

## Association of Matrix Metalloproteinase-2 Genotypes With Prostate Cancer Risk

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**Abstract.** *Background/Aim:* Prostate cancer is one of the most commonly diagnosed malignancies among males, especially in Western populations. Matrix metalloproteinase-2 (MMP-2) plays a critical role in extracellular regulation and metastasis. However, its genotypes have seldom been examined among patients with prostate cancer (PCa). Therefore, the purpose of the study was to evaluate the association of genotypes at MMP-2 promoter -1306 (rs243865) and -735 (rs2285053) with PCa risk in a Taiwanese cohort. *Materials and Methods:* The profiles of MMP-2 rs243865 and rs2285053 genotypes were examined among 218 PCa patients and 436 healthy controls by polymerase chain reaction-restriction fragment length polymorphism methodologies. *Results:* The percentages of wild-type CC, and variant CT and TT genotypes on MMP-2 rs243865 were 88.5, 10.6, and 0.9% in the PCa case group and 85.6, 13.5, and 0.9% in the control group, respectively (*p* for

trend=0.5544). The allelic frequency distribution showed that the variant T allele at MMP-2 rs24386 5 was not associated with PCa risk (*p*=0.3250). As for MMP-2 rs2285053, the results were also non-significant. In addition, there was no association between the genotypes of MMP-2 rs243865 or rs2285053 with age or smoking status on PCa risk. *Conclusion:* rs11568818 and rs11568819 at MMP-2 promoter region played minor roles in determining individual PCa risk.

Prostate cancer (PCa) is the second most prevalent malignancy, and the fifth leading death-causing cancer among males worldwide, with about 1,414,000 newly diagnosed cases and 375,304 deaths in 2020 (1). According to global cancer statistics, PCa is the most frequently diagnosed cancer in 112 countries, and the leading death-causing malignancy in 48 countries including USA (2). According to world cancer statistics, PCa cases are predicted to continue to increase due to the trend of global aging (3). From the epidemiological viewpoint, black race, family cancer history, and aging, are three most well-known risk factors for PCa (4). In addition, fitness (5), diabetes mellitus (6), obesity (7), risky diet (8), and over-supplementation of vitamin E (9) may also contribute to the etiology of PCa. However, lack of targets in PCa therapy urge the identification of genetic markers.

The extracellular matrix (ECM) is a meshwork of crosslinked macromolecules that form a dynamic scaffold outside of the cells. It provides homeostasis of the micro-environment, and its imbalances may associate with cancer progression and metastasis (10, 11). Noticeably, matrix metalloproteinases (MMPs, also named matrix metalloproteinases or matrixins) play

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**Key Words:** Genotype, MMP-2, polymorphism, prostate cancer.



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Table I. Demographics of the prostate cancer cases and control subjects.

Characteristics	Controls (n=436)			Cases (n=218)			p-Value
	n	%	Mean±SD	n	%	Mean±SD	
Age (years)			63.9±6.6			63.6±6.9	0.58 <sup>a</sup>
<55	275	63.1%		142	65.1%		0.67 <sup>b</sup>
≥55	161	36.9%		76	34.9%		
Smoking behavior							
Ever smoker	336	77.0%		177	81.2%		0.27 <sup>b</sup>
Non-smoker	100	23.0%		41	18.8%		
Family history							
First degree (Father, brother and/or son)	5	1.1%		17	7.8%		<0.001 <sup>b</sup>
Second degree	2	0.5%		4	1.8%		
No history	429	98.4%		197	90.4%		

<sup>a</sup>Based on unpaired Student's *t*-test; <sup>b</sup>based on Chi-square test.

a critical role in tissue remodeling, which is associated with multiple physiological or pathological processes such as angiogenesis, cirrhosis, arthritis, and metastasis *via* their degradation of the ECM components (11-13). In literature, MMP-2 has been shown to closely relate to the metastatic behavior of tumors (14-17). In addition, mounting evidence has shown that MMP-2 over-expression was associated with higher risk of metastasis among various types of cancer (18-23).

MMP-2 is located on chromosome 16q21. This endopeptidase is expressed in a variety of tissues throughout the body (24-26). One of the main functions of MMP-2 is to digest type IV collagen, the major constituent of the cell membrane (27). In literature, it has been reported that MMP-2 rs243865 and rs2285053 may affect its mRNA and protein expression levels, leading to an increase in the metastatic potential of several types of cancer, such as breast, esophageal, colorectal, oral cancer, and leukemia (28-32). In 2014, MMP-2 rs243865 genotypes were first investigated for their association with PCa in Turkey (33). In that study, 61 PCa patients and 46 healthy subjects were examined for their MMP-2 rs243865 genotypes. The MMP-2 rs243865 CT genotypes were found to be 2.17 times more frequent in the PCa patient group than in the control group without statistical significance ( $p=0.149$ ) (33). Furthermore, Adabi *et al.* examined the genetic contribution of MMP-2 rs243865 to PCa in Iran in 2015. They recruited 139 benign prostatic hyperplasia patients as controls and found no association between MMP-2 rs243865 polymorphism and PCa risk (34). In 2018, Bialkowska *et al.* reported that there is no positive association between MMP-2 rs243865 genotypes and PCa risk (35). In that study, they recruited 197 healthy men and 197 PCa patients from Poland. Evidence for the association of MMP-2 rs2285053 genotypes with cancers is inconclusive, and there is none about PCa (36, 37). Another study investigated 150 patients with cervical cancer and 120 healthy individuals in China and reported that MMP-2

rs2285053 genotypes were associated with cervical cancer susceptibility (36). Also, T allele in MMP-2 rs2285053 were associated with reduced risk of breast cancer (37).

According to the above information, we aimed at evaluating the association of MMP-2 rs243865 and rs2285053 genotypes with PCa risk in a representative (case:control=436:218) Taiwanese population for the first time.

## Materials and Methods

**PCa study population.** The current study was approved and supervised by the IRB of China Medical University Hospital (DMR104-IRB-158). All the research protocols were conducted according to the principles of the Declaration of Helsinki. The 436 healthy controls were matched according to age and sex from the Health Examination Cohort of China Medical University Hospital by two folds in sample size of the PCa cases (n=218). The inclusion and exclusion criteria of sampling have been published in our previous papers (38, 39). Some demographic characteristics for all the participants in this study are summarized and compared in Table I.

**MMP-2 rs243865 and rs2285053 genotyping.** DNA was extracted from the whole blood of each participant as previously published (40-42). In the present study, the profiles of MMP-2 rs243865 and rs2285053 genotypes among 218 PCa and 436 controls were determined by using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) methodology. The sequences of forward and reverse primers for MMP-2 rs243865 are: 5'-CTTCCTAGGCTGGT CCTTACTGA-3' and 5'-CTGAGACCTGAAGAGCTAAAGAGCT-3', and those for MMP-2 rs2285053 are 5'-GGATTCTTGGCTTGGC GCAGGA-3' and 5'-GGGGGCTGGGTAAAATGAGGCTG-3'. The primers for MMP-2 rs243865 and rs2285053 genotyping are the same as we have previously published (42, 43). The PCR condition was set as: 5 min initial step at 94°C; 40 cycles of 94°C for 30 s, 55°C for 30 s, and 72°C for 30 s; and a final extension step at 72°C for 10 min. Then, the PCR adducts were subjected to full digestion by *Xsp* I (for MMP-2 rs243865) and *Hinf* I (for MMP-2 rs2285053) overnight. The profiles of MMP-2 rs243865 and rs2285053 of each sample were identified by 3% agarose gel electrophoresis and imaged under UVC irradiation.

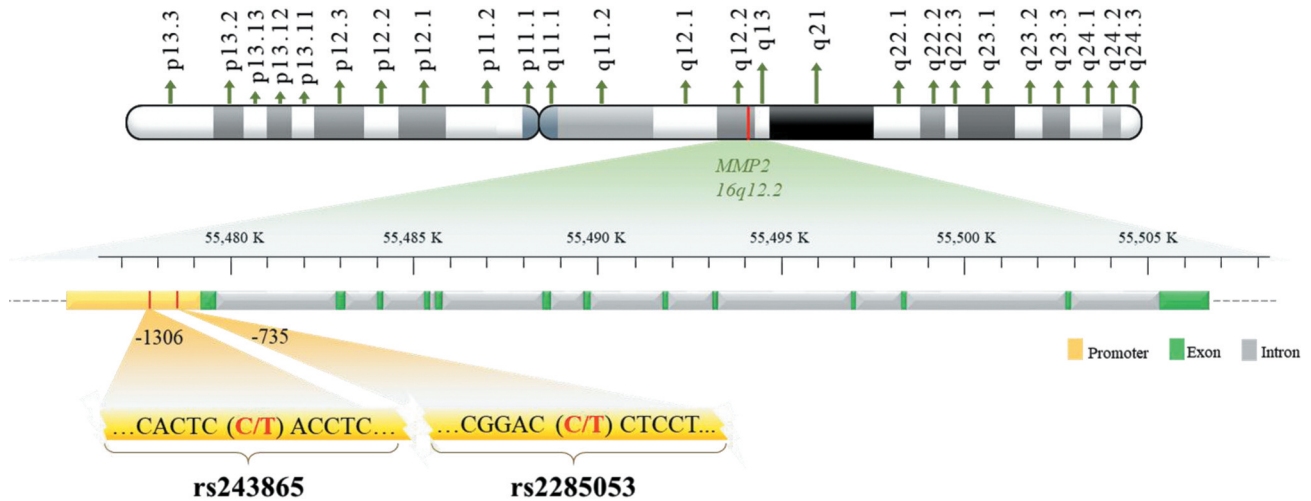


Figure 1. Physical map of *MMP-2* rs243865 and rs2285053 polymorphic sites.

*MMP-2* rs243865 and rs2285053 statistical analysis. The comparison of the ages between the PCa patient and control groups is presented as the mean plus standard deviation (SD), and unpaired *Student's t*-test was used. The Pearson's chi-square or Fisher exact test was used for the evaluation of the associations of *MMP-2* rs243865 and rs2285053 genotypes, and the significant associations were also evaluated as odds ratios (ORs) and 95% confidence intervals (CIs). Results were considered statistically significant at  $p$ -value  $<0.05$ .

## Results

*Comparison of selected demographics between the PCa patient and control groups.* We stratified the 218 PCa cases and 436 controls according to their age and found no difference in the distribution of younger ( $<50$ -years-old) or elder ( $\geq 50$  years old) age among the PCa cases and controls. Furthermore, there is no difference in the distribution of ever smokers or non-smokers between the PCa case and control groups. Moreover, 7.8% and 1.8% of the PCa patients had first- and second-degree relatives suffering from any type of cancer, respectively, whereas only 1.1% and 0.5% of the controls, respectively had a family history of the disease (Table I). This difference was found to be significant ( $p<0.001$ ).

*Association of *MMP-2* rs243865 and rs2285053 genotypes and PCa risk.* The physical map of *MMP-2* rs243865 and rs2285053 is shown in Figure 1. The genotypic frequency of *MMP-2* rs243865 and rs2285053 in the control group fitted well with the Hardy-Weinberg equilibrium ( $p=0.1357$  and  $0.1511$  for *MMP-2* rs243865 and rs2285053, respectively) (Table II). The genotypic frequency of *MMP-2* rs243865 was not differentially distributed between the PCa patient and

control groups ( $p$  for trend= $0.5544$ ) (Table II, top panel). In detail, the CT and TT at *MMP-2* rs243865 were not associated with any altered risk for PCa (OR= $0.75$  and  $0.97$ , 95%CI= $0.45$ - $1.26$  and  $0.18$ - $5.32$ ,  $p=0.3366$  and  $1.0000$ , respectively) (Table II, top panel). In the dominant model, combined CT and TT genotypes conferred no altered risk for PCa (OR= $0.77$ , 95%CI= $0.47$ - $1.26$ ,  $p=0.3514$ ) (Table II, top panel). As for *MMP-2* rs2285053, the genotypic frequency was not differentially distributed between the PCa patient and control groups ( $p$  for trend= $0.7464$ ) (Table II, bottom panel). In detail, the CT and TT at *MMP-2* rs2285053 were not associated with any altered risk for PCa (OR= $1.11$  and  $1.25$ , 95%CI= $0.77$ - $1.59$  and  $0.60$ - $2.63$ ,  $p=0.6340$  and  $0.6913$ , respectively) (Table II, bottom panel). In the dominant model, combined CT and TT genotypes conferred no altered risk for PCa (OR= $1.13$ , 95%CI= $0.80$ - $1.59$ ,  $p=0.5398$ ) (Table II, bottom panel).

*Association of *MMP-2* rs243865 and rs2285053 allelic frequencies and PCa risk.* The results of the allelic analysis showed that the variant T allele at *MMP-2* rs243865 was not significantly associated with PCa risk (OR= $0.79$ , 95%CI= $0.50$ - $1.26$ ,  $p=0.3250$ ). In detail, the distribution of T allele frequencies was not significantly different (7.7% and 6.2%) in the healthy control and PCa case groups, respectively (Table III). As for *MMP-2* rs2285053, the results of the allelic analysis showed that the variant T allele was not significantly associated with PCa risk (OR= $1.12$ , 95%CI= $0.84$ - $1.50$ ,  $p=0.4291$ ). In detail, the distribution of T allele frequencies was not significantly different (18.8% and 20.6%) in the healthy control and PCa case groups, respectively (Table III).

Table II. Genotypic frequency distributions of matrix metalloproteinase-2 rs243865 and rs2285053 among the prostate cases and healthy controls.

Genotypes	Controls, n (%)	Cases, n (%)	OR (95%CI)	p-Value <sup>a</sup>
Promoter -1306 rs243865				
CC	373 (85.6)	193 (88.5)	1.00 (Reference)	
CT	59 (13.5)	23 (10.6)	0.75 (0.45-1.26)	0.3366
TT	4 (0.9)	2 (0.9)	0.97 (0.18-5.32)	1.0000
CT+TT	63 (14.4)	25 (11.5)	0.77 (0.47-1.26)	0.3514
<i>P</i> <sub>trend</sub>				0.5544
<i>P</i> <sub>HWE</sub>				0.1357
Promoter -735 rs2285053				
CC	292 (67.0)	140 (64.2)	1.00 (Reference)	
CT	124 (28.4)	66 (30.3)	1.11 (0.77-1.59)	0.6340
TT	20 (4.6)	12 (5.5)	1.25 (0.60-2.63)	0.6913
CT+TT	144 (33.0)	78 (35.8)	1.13 (0.80-1.59)	0.5398
<i>P</i> <sub>trend</sub>				0.7464
<i>P</i> <sub>HWE</sub>				0.1511

OR: Odds ratio; CI: confidence interval; <sup>a</sup>data based on Chi-square test with Yates' correction ( $n \geq 5$ ) or Fisher's exact test ( $n < 5$ ); *p*<sub>trend</sub>: *p*-value based on trend analysis; *p*<sub>HWE</sub>: *p*-value based on Hardy-Weinberg Equilibrium.

Table III. Allelic frequencies for matrix metalloproteinase-2 rs243865 and rs2285053 polymorphisms among the prostate cases and healthy controls.

Genotypes	Controls, n (%)	Cases, n (%)	Odds ratio (95% Confidence interval)	p-Value <sup>a</sup>
rs243865				
Allele C	805 (92.3)	409 (93.8)	1.00 (Reference)	
Allele T	67 (7.7)	27 (6.2)	0.79 (0.50-1.26)	0.3250
rs2285053				
Allele C	708 (81.2)	346 (79.4)	1.00 (Reference)	
Allele T	164 (18.8)	90 (20.6)	1.12 (0.84-1.50)	0.4291

<sup>a</sup>Data based on Chi-square test with Yates' correction.

## Discussion

The incidence of PCa has been increasing in Taiwan since 1979 (44). In the present study, the contribution of *MMP-2* rs243865 and rs2285053 genotypes to PCa susceptibility among males in Taiwan was firstly investigated. According to the literature, *MMP-2* is responsible for regulating the ECM contents and closely relates to the metastatic behaviors of a panel of cancers. *MMP-2* rs243865 T allele has also been associated with elevated PCa risk in a meta-analysis in 2017 (45).

To our surprise, the T allele of *MMP-2* rs243865 was not a contributor of personal PCa susceptibility (Table II and Table III). On the contrary, it seems to be a protective factor (Table II). To the best of our knowledge, the current study is the first to reveal the contribution of *MMP-2* promoter genotypes to PCa in Taiwan. When comparing the findings of Weng's and ours, our samples are more genetically conserved (all Taiwanese) and representative (case:control=218:436). They collected 6 reports from USA, Brazil, India, Turkey, and Iran

(45). had a smaller sample size (with the exception of that from the USA), not larger than 200 controls and 200 cases. In the USA, they used mixed ethnicities for genotyping investigation (45). Therefore, the difference in the genetic patterns and the small sample size may have caused the different results and conclusion of this study with our own.

The minor allelic frequencies of *MMP-2* rs243865 and rs2285053 were 7.7% and 18.8% in our study (Table III), very similar to those of 5.5% and 24.2% in East Asian as seen on NCBI (<https://www.ncbi.nlm.nih.gov/snp/rs243865> and <https://www.ncbi.nlm.nih.gov/snp/rs2285053>).

We have also examined the associations of *MMP-2* rs243865 and rs2285053 genotypes with age and smoking behaviors. There was no difference in the distributions of *MMP-2* rs243865 or rs2285053 genotypes among PCa patients and controls stratified by younger (<50-years-old) or elder (≥50-years-old) (data not shown). In addition, there was no difference in the distributions of *MMP-2* rs243865 or rs2285053 genotypes among PCa patients and controls



stratified by their smoking behavior (data not shown). Unfortunately, clinical data, such as metastatic status and survival time, were not available for analysis. We now aim to collect fresh samples from PCa patients for genotype-phenotype analysis. It has been shown many times that *MMP-2* plays a critical role in PCa cell and animal models; however, no report has directly provided evidence that *MMP-2* genotypes may be involved in the etiology of PCa (22, 23).

In 2020, Kiani *et al.* reported that the frequency of *MMP-2* promoter -1575 A/A+A/G genotypes was higher in PCa-patients with diabetes mellitus ( $p=0.003$ ) and in smokers ( $p=0.005$ ) and was associated with an elevated risk of PCa (46). This result suggested that *MMP-2* polymorphic sites, other than the commonly studied ones (such as rs243865 and rs2285053) should be evaluated. Our results do not support the hypothesis of Weng's meta-analysis reporting that *MMP-2* rs243865 T allele was associated with an elevated PCa risk (45). On the contrary, our results are more consistent with the hypothesis of Zhou's meta-analysis indicating that *MMP-2* rs243865 genotypes are not associated with PCa risk (47). Although the current evidence showed that *MMP-2* rs243865 genotypes seem not to contribute to the determination of personal PCa susceptibility; they may contribute to the prediction of metastasis and prognosis of PCa, which have not been well-studied. In addition, it is not exclusive that other *MMP-2* polymorphic sites may serve as novel PCa markers for diagnosis and/or prognosis. The role of *MMP-2* rs243865 and rs2285053 genotypes in PCa should be validated in larger and multiple populations.

In conclusion, this study examined the genotypic patterns of *MMP-2* rs243865 and rs2285053 among Taiwanese and revealed that neither *MMP-2* rs243865 nor rs2285053 was associated with personal susceptibility to PCa. Further studies with larger and multiple populations are needed to validate the current findings.

## Conflicts of Interest

The Authors declare no conflicts of interest regarding this study.

## Authors' Contributions

Research design: Li PH, Liao CH, and Huang WC; patient and questionnaire summary: Wu HC, Liao CH, and Hsu SW; experimental work: Tsai CW, Wang ZH and Chang WS; statistical analysis: Chen KY, Hsia TC and Li PH; article writing: Tsai CW and Bau DT; manuscript preparation and discussing: Li PH, Liao CH, Huang WC, Chang WS, Wu HC, Hsu SW, Chen KY, Hsia TC, Wang ZH, Tsai CW and Bau DT.

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