancer cell lines [33]. In these studies Bmi-1 was detected at protein level by IHC method. Here we detected Bmi-1 at mRNA level by QRT-PCR method and found that Bmi-1 is overexpressed in gastric tumors and Bmi-1 overexpression...
correlates with tumor size, depth of invasion (T classification), or lymph node metastasis (N classification), which confirms previous observation of Bmi-1 at protein level. It suggests that Bmi-1 may play a crucial role and act as an oncogene in gastric cancer, and associated with the carcinogenesis, progression, and metastasis of gastric cancer.

Mel-18 was originally cloned from B16 mouse melanoma cells [62]. Mel-18 may bind to the nucleotide sequence 5'-GACTNGACT-3', which is present in the promoter region of certain genes. One of the unique target genes of Mel-18 is c-Myc transcriptionally repressed by Mel-18. In mature resting B cells, Mel-18 negatively regulates B cell receptor-induced proliferation through the down-regulation of the c-Myc/cdc25 cascade [63,64]. Our previous studies suggest that Mel-18 is a physiologic regulator of Bmi-1 expression and transcriptionally down-regulates Bmi-1 expression during senescence in human fibroblasts and acts as a tumor suppressor in breast cancer [38,43]. Our previous data also showed an inverse correlation between Bmi-1 and Mel-18 expression at protein level in breast cancer and gastric cancer [33,38]. However, there was no correlation between Mel-18 expression at protein level and clinicopathological factors in in vivo study, which was not accordance with the results in in vitro study that Mel-18 overexpression was accompanied by decreased transformed phenotype and migration ability in gastric cancer cell lines [33]. One of the reasons may due to the reliability of IHC method depends on the specific of antibody. Mel-18 antibody is rabbit polyclonal and its specific is not so good as Bmi-1 antibody which is mouse monoclonal. So we suspect the results of Mel-18 expression in tumor tissues at protein level detected by IHC may be not too reliable. To clarify this problem and further explore the role of Mel-18 in gastric cancer,
we detected it’s expression at mRNA level by QRT-PCR in the present study. We found that most gastric tumor tissues (64.79%) expressed decreased mRNA levels of Mel-18, and there was a strong negative correlation between Bmi-1 and Mel-18 expression at mRNA level. The results confirm the expression of Mel-18 and its’ relationship with Bmi-1 at protein level in our previous study. More important, we also found that decreased expression of Mel-18 correlated with lymph node metastasis or the clinical stage, which was accordance with the results in in vitro study that Mel-18 overexpression was accompanied by decreased transformed phenotype and migration ability in gastric cancer cell lines in our previous study[33]. It provides more convincing in vivo data to suggest that Mel-18 may play a crucial opposite role to Bmi-1 and act as a tumor suppressor in gastric cancer, and associated with the carcinogenesis, progression, and metastasis of gastric cancer.

In the current study we demonstrated that neoplastic cells in gastric cancer can’t normally express Bmi-1 and Mel-18. We propose that abnormal PcG expression results in an altered composition of the PRC1 in gastric cancer cells, which probably affects expression of target genes involved in regulation of senescence and/or the cell cycle. Our observations add to the increasing evidence that PcG genes are very important contributors to the carcinogenesis and progression of human tumors. We additionally found that both Mel-18 and Bmi-1 correlated with lymph node metastasis. The mechanisms that they regulate cancer cells metastasis need to be further studied.

This research is the first time to study the correlation between Mel-18 or Bmi-1 expression at mRNA level and clinicopathological characteristics of gastric cancer by quantitative method. The expression of Bmi-1 and Mel-18 was correlated with gastric cancer progress, advanced gastric cancer more likely expressed higher Bmi-1 and lower Mel-18. Its clinical value deserves further study in a larger patient population.

### Conclusions

In conclusion, our results suggest that Bmi-1 and Mel-18 are coordinately deregulated. Interestingly, we observed a reverse correlation between the expression levels of Bmi-1 and Mel-18 in gastric cancer. Both Bmi-1 and Mel-18 are involved in the development and progression of gastric cancer. Bmi-1 and Mel-18 might be novel molecular markers for gastric cancer. But, the detailed mechanisms of regulation of Bmi-1 and Mel-18 remained to be elucidated.

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### Authors’ contributions

LYW performed the experiment and prepared the manuscript; LJ supervised the experiment; GWJ designed the experiment and supervised the project. All authors have read and approved the final manuscript.

### Competing interests

The authors declare that they have no competing interests.

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**Table 2 Correlations between the expression level of Bmi-1 or Mel-18 and clinical-pathologic variables**

| Variable | Bmi-1 | Mel-18 |
|----------|-------|--------|
| Gender   |       |        |
| Male     | n GA  | P n GA  | P |
| Female   | 58 1.568 0.687 58 0.259 0.309 |
| Age(>5)  |       |        |
| <60      | 44 1.584 0.832 44 0.188 0.166 |
| ≥60      | 27 1.715 27 0.336 |
| Size(cm) |       |        |
| <4.5     | 26 0.965 0.049* 26 0.206 0.335 |
| ≥4.5     | 45 2.213 45 0.313 |
| Histology|       |        |
| Moderately differentiated | 13 0.899 0.248 13 0.185 0.584 |
| Poorly differentiated | 58 1.827 58 0.247 |
| T classification |       |        |
| T1/2 | 12 0.635 0.036* 12 0.399 0.242 |
| T3/4 | 59 1.979 59 0.210 |
| LNM     |       |        |
| Negative | 16 0.762 0.044* 16 0.513 0.037* |
| Positive | 55 2.038 55 0.186 |
| Distant metastasis |       |        |
| Negative | 68 1.663 0.597 68 0.232 0.645 |
| Positive | 3 2.932 3 0.372 |
| Clinical Stage |       |        |
| I/II | 22 0.949 0.075 22 0.506 0.010* |
| III/IV | 49 2.084 49 0.166 |

Abbreviations: LNM, lymph node metastases; GA, geometrical average; *, Statistically significant. Statistically significant at 0.05 level (bilateral).
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