

The Association of *MMP9* Promoter Rs3918242 Genotype With Gastric Cancer

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Abstract. *Background/Aim:* Matrix metalloproteinase 9 (*MMP9*) is highly expressed in gastric cancer but the role of *MMP9* is unclear. This study aimed at revealing the association of *MMP9* promoter rs3918242 genotypes with gastric cancer risk. *Materials and Methods:* *MMP9* rs3918242 genotypes of 121 patients with gastric cancer and 363 healthy individuals were examined by polymerase chain reaction-restriction fragment length polymorphism methodology using serum samples. *Results:* *MMP9* rs3918242 TT genotype carriers had an elevated gastric cancer risk compared to wild-type CC carriers (odds ratio=3.92, 95% confidence interval=1.28-11.99; $p=0.0103$). Patients with CT/TT genotypes were at higher risk of metastasis ($p=0.0178$) than those with CC. No correlation was found between *MMP9* rs3918242 genotype and gastric cancer risk with smoking or alcohol behavior, nor *Helicobacter pylori* infection. No correlation was observed for *MMP9* rs3918242 genotypic distributions with age, gender, or body mass index. *Conclusion:* Carrying a T allele

for *MMP9* rs3918242 may be predictive for higher gastric cancer risk, and as a predictor for higher risk of metastasis.

Gastric cancer has been listed as the fourth most prevalent cancer and the second most common cause of cancer-related death worldwide (1). Epidemiologically speaking, lifestyle, dietary habits and genomic factors combine to cause the etiology of gastric cancer, while personalized predictive strategy based on genomics for gastric cancer remains unestablished. In literature, dietary habits (2, 3), obesity (4), alcoholism (4-6), cigarette consumption (4), *Helicobacter pylori* infection (7), occupational exposure status (8-10), and inherited genetic polymorphisms (11) may all be involved in the development of gastric carcinogenesis but their interactions are largely unknown. In Taiwan, gastric cancer is the 10th most prevalent type of cancer (7th in males and 10th in females) and the 8th cause of cancer-related deaths (12). In recent years, several population-based genomic studies focusing on evaluating the association of genomic markers with the risk of gastric cancer in Taiwan have some novel findings (13-16), although these have not yet found use in clinical practice.

Matrix metalloproteinases (MMPs), a family of proteins with individual capacities to degrade specific substrates (17), are responsible for the complex and subtle regulation of the extracellular matrix, an imbalance of which may result in tumorigenesis (18). Alteration of expression patterns of MMPs and imbalance of the extracellular microenvironment are frequently observed in various types of cancer, including gastric cancer (19). For instance, *MMP2* and *MMP9* have

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Table I. Basic characteristics of the control and gastric cancer patient groups.

Character		Cases (n=121)	Controls (n=363)	p-Value ^a
Age, years	Mean±SD	51.3±9.4	53.2±8.1	0.8918
Gender	Female/male	56/65	168/195	0.9999
BMI, kg/m ²	Mean±SD	27.1±5.8	26.7±6.6	0.9344
Alcohol consumption, n (%)	Never drinker	70 (57.9)	268 (73.8)	
	Drinker	39 (32.2)	84 (23.1)	0.0538
	Heavy drinker ^b	12 (9.9)	11 (3.1)	0.0049
Cigarette consumption, n (%)	Never smoker	66 (54.6)	286 (78.8)	
	Smoker	42 (34.7)	71 (19.5)	0.0012
	Heavy smoker ^c	13 (10.7)	6 (1.7)	0.0001
<i>Helicobacter pylori</i> infection, n (%)	Yes	85 (70.2)	188 (51.8)	0.0005
Tumor location, n (%)	Upper	17 (14.1)		
	Middle	54 (44.6)		
	Lower	50 (41.3)		
Metastasis, n (%)	No	52 (43.0)		
	Yes	69 (57.0)		

BMI: Body mass index; SD: standard deviation. ^aBased on chi-square test. ^bUnable to walk straight, or respond to common questions properly in speech more than twice weekly after drinking or drinking more than 100 ml per day for at least half year. ^cMore than 1 pack per day for at least half a year. Significant p-values (p<0.05) are shown in bold.

been found to be up-regulated in gastric cancer tissues (20). On the contrary, down-regulation of *MMP3* and *MMP13* have been found to effectively suppress gastric cancer fibroblast proliferation and migration (21, 22). It is evident that MMPs may be involved in the progression of gastric cancer, as part of a complex network.

Twenty-eight MMP family members that are responsible for regulating the components of the extracellular matrix have been identified, and their functions are becoming revealed (23, 24). MMP9 is one of the most important enzymes involved in the breakdown of the extracellular matrix, which plays a crucial role in various types of cancer (25). Among sites of single nucleotide polymorphisms of *MMP9*, C1562T (rs3918242), located in the promoter region, is the most well-known and most frequently examined. *MMP9* rs3918242 polymorphisms have been reported to be associated with risk for several types of cancer, including of the lung (26), prostate (27), breast (28), and colorectum (29, 30). In addition, gain of 20q12-1q13 (where *MMP9* is located) has been identified one of the most frequent regions with genomic gains in gastric cancer (31-34). Moreover, some reports have suggested that the gain at 20q may contribute to gastric cancer lymph node metastasis (35, 36). From the information above, it is apparent that the progression of gastric cancer is influenced by alterations in *MMP9* expression, while the effects of genomic variations are largely unknown. Therefore, in the current study, we aimed at evaluating its association with gastric cancer risk in a Taiwanese population and revealing its interactions with clinical and lifestyle factors.

Materials and Methods

Collection of gastric cancer cases and controls. During 2005 to 2007, 121 gastric cancer cases were collected at the China Medical University Hospital by Dr. Yang and his colleagues. Well matched in aspects of age and gender, a three-fold number of healthy people were enrolled from the Health Examination Cohort of the same Hospital. The design and protocol of this study was approved by the Institutional Review Board (IRB number: DMR100-IRB-107) and informed consent was obtained with the great help of the Tissue Bank. Selected demographic characteristics of the two groups are summarized and evaluated in Table I.

Methodology for the determination of *MMP9* rs3918242 genotype. DNA was extracted using QIAamp Blood Mini Kit (Blossom, Taipei, Taiwan) as previously described (37-40), and *MMP9* rs3918242 genotyping was conducted as per our previous practice (41, 42). Briefly, the primer sequences for *MMP9* rs3918242 genotyping were 5'-TGGTCAACGTAGTGAAACCCCATCT-3' and 5'-TCCAGCCCCAATTATCACACTTAT-3'. The PCR conditions were set as one cycle at 94°C for 5 min, then 35 cycles at 94°C for 30 s, then 59°C for 30 s and 72°C for 30 s, and a terminal extension at 72°C for 10 min. The restriction endonuclease, SphI (New England Biolabs, Taipei, Taiwan, ROC) was applied. The DNA adducts of CC, CT and TT genotypes after enzyme cutting were 386 bp only, 386+320+66 bps, and 320+66 bps, respectively.

Methodology of statistical analysis. Pearson's chi-square test without Yates' correction and Fisher exact test were applied for all comparisons, except Student's *t*-test was applied for the comparison of distribution of the ages between the case and control groups. The associations between the *MMP9* polymorphisms and gastric cancer risk were evaluated with odds ratios (ORs), as well as the corresponding 95% confidence intervals (CIs) after adjustment for

Table II. Distribution of matrix metalloproteinase-9 rs3918242 genotypic frequencies among the controls and patients with gastric cancer.

Genotype	Frequency, n (%)		OR (95% CI) ^a	p-Value ^b
	Cases (n=121)	Controls (n=363)		
rs3918242				
CC	83 (68.6)	279 (76.9)	1.00 (Reference)	
CT	31 (25.6)	78 (21.5)	1.34 (0.82-2.17)	0.2388
TT	7 (5.8)	6 (1.6)	3.92 (1.28-11.99)	0.0103
<i>P</i> _{trend}				0.0262
Carrier comparison				
CC+CT	114 (94.2)	357 (98.4)	1.00 (Reference)	
TT	7 (5.8)	6 (1.6)	3.65 (1.20-11.09)	0.0149
CC	83 (68.6)	279 (76.9)	1.00 (Reference)	
CT+TT	38 (31.4)	84 (23.1)	1.52 (0.96-2.40)	0.0698

CI: Confidence interval; OR: odds ratio. ^aAdjusted for age, gender, smoking, alcohol and *Helicobacter pylori* infection. ^bBased on chi-square test without Yates' correction. Significant *p*-values (*p*<0.05) are shown in bold.

Table III. Allelic frequencies for matrix metalloproteinase-9 rs3918242 in the control and gastric cancer patient groups.

Allelic type	Frequency, n (%)		Adjusted OR (95% CI) ^a	p-Value ^b
	Cases (n=242)	Controls (n=726)		
C	197 (81.4)	636 (87.6)	1.00 (Reference)	
T	45 (18.6)	90 (12.3)	1.61 (1.12-2.43)	0.0159

CI: Confidence interval; OR: odds ratio. ^aAdjusted for age, gender, smoking, alcohol and *Helicobacter pylori* infection. ^bBased on chi-square test without Yates' correction. Significant *p*-values (*p*<0.05) are shown in bold.

some factors including age, gender and other indices (Table I). Any *p*-value less than 0.05 was considered significant.

Results

Analysis of basic characteristics between the gastric cancer and control groups. The demographic indices of the 121 gastric cancer cases and the 363 controls are shown in Table I. Firstly, age and gender were well matched between the case and control groups (*p*=0.8918 and 0.9999, respectively). Secondly, the average body mass indices were of the same level (*p*=0.9344) for the case and control groups. Thirdly, alcohol consumers comprised a significantly higher percentage of the gastric cancer group than that of the control group (42.1% versus 26.2%) (*p*<0.05). Fourthly, the gastric cancer group had a significantly higher percentage of cigarette smokers, especially heavy smokers, than those of the control group (34.7% vs. 19.5%, and 10.7% vs. 1.7%, *p*=0.0012 and 0.0001, respectively). Fifthly, 70.2% of the patients with gastric cancer were positive for *Helicobacter pylori* infection, significantly higher than that of 51.8% for the control group (*p*=0.0005).

Association of *MMP9* rs3918242 genotypes with gastric cancer risk. The genotypic results for *MMP9* rs3918242 among the 121 patients with gastric cancer and the 363 controls are presented in Table II. The genotypic distribution for *MMP9* rs3918242 in the control group fits well under the Hardy-Weinberg equilibrium (*p*=0.8386). The genotypic frequency distributions for *MMP9* rs3918242 were significantly different between the gastric cancer and control groups (*p* for trend=0.0262) (Table II). In detail, *MMP9* rs3918242 heterozygous CT genotype seemed not to be associated with risk for gastric cancer (*p*=0.2388). On the contrary, the homozygous variant TT genotype exhibited a significant association with gastric cancer risk (adjusted OR=3.92, 95% CI=1.28-11.99; *p*=0.0103). We also compared those carrying the TT genotype with those with CC or CT genotype, and the results showed that the TT genotype at *MMP9* rs3918242 conferred a 3.65-fold odds of gastric cancer (adjusted OR, 95% CI=1.20-11.09, *p*=0.0149) (Table II). On the contrary, people carrying CT or TT genotypes had a non-significant risk of gastric cancer (adjusted OR=1.52, 95% CI=0.96-2.40; *p*=0.0698), compared with the CC genotype (Table II).

Table IV. Correlation between matrix metalloproteinase-9 rs3918242 genotype and clinicopathological features of 121 patients with gastric cancer.

Characteristic	Subgroup	Patients, n	MMP9 rs3918242 genotype, n (%)			p-Value ^a
			CC	CT	TT	
Age	≤50 Years	54	38 (71.7)	12 (22.7)	3 (5.6)	0.7940
	>50 Years	67	45 (66.2)	19 (27.9)	4 (5.9)	
Gender	Male	65	46 (70.8)	16 (24.6)	3 (4.6)	0.7849
	Female	56	37 (66.1)	15 (26.8)	4 (7.1)	
BMI	≤25 kg/m ²	45	28 (62.2)	14 (31.1)	3 (6.7)	0.5057
	>25 kg/m ²	76	55 (72.4)	17 (22.4)	4 (5.2)	
Alcohol drinker	Never	70	51 (72.9)	16 (22.9)	3 (4.2)	0.4538
	Ever	51	32 (62.7)	15 (29.4)	4 (7.9)	
Cigarette smoker	Never	66	47 (70.1)	16 (23.9)	4 (6.0)	0.8874
	Ever	55	36 (66.7)	15 (27.8)	3 (5.5)	
<i>Helicobacter pylori</i>	Negative	36	21 (58.3)	12 (33.3)	3 (8.3)	0.2791
	Positive	85	62 (72.9)	19 (22.4)	4 (4.7)	
Metastasis	Negative	51	42 (82.4)	8 (15.6)	1 (2.0)	0.0178
	Positive	70	41 (58.6)	23 (32.8)	6 (8.6)	

^aBased on Fisher's exact test; Significant p-values ($p < 0.05$) are shown in bold.

Association of MMP9 rs3918242 allelic frequencies with gastric cancer risk. To validate the genotypic findings deduced from Table II, we further conducted allelic frequency analysis for the association of *MMP9* rs3918242 with gastric cancer risk and the results are presented in Table III. There was a significant difference in the distribution of variant alleles between the gastric cancer and control groups for *MMP9* rs3918242 ($p = 0.0159$, Table III), with an adjusted OR for those carrying the variant T allele of 1.61 (95% CI=1.12-2.43) compared to those carrying the wild-type C allele (Table III). Thus, the results of allelic frequency analysis support the idea that the T allele was associated with an increased risk of gastric cancer.

Interaction analysis of MMP9 rs3918242 genotypes and clinical and lifestyle factors. We are interested in genetic-lifestyle interactions and therefore the interaction between *MMP9* rs3918242 and clinical and lifestyle indices in their effect on gastric cancer risk was evaluated (Table IV). Firstly, we sub-grouped the patients according to their age, finding that the distributions of genotypes of *MMP9* rs3918242 did not differ among those older and younger than 50 years old ($p = 0.7940$). Moreover, when we analyzed the distributions of gender, they were also similar ($p = 0.7849$) (Table IV). Secondly there was also no difference in distribution observed for those with body mass index using a cut-off of 25 kg/m² ($p = 0.5057$). Thirdly, for alcohol drinking, cigarette smoking and *H. pylori* infection status, the results remained non-significant (all $p > 0.05$). Last but not least, there was an obvious association of metastasis in patients with gastric cancer carrying a T allele for *MMP9* rs3918242 ($p = 0.0178$).

Discussion

The overexpression of *MMP9* has been observed in many types of cancer, including gastric cancer (43-45). It is reasonable that single nucleotide polymorphisms on the *MMP9* promoter region may control regulation of the expression of *MMP9* (46). Among *MMP9* single nucleotide polymorphisms, rs3918242 is the most investigated. For instance, Xing *et al.* has provided evidence supporting the contribution of *MMP9* rs3918242 to colorectal cancer (29). They found that the *MMP9* rs3918242 T allele was associated with an increased risk of colorectal cancer among the elderly (>60 years old) and contributed to elevating the risk of metastasis (29). However, there is no direct evidence of its role in gastric cancer.

In this study, we concluded that the TT genotype of *MMP9* rs3918242 is associated with elevated risk of gastric cancer (Table II), and this finding is consistent with the previous finding in Turkish population with relatively small sample size (case/control=79/65) (47). As far as we are concerned, the present study revealed the genotypic contribution of *MMP9* rs3918242 genotype to gastric cancer in Taiwan. We do not find any difference in age, gender, and other factors (Table IV). A highlight of our finding is that the genetic variants in *MMP9* may play a critical role in metastasis (Table IV). Yang and colleagues found another two *MMP9* polymorphic sites, R279Q and P574R, to be associated with gastric cancer metastasis (48). In literature, there is mounting evidence showing that the expression of *MMP9* is correlated with the metastatic behavior of gastric cancer cells (49-52). Further investigations of the underlying

molecular mechanism of its involvement in metastasis using gastric cancer samples are urgently warranted to understand the role of *MMP9* in gastric cancer.

There are several directions for further examining the role of *MMP9* in gastric carcinogenesis. One of the missions should be to enlarge the collection sample size. Only in this way could other East-Asian data with similar genetic backgrounds be incorporated together for meta-analyses. A platform of primary cultured cells from tumoral and non-tumoral sites of patients of gastric cancer (and control counterparts) would also be helpful to further understand the role of *MMP9* in aspects of its transcripts, protein level and activity. Although no interaction of body mass index and *MMP9* genotype was found (Table IV), a further understanding of the *MMP9* genotype in joint effects with the diet of patients would be very helpful in understanding the role of *MMP9* in the development of gastric cancer.

In conclusion, this study provided evidence for the significant association of *MMP9* promoter rs3918242 T allele with gastric cancer risk. In addition, *MMP9* rs3918242 appears to play an important role in metastasis. It might serve as both a predictive marker for personal susceptibility and for metastasis of gastric cancer.

Conflicts of Interest

All the Authors declared no conflicts of interest.

Authors' Contributions

Research design: Fu CK, Chang WS and Tsai CW; patient and questionnaire summaries: Fu CK, Hsu HS and Yang MD; experimental work: Wang YC, Chang WS and Yu CC; statistical analysis: Chao CY, Chen JS and Pei JS; article writing: Tsai CW and Bau DT; review and revision: Bau DT.

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