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Relationships between *MGMT* promoter methylation and gastric cancer: a meta-analysis

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Abstract: A DNA repair enzyme, O6-methylguanine-DNA methyltransferase (*MGMT*), plays an important role in the development of gastric cancers. However, the role of *MGMT* promoter methylation in the occurrence of gastric cancer and its relationships with clinicopathologic characteristics has not been fully clarified. Thus, we performed a meta-analysis to evaluate the associations between *MGMT* promoter methylation and gastric cancer. Electronic databases, including PubMed and Web of Science, were used to systematically search related clinical studies published in English until April 1, 2016. Odds ratios (ORs) and 95% confidence intervals (95% CIs) were calculated to evaluate the associations between *MGMT* promoter methylation and gastric cancer risk or clinicopathologic characteristics. A total of 16 studies including 1,935 patients and 1,948 control persons were included in the analysis. Our study suggested that *MGMT* promoter methylation frequency was associated with gastric cancer (OR=3.46, 95% CI: 2.13–5.61, $P<0.001$). Moreover, the frequency of *MGMT* promoter methylation in the no lymph node metastasis group was lower than that in lymph node metastasis group, with marginal significance (OR=0.65, 95% CI: 0.42–1.01, $P=0.05$). Additionally, the methylation rate of the *MGMT* promoter was much lower in patients without distant metastases than in those with metastases (OR=0.27, 95% CI: 0.18–0.40, $P<0.001$). No significant association of *MGMT* promoter methylation with Lauren classification, tumor location, tumor invasion, or *Helicobacter pylori* infection was found. In conclusion, the methylation status of the *MGMT* promoter was related to gastric cancer risk, distant metastasis, and lymph node metastasis, which indicates that *MGMT* promoter methylation may play an important role in gastric cancer development.

Keywords: gastric cancer, tumor suppressor gene, cancer risks

Introduction

Gastric cancer is one of the most common cancers worldwide, with an estimated 951,600 new stomach cancer cases and 723,100 deaths in 2012.[1] Although diagnostic methods, surgical techniques, and targeted therapy have improved, gastric cancer remains a notable clinical challenge.[2] Many studies indicate that epigenetic alterations in tumor suppressor genes, such as cadherin 13,[3] Ras association domain family member 1,[4] methylation of O6-methylguanine-DNA methyltransferase (*MGMT*),[5] and adenomatosis polyposis coli,[6] play an important role in the initiation and progression of human cancer. DNA methylation is one of the most significant processes involved in epigenetic modifications and has an important effect on the development and prognosis of human cancer.[7–10] In gastric cancer, hypermethylation of tumor suppressor genes has been frequently found.[11]

Among these tumor suppressor genes, *MGMT* in gastric cancer has often been investigated. The *MGMT* gene, located at chromosome 10q26, includes one noncoding and four

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coding exons.[12] *MGMT*, a DNA repair enzyme, mainly defends cells against the carcinogenic effects of adducts by eliminating alkyl groups from the O6-position of guanine and then transferring them into its active center.[13] O6-methylguanine (O6-mG) is the most potent mutagenic lesion that leads to a G-C to A-T transition mutation. *MGMT* can restore this mutagenesis of endogenous DNA damage and play an important role in maintaining normal cell physiology and genomic stability.[14] Thus, loss of MGMT function can cause mutations, leading to human carcinogenesis.[15] *MGMT* promoter methylation resulting in gene silencing and loss of function was found in many tumors, including colorectal cancer,[16] non-small-cell lung cancer,[17] gliomas,[18] and gastric cancer.[19] Oue et al[20] first found that *MGMT* promoter methylation may play a role in carcinogenesis in the stomach. Subsequently, many studies have demonstrated that *MGMT* methylation has been observed more frequently in gastric cancer tissues than in noncancer tissues,[21–23] suggesting that *MGMT* methylation may be associated with an increased gastric cancer risk. However, contradictory results also existed. Therefore, we performed a meta-analysis to elucidate the associations between *MGMT* promoter methylation and gastric cancer.

Methods

Search strategy

Electronic databases, including Web of Science, and PubMed, were used to systematically search related clinical studies published in English until April 1, 2016. The following terms were used: (methylation or DNA methylation or hypermethylation or demethylation), (gastric cancer or gastric carcinoma or gastric tumor), and (O-6-methylguanine-DNA methyltransferase or *MGMT*).

Inclusion and exclusion criteria

Eligible studies met the following standards: 1) assessed the association between *MGMT* methylation and gastric cancer; 2) case–control or cohort studies; 3) studies with sufficient data for calculating odds ratios (ORs) and their 95% confidence intervals (CIs); 4) at least three case and control groups; 5) patients had a definite diagnosis of gastric cancer by pathological or histological examination. For duplicated data, only the most recent or comprehensive studies were included. Moreover, reviews, meta-analysis, case reports, letters, and animal and cell studies were excluded.

Data extraction

Data from the included studies were extracted independently by two authors. The following data were recorded from each study: First author's last name, year of publication, ethnicity, the frequency of *MGMT* methylation in case and control groups, detection method, sample type, source of samples, the number of patients with distant metastasis status having a methylated and unmethylated status, lymph node status, sex, Lauren classification and *Helicobacter pylori* infection. Any differences of opinion were discussed till an agreement was reached.

Statistical analysis

Stata 12.0 (Stata Corporation, TX, USA) and Review Manager 5.2 (Cochrane Collaboration, Oxford, UK) were used in this meta-analysis. The ORs and 95% CIs were used to evaluate the association between *MGMT* promoter methylation and gastric cancer risk or clinicopathologic features. Heterogeneity between studies was evaluated by the Q-test based on the χ^2 statistic and I^2 statistics.[24] If substantial heterogeneity existed ($P<0.05$ for the Q statistic or $I^2>50\%$), a random effect model was applied to pool the ORs; otherwise, a fixed effect model was conducted.[25] A meta-regression analysis was conducted to explore reasons for statistical heterogeneity. Additionally, subgroup analysis was performed based on sex, ethnicity, and sample size to determine the source of heterogeneity. A sensitivity analysis was conducted to assess the effect of single studies on the overall estimate by omitting one study at a time. A funnel plot, trim and fill method, and Egger's test were used to assess for publication bias. All tests were two-sided, and $P<0.05$ denoted statistical significance.

Results

Study selection and characteristics

A total of 72 relevant articles were identified from electronic databases. After reading the titles, abstracts, and full text, 56 studies were excluded, because of irrelevant content, duplicated articles, non-English articles, inadequate data, and cell lines research. Finally, a total of 16 studies,[21–23,26–38] consisting of 1,935 cases and 1,948 controls, were included in the analysis. The study selection process is shown in Figure 1. The methylation rate ranged from 6.9% to 70% in the cancer group and 0% to 44.9% in the control group. Among these studies, 4 studies were conducted on Caucasian, 11 studies on Asian, and 1 study on African individuals. Fourteen studies explored MGMT promoter methylation in tissues and two studies explored MGMT promoter methylation in blood. The basic characteristics of the included studies are shown in Table 1.

Meta-analysis

MGMT promoter methylation and gastric cancer risk

Our results revealed that the frequency of *MGMT* promoter methylation was increased in patients with gastric cancer

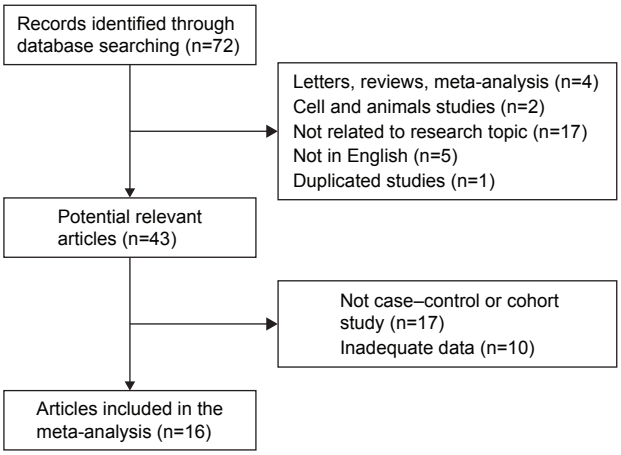

Figure 1 Flow chart of study selection.

compared with control groups under the random-effects model (OR=3.46, 95% CI: 2.13–5.61, $P<0.001$, Figure 2). Because of marked heterogeneity ($P_h<0.001$, $I^2=75\%$), a random effect model was performed. Subgroup analyses by ethnicity, sex, and case sample size were conducted to evaluate the potential source of heterogeneity. In the subgroup analysis based on ethnicity, the pool OR for *MGMT* promoter in the Caucasian subgroup was 2.70 (95% CI: 0.61–12.06, $P=0.19$) within a random effect model, and that for the Asians subgroup was 3.29 (95% CI: 1.99–5.44, $P<0.001$) under a random effect model. Subgroup analysis based on the case sample size indicated that in the >60 case group, the OR was 3.25 (95% CI: 1.83–5.77, $P<0.001$) with a random effect model, in the <60 case group, the OR was 4.14 (95% CI: 2.22–7.73, $P<0.001$) with a fixed effect model. Subgroup analysis by sex suggested no significant association between samples from female patients and those from male patients (OR=0.75, 95% CI: 0.51–1.11, $P=0.15$) based on a random effect model. Detailed results are summarized in Table 2.

Meta-regression analyses with the covariates of case sample size ($P=0.774$) and ethnicity ($P=0.502$) indicated no source of significant heterogeneity. Sensitivity analyses were conducted by excluding every study in turn to assess the stability of the overall results. The pooled OR with 95% CI changed from 2.83 (1.80, 4.44) to 3.95 (2.44, 6.40) under a random effect model, indicating that pooled OR between *MGMT* promoter methylation and gastric cancer was not a significant change. This also showed that our results were reliable and stable.

MGMT promoter methylation and clinicopathologic features in gastric cancer

In terms of lymph node status in patients with gastric cancer, our results showed that the frequency of *MGMT* promoter methylation in the no-lymph node metastasis group was lower than that in the lymph node metastasis group (OR=0.65, 95% CI: 0.42–1.01, $P=0.05$, Figure 3) under a random effect model. Additionally, the rate of *MGMT* promoter methylation was much lower in patients without distant metastases than in patients with metastases (OR=0.27, 95% CI: 0.18–0.40, $P<0.001$, Figure 4) with a fixed effect model. Results revealed no significant association of *MGMT* promoter methylation with Lauren classification (OR=0.95, 95% CI: 0.62–1.47, $P=0.82$), tumor invasion (OR=0.79, 95% CI: 0.60–1.04, $P=0.09$), tumor location (OR=0.90, 95% CI: 0.68–1.20, $P=0.049$), or *H. pylori* infection (OR=1.02, 95% CI: 0.54–1.93, $P=0.94$) with a fixed effect model. The detailed results are shown in Table 3.

Publication bias

The shapes of funnel plots, trim and fill method, and Egger's linear regression test were used to evaluate the publication bias. Slight asymmetry was observed in funnel plots, indicating that publication bias existed in evaluating the association of *MGMT* promoter methylation with gastric cancer risk (Figure 5); however, the *P*-value of Egger's test was greater at 0.076. Trim and fill analysis was performed, and the pooled OR was 2.05 (95% CI: 1.26–3.33, $P<0.001$). The results were similar to the crude meta-analysis, suggesting that our analyses were reliable.

Discussion

Gastric cancer is still a major clinical challenge with poor prognosis in recent years. A useful detection biomarker for the early diagnosis and prognosis evaluation is needed. Silencing tumor suppressor genes expression by aberrant methylation of the promoter regions has been found in the process of tumors.[39] Thus, by pooling the data from 16 studies, we investigated the associations of *MGMT* promoter methylation with gastric cancer risk and its clinicopathologic features. According to our meta-analysis, *MGMT* promoter methylation was significantly correlated with the gastric cancer risk. Our results also suggested that the frequency of *MGMT* promoter methylation was lower in the no-lymph node metastasis group than in the lymph node metastasis group, with marginal significance. More importantly, we found that distant metastasis was associated with increased *MGMT* promoter hypermethylation.

The current meta-analysis revealed an association between *MGMT* promoter methylation and gastric cancer risk. This was in line with previous studies in which the frequency of *MGMT* promoter methylation in tumors was increased compared with control groups,[23,27,28] although a

Table 1 Characteristics of the studies included in the meta-analysis

Reference	Country	Case (M/U)	Control (M/U)	Method	Sample type	Source of control	Source of case	Gender (M/U)		Lauren classification (M/U)		Tumor invasion (M/U)		Lymph node status (M/U)		Distant metastasis (M/U)		*H. pylori* infection (M/U)	
								Male	Female	Intestinal	Diffuse	T1-T2	T3-T4	Negative	Positive	Negative	Positive	Negative	Positive
Jin et al[21] (2014)	People's Republic of China	90/193	49/234	MSP	Tissue	AT	CL	49/103	41/90	NA	NA	34/88	56/105	40/118	50/75	73/185	17/8	NA	NA
Wang et al[22] (2014)	People's Republic of China	24/110	0/146	Methlight	Tissue	AT	CL	19/90	5/20	7/45	13/54	NA	NA	NA	NA	NA	NA	NA	NA
Song et al[23] (2013)	People's Republic of China	89/233	52/270	MSP	Tissue	AT	CL	49/124	40/109	NA	NA	35/104	54/129	41/139	48/94	74/220	15/13	NA	NA
Kupčinskaitė-Noreikienė et al[26] (2013)	Lithuania	25/44	31/38	MSP	Tissue	AT	CL	11/28	14/16	10/25	14/18	6/7	18/35	10/15	14/28	NA	NA	NA	NA
Xiong et al[27] (2013)	People's Republic of China	114/299	48/365	MSP	Tissue	AT	CL	63/159	51/140	NA	NA	35/143	54/181	41/190	48/134	74/303	15/21	NA	NA
Hiraki et al[28] (2010)	Japan	26/23	15/34	MSP	Tissue	AT	CL	14/16	12/7	13/14	13/9	NA	NA	5/15	21/18	NA	NA	NA	NA
Ksiaa et al[29] (2009)	Tunisia	25/43	3/50	MSP	Tissue	AT	APETT	15/25	10/18	11/14	14/29	3/9	22/34	15/23	10/20	21/39	4/4	15/23	10/20
Kolesnikova et al[30] (2008)	Russia	14/6	8/14	MSP	Blood	H	H	8/4	6/2	NA	NA	6/4	8/2	5/4	9/2	10/60	4/0	NA	NA
Zhao et al[31] (2007)	People's Republic of China	7/94	0/26	MSP	Tissue	AT	CL	6/77	1/17	NA	NA	NA	NA	4/27	3/67	6/89	1/5	5/60	2/33
Oue et al[32] (2006)	Japan	20/55	2/33	MSP	Tissue	MIX	CL	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Schildhaus et al[33] (2005)	Germany	2/5	0/7	MSP	Tissue	AT	CL	NA	NA	NA	NA	1/2	0	2/5	NA	NA	NA	NA	NA
Hong et al[34] (2005)	Korea	25/75	4/234	MSP	Blood	H	H	7/57	18/18	8/22	13/32	NA	NA	NA	NA	NA	NA	8/29	17/46
Sabbioni et al[35] (2003)	Italy	11/10	0/6	MSP	Tissue	H	CL	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Kang et al[36] (2003)	Korea	11/63	17/63	MSP	Tissue	NT	CL	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Bae et al[38] (2002)	Korea	21/128	0/149	MSP	Tissue	AT	CL	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Oue et al[37] (2001)	Japan	8/42	0/50	MSP	Tissue	AT	CL	NA	NA	7/17	1/25	NA	NA	NA	NA	NA	NA	NA	NA

Abbreviations: APETT, archival paraffin embedded tumor tissues; AT, normal gastric adjacent the tumor; CL, cancer lesions; H, healthy controls; *H. pylori, Helicobacter pylori*; M, methylations; MIX, mixed controls; MSP, methylation-specific; PCR, polymerase chain reaction; NA, not available; NT, normal gastric tissue; U, unmethylations.

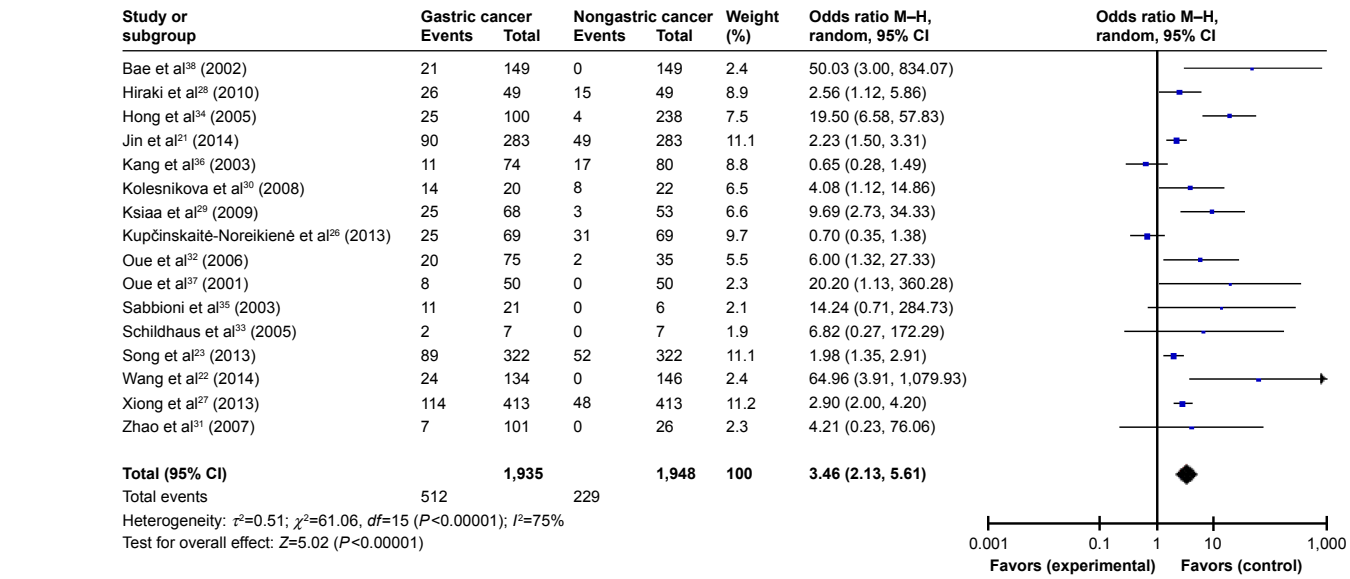

Figure 2 Forest plot for evaluating the association between MGMT promoter methylation and gastric cancer risk. Random-effect model was used for the analysis.
Note: The pooled OR from 16 studies included 1,935 gastric cancer and 1,948 noncancer tissues (OR=3.46, 95% CI: 2.13–5.61, P<0.0001).
Abbreviations: MGMT, O6-methylguanine-DNA methyltransferase; CI, confidence interval; M–H, Mantel–Haenszel; OR, odds ratio.

study by Kupčinskaitė-Noreikienė et al[26] revealed no significant association between *MGMT* promoter methylation and gastric cancer. *MGMT* promoter methylation could be considered as a risk factor for the development of gastric cancer after large-scale studies are conducted. Silencing *MGMT* expression by hypermethylation has two consequences for cancer.[40] First, *MGMT* can defend cell against alkylation-induced gene mutations, toxicity, and carcinogenicity.[41] Alkylating agent can result in alkylation of O6 guanine in DNA. O6-methylguanine preferentially pairs with thymine in DNA replication leading to a G-C to A-T transition mutation[42] and can lead to cross-linking reactions with cytosine on the side chain, resulting in termination of DNA synthesis. These changes may result in K-ras mutation or p53 mutation[38] leading to the development of cancer.

Table 2 Stratified analysis of the frequency of MGMT promoter methylation in gastric cancers compared with noncancer controls

Study group	N	OR (95% CI)	I^2 (%)	P_h	P_{bias}	*P*-value
Total	16	3.46 (2.13, 5.61)	75	**<0.001**	0.076	**<0.001**
Ethnicity						
Caucasian	4	2.70 (0.61, 12.06)	69	**0.02**	0.126	0.19
Asians	11	3.29 (1.99, 5.44)	73	**<0.001**	0.063	**<0.001**
Africans	1	9.69 (2.73, 34.33)	NA	NA	NA	**<0.001**
Case sample size						
<60	5	4.14 (2.22, 7.73)	0	0.52	**0.021**	**<0.001**
>60	11	3.25 (1.83, 5.77)	82	**<0.001**	0.120	**<0.001**

Note: Values in bold indicate statistical significance.
Abbreviations: CI, confidence interval; MGMT, O6-methylguanine-DNA methyltransferase; N, total number of eligible studies; NA, not available; OR, odds ratio; P_{bias}, *P*-value of Egger linear regression test for evaluating publication bias; P_h, *P*-value of Q test for heterogeneity among studies.

Unrepaired DNA damage is a major source of potentially mutagenic lesions that may lead to cancer.[43] Second, *MGMT* hypermethylation in tumors is sensitive to alkylating drugs used in chemotherapy. *MGMT* promoter methylation has been associated with chemo-responsiveness with alkylating agent drugs in glioma, Hodgkin's lymphoma cells and other tumor models.[44,45] Silencing *MGMT* gene expression by promoter methylation can increase the sensitivity to temozolomide, which is considered a therapeutic option for some gastric cancers. Additionally, Miura et al indicated that negative expression of the *MGMT* gene was observed in 45% of the gastroesophageal tumors on the basis of biomarker profiling, suggesting potential sensitivity to temozolomide.[46] Therefore, it is necessary to detect the *MGMT* promoter methylation status in patients with gastric cancer to develop individualized treatment programs when they are treated with temozolomide.

In the subgroup analysis based on ethnicity, a significant association between *MGMT* promoter methylation and gastric cancer risk was observed in Asians, but no significant difference was found in Caucasians. It suggested that a combination of differences in gene backgrounds and the environment may have certain impact on the prevalence of *MGMT* methylation. Furthermore, limited studies were conducted on Caucasians, which may bring about a false-negative result. Further study is warranted to investigate the association between *MGMT* promoter methylation and gastric cancer in Caucasians. In the subgroup analysis of sample size, statistical associations were found for all

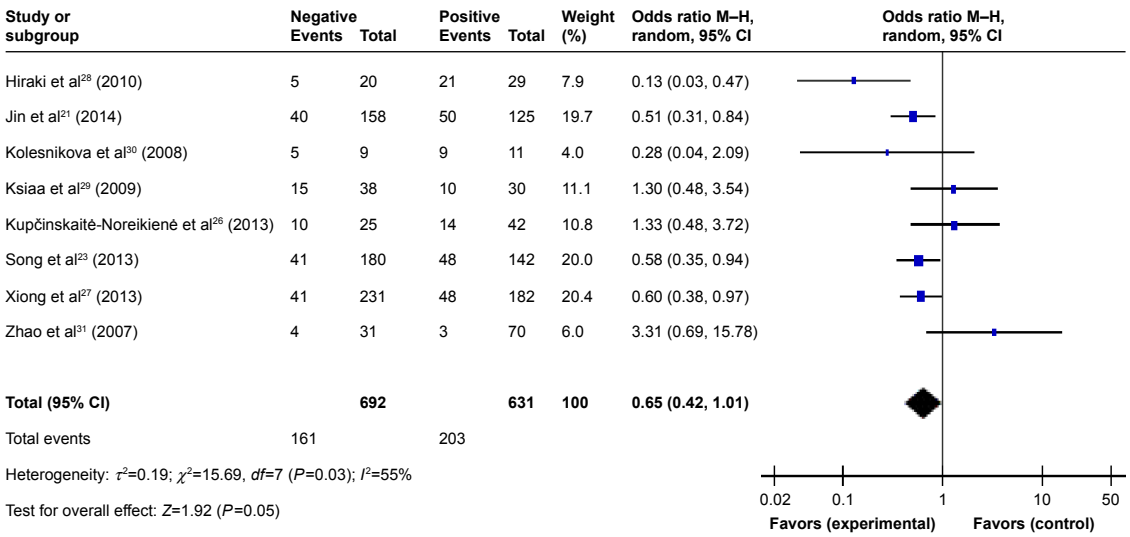

Figure 3 Forest plot for evaluating the association between MGMT promoter methylation and lymph node metastasis. Random-effect model was used for the analysis.
Notes: The pooled OR from 9 studies included 692 gastric cancer patients with no lymph node metastasis and 638 patients with lymph node metastasis (OR=0.65, 95% CI: 2.13–0.42, *P*=0.05). Negative: patients with no lymph node metastasis, positive: patients with lymph node metastasis.
Abbreviations: MGMT, O6-methylguanine-DNA methyltransferase; CI, confidence interval; M–H, Mantel–Haenszel; OR, odds ratio.

subgroups. Additionally, the results of subgroup analysis based on sex revealed that *MGMT* promoter methylation has no relationship with sex in patients with gastric cancer patients.

The associations between *MGMT* promoter methylation and Lauren classification, *H. pylori* infection, tumor location, distant metastasis, and lymph node status were also investigated. Our results showed that *MGMT* promoter methylation was related to lymph node metastasis and distant metastasis was observed in our study, indicating that *MGMT* promoter methylation may be involved in the metastasis of gastric cancer. The tumor microenvironment plays an important role in tumor progression and may exert an influence on the epigenetic status of micrometastatic colonies in the lymph nodes.[47] Therefore, the frequency of methylation differs depending on whether lymph node metastasis has occurred. Therefore, it was hypothesized that *MGMT* promoter methylation may serve as a biomarker for monitoring gastric cancer metastasis. Furthermore, Li et al[48] investigated the role of *MGMT* in gastric cancer cell migration, invasion, and metastatic potential. They demonstrated that loss of *MGMT* expression induced increases in gastric cancer cell metastasis

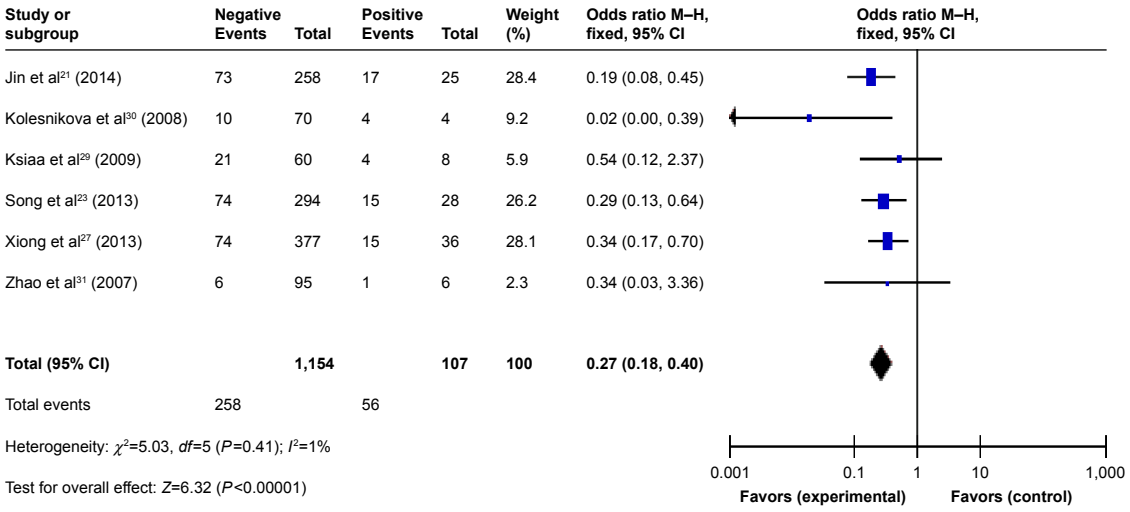

Figure 4 Forest plot for evaluating the association between MGMT promoter methylation and distant metastasis. Fixed-effect model was used for the analysis.
Notes: The pooled OR from 6 studies included 1,154 gastric cancer patients with no distant metastasis and 107 patients with distant metastasis (OR=0.27, 95% CI: 0.18–0.40, *P*<0.0001). Negative: patients with no distant metastasis, positive: patients with distant metastasis.
Abbreviations: MGMT, O6-methylguanine-DNA methyltransferase; CI, confidence interval; M–H, Mantel–Haenszel; OR, odds ratio.

Table 3 Association of MGMT promoter methylation with clinicopathologic features in gastric cancer

Clinicopathological characteristics	N	OR (95% CI)	I^2 (%)	P_h	P_{bias}	*P*-value
Gender	10	0.75 (0.51, 1.11)	52	***P*=0.03**	*P*=0.170	0.15
Lauren classification	6	0.95 (0.62, 1.47)	38	*P*=0.15	*P*=0.079	0.82
Tumor invasion	7	0.79 (0.60, 1.04)	0	*P*=0.86	*P*=0.945	0.09
Distant metastasis	6	0.27 (0.18, 0.40)	1	*P*=0.41	*P*=0.435	**<0.001**
Lymph node status	9	0.65 (0.42, 1.01)	55	***P*=0.03**	*P*=0.674	**0.05**
H. pylori infection	3	1.02 (0.54, 1.93)	0	*P*=0.68	*P*=0.881	0.94
Tumor location	3	0.9 (0.68, 1.20)	0	*P*=0.80	*P*=0.470	0.49

Note: Values in bold indicate statistical significance.
Abbreviations: *H. pylori*, *Helicobacter pylori*; MGMT, O6-methylguanine-DNA methyltransferase; N, total number of eligible studies; P_{bias}, *P*-value of Egger linear regression test for evaluating publication bias; P_h, *P*-value of Q test for heterogeneity among studies.

by downregulation of matrix metalloproteinase 2. However, no obvious association of *MGMT* promoter methylation and Lauren classification was found in our meta-analysis, suggesting that *MGMT* promoter methylation had no effect on the different pathological types of gastric cancer. Additionally, no significant association was identified between *MGMT* promoter methylation and tumor invasion. Multiple high-quality studies are needed to further investigate these associations. Recent studies have indicated that viral or bacterial infections were related to aberrant DNA methylation.[49] The increased DNA methylation levels of some tumor-suppressor genes, such as p16 (*INK4a*), angiopoietin like 4s (ANGPTL4), *MGMT*, and four and a half LIM domains 1 (FHL1) owing to *H. pylori* infection were observed in the gastric mucosa.[50] However, no significant correlation was found between *MGMT* promoter methylation and *H. pylori* infection in our meta-analysis, which included three studies. This clear mechanism needs further study. Kupcinskaite-Noreikiene et al[51] suggested that the rate of methylation of the *MGMT* promoter was higher in the lower third of the stomach than in the upper third, so we divided our studies into two groups according to the primary tumor location. Stratification by tumor location revealed that no associations between *MGMT* promoter methylation and tumor location (OR=0.90, 95% CI: 0.68–1.20, *P*=0.49) within a fixed effect model, because the number of patients in the meta-analysis was relatively small. Further studies are needed to clarify this.

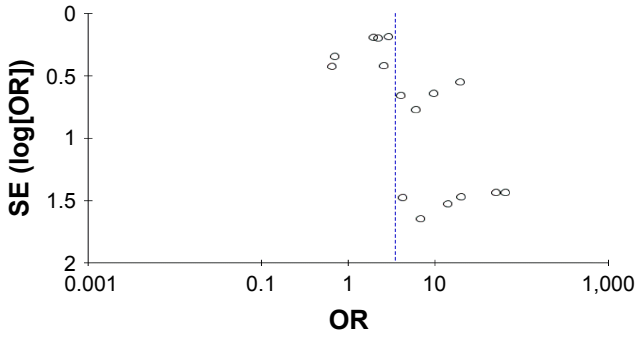

Figure 5 Funnel plot for evaluating the association of MGMT promoter methylation with gastric cancer risk.
Note: The funnel plot from 16 studies determined the relationship between MGMT hypermethylation and gastric cancer.
Abbreviations: MGMT, O6-methylguanine-DNA methyltransferase; OR, odds ratio; SE, standard error.

Several potential limitations were noted in this meta-analysis. First, significant heterogeneity between studies existed, but no sources of heterogeneity were found by meta-regression and subgroup analysis. The control group consisted of both normal gastric tissue adjacent to the tumor and normal gastric tissue, thus, the diversity of control groups may have effected on our research results. Thus, the nonuniform definition of control groups may lead to some heterogeneity. Second, many other factors, such as age as a risk factor for gastric cancer, *MGMT* mRNA expression, tumor grade, 10-year disease-free survival, disease-specific survival, and general demographic information, could not be assessed because of inadequate data. Large detailed studies should be included in further research. Third, we chose the only studies published in English, and this may contribute to potential selection bias, which may not be possible to avoid entirely. Finally, all included studies were retrospective; hence, it is impossible to determine whether *MGMT* promoter methylation is an early cancer-causing aberration or an influence of cancer progression. In the future, multiple prospective studies should be conducted to clarify this.

Although this study does have some limitations, it also has some strengths. Most importantly, our study showed a strong association of *MGMT* promoter methylation with risk of gastric cancer, which is consistent with previous findings that *MGMT* promoter methylation could be a risk factor for other types of cancer, such as colon adenocarcinoma,[52] breast cancer,[4] and non-small-cell lung cancer.[53] Moreover, we found that *MGMT* promoter methylation may serve as a biomarker for monitoring gastric cancer metastasis, although many future studies are recommended to repeat these findings. *MGMT* promoter methylation has been associated with chemo-responsiveness with alkylating agent drugs; therefore, it is essential to detect the *MGMT* promoter methylation status in patients if they need treatment with alkylating agent drugs.

In summary, *MGMT* promoter hypermethylation is associated with gastric risk, distant metastasis and lymph node metastasis, which indicates that *MGMT* promoter methylation may play an important role in gastric cancer. However,

large-scale multicenter and well-matched cohort research studies are warranted to confirm our results and elucidate the exact mechanisms involved.

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Disclosure

The authors report no conflicts of interest in this work.

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