**Name of Journal:** *World Journal of Gastroenterology*

**Manuscript NO:** 67139

**Manuscript Type:** ORIGINAL ARTICLE

***Retrospective Cohort Study***

***MTNR1B* polymorphisms with *CDKN2A* and *MGMT* methylation status are associated with poor prognosis of colorectal cancer in Taiwan**

Lee CC *et al*. *MTNR1B* polymorphisms with *CDKN2A* and *MGMT* methylation

Chia-Cheng Lee, Yu-Cheng Kuo, Je-Ming Hu, Pi-Kai Chang, Chien-An Sun, Tsan Yang, Chuan-Wang Li, Chao-Yang Chen, Fu-Huang Lin, Chih-Hsiung Hsu, Yu-Ching Chou

**Chia-Cheng Lee, Je-Ming Hu, Pi-Kai Chang, Chao-Yang Chen,** Division of Colorectal Surgery, Department of Surgery, Tri-Service General Hospital, National Defense Medical Center, Taipei 114, Taiwan

**Chia-Cheng Lee,** Medical Informatics Office, Tri-Service General Hospital, National Defense Medical Center, Taipei 114, Taiwan

**Yu-Cheng Kuo, Fu-Huang Lin, Chih-Hsiung Hsu, Yu-Ching Chou,** School of Public Health, National Defense Medical Center, Taipei 114, Taiwan

**Chien-An Sun,** Department of Public Health, College of Medicine, Fu-Jen Catholic University, New Taipei City 24205, Taiwan

**Chien-An Sun,** Big Data Research Center, College of Medicine, Fu-Jen Catholic University, New Taipei City 24205, Taiwan

**Tsan Yang,** Department of Health Business Administration, Meiho University, Pingtung 91202, Taiwan

**Chuan-Wang Li,** Department and Graduate Institute of Microbiology and Immunology, National Defense Medical Center, Taipei 114, Taiwan

**Chuan-Wang Li,** Institute of Preventive Medicine, National Defense Medical Center, New Taipei City 237, Taiwan

**Author contributions:** Hsu CH and Chou YC contributed equally to this work;Lee CC, Hsu CH and Chou YC designed the research; Sun CA, Yang T and Li CW performed the research; Hu JM, Chang PK and Chen CY collected the data; Lee CC, Kuo YC, Hsu CH, Lin FH and Chou YC analyzed the data; Lee CC, Hsu CH and Chou YC wrote the paper.

**Supported by** the grant from the Ministry of National Defense-Medical Affairs Bureau, Taiwan, No. MND-MAB-110-109 and No. MND-MAB-D-111059.

**Corresponding author: Yu-Ching Chou, PhD, Professor,** School of Public Health, National Defense Medical Center, No. 161 Sec. 6, Minquan E. Road, Neihu District, Taipei 114, Taiwan. trishow@mail.ndmctsgh.edu.tw

**Received:** April 15, 2021

**Revised:** June 30, 2021

**Accepted:** August 23, 2021

**Published online:** September 14, 2021

**Abstract**

BACKGROUND

Identifying novel colorectal cancer (CRC) prognostic biomarkers is crucial to helping clinicians make appropriate therapy decisions. Melatonin plays a major role in managing the circadian rhythm and exerts oncostatic effects on different kinds of tumours.

AIM

To explore the relationship between *MTNR1B*single-nucleotide polymorphism (SNPs) combined with gene hypermethylation and CRC prognosis.

METHODS

A total of 94 CRC tumour tissues were investigated. Genotyping for the four *MTNR1B* SNPs (rs1387153, rs2166706, rs10830963, and rs1447352) was performed using multiplex polymerase chain reaction. The relationships between the *MTNR1B* SNPs and CRC 5-year overall survival (OS) was assessed by calculating hazard ratios with 95%CIs.

RESULTS

All SNPs (rs1387153, rs2166706, rs10830963, and rs1447352) were correlated with decreased 5-year OS. In stratified analysis, rs1387153, rs10830963, and rs1447352 risk genotype combined with CDKN2A and MGMT methylation status were associated with 5-year OS. A strong cumulative effect of the four polymorphisms on CRC prognosis was observed. Four haplotypes of *MTNR1B* SNPs were also associated with the 5-year OS. *MTNR1B* SNPs combined with *CDKN2A* and *MGMT* gene methylation status could be used to predict shorter CRC survival.

CONCLUSION

The novel genetic biomarkers combined with epigenetic biomarkers may be predictive tool for CRC prognosis and thus could be used to individualise treatment for patients with CRC.

**Key Words:** Colorectal cancer; Melatonin; Hypermethylation; Polymorphism; Prognosis; Biomarker

**©The** **Author(s) 2021.** Published by Baishideng Publishing Group Inc. All rights reserved.

**Citaton:** Lee CC, Kuo YC, Hu JM, Chang PK, Sun CA, Yang T, Li CW, Chen CY, Lin FH, Hsu CH, Chou YC. MTNR1B polymorphisms with CDKN2A and MGMT methylation status are associated with poor prognosis of colorectal cancer in Taiwan. *World J Gastroenterol* 2021; 27(34): 5737-5752

**URL:** https://www.wjgnet.com/1007-9327/full/v27/i34/5737.htm

**DOI:** https://dx.doi.org/10.3748/wjg.v27.i34.5737

**Core Tip:** In this retrospective cohort study, we found that *MTNR1B* single-nucleotide polymorphism were associated with a significantly increased risk of colorectal cancer (CRC) 5-year overall survival. A strong cumulative effect of the four polymorphisms on CRC prognosis was observed. This study indicated the novel genetic biomarkers, *MTNR1B*, combined with *CDKN2A* and *MGMT* gene methylation statuses, maybe a predictive tool for CRC prognosis.

**INTRODUCTION**

Colorectal cancer (CRC) is the third most newly diagnosed cancer and second most frequent cause of cancer-related deaths worldwide[1]. The sudden increase in the incidence of CRC in Taiwan may be associated with obesity, a sedentary lifestyle, and unhealthy dietary habits resulting from improvement of the economy[2]. However, these well-known risk factors cannot wholly account for the increased incidence of CRC. Extensive studies have demonstrated that genetic and epigenetic variations influence personal CRC susceptibility and prognosis[3-6]. Finding novel CRC prognostic biomarkers is crucial because it would help clinicians in making appropriate decisions. Melatonin, which plays a central role in the management of circadian rhythm, has been identified in the pineal retina, lymphocytes, bone marrow, and gastrointestinal tract[7]. Several epidemiological studies have indicated that melatonin exerts oncostatic effects, including antioxidant activity, stimulation of apoptosis, regulation of prosurvival signalling and tumour metabolism, inhibition of angiogenesis, metastasis, and induction of epigenetic alteration[8] on different types of tumours[9-11]. Melatonin prevents metastases, increases the 1-year longevity of patients with resected CRC, and enhances myelotoxicity, lymphocytopenia, and other undesirous haematological and immunological side effects. Furthermore, melatonin reduces neurotoxicity, weakness, insomnia, and psychological stress. These effects have been reported when melatonin is administered as a single pharmaceutical agent or coadministered with the usual first-line and second-line schedules for radiotherapy and chemotherapy[12]. The growing interest in understanding the association between melatonin and colorectal carcinogenesis has led to thorough studies regarding the presence of unique melatonin binding sites in the human colon's intestinal mucosa and submucosa. The melatonin receptor MT2, one of the largest superfamilies of G-protein linked receptors and encoded by *MTNR1B,* is generally responsible for mediating the downstream effects of melatonin[13]. In 2006, Ekmekcioglu *et al*[14] reported that MT2 was involved in the antiproliferative action of melatonin. Some research demonstrated that the levels of melatonin are regulated through its biosynthesis from the amino acid tryptophan, which is mediated by MT2[15]. Research analyses have demonstrated reduced expression of MT2 in tumour mucosa compared with the normal mucosa in patients with CRC[16,17]. This may be caused by MT2 downregulation, which reduces protection against CRC and facilitates the development of CRC tumours. In vitro findings indicate that melatonin triggers p53 phosphorylation through the activation of MT2[18].

Studies have reported an association between *MTNR1B* gene polymorphisms and impaired insulin secretion, higher fasting glucose level, increased risk of type 2 diabetes, and gestational diabetes[19,20]. However, the effect of *MTNR1B* gene polymorphisms on CRC sensitivity is little understood. Many studies have demonstrated that *CDKN2A* is more frequently methylated in poorly differentiated, lymphatic metastasis of CRC[21]. In addition, the hypermethylation state of DNA repair genes, *MGMT* and *MLH1*, which are silenced, and have been shown to be correlated with specific mutations in tumor DNA, such as *KRAS* mutations or microsatellite instability, respectively[22]. Furthermore, aberrant promoter methylation of the *CDKN2A,* *MGMT*, and *MLH1* genes has been reported to be related to adenoma-carcinoma sequence and could serve as a diagnostic prognostic marker of CRC[23,24].

In the present study, a hospital-based retrospective cohort study was conducted to evaluate the effects of *MTNR1B* gene polymorphisms rs1387153, rs2166706, rs10830963, and rs1447352 and their haplotypes on the 5-year overall survival (OS) of patients with CRC and to analyse interactions based on the methylation status of the *CDKN2A* and *MGMT* genes. We hypothesised that the influence of *MTNR1B* gene variation combined with the hypermethylation of *CDKN2A* and *MGMT* genes would predict the prognosis and provide clinical recommendations for optimal treatment of CRC.

**MATERIALS AND METHODS**

***Samples and DNA extraction***

A retrospective cohort study, described in detail elsewhere[24-27], was conducted to predict the OS of patients with CRC in Taiwan. Among this cohort, 94 tumour tissues were collected from patients with CRC, which was diagnosed in the Tri-Service General Hospital (TSGH), Taiwan, from 2006 to 2010. The 5-year prognosis was assessed using the tumour tissues. The TSGH Colon and Rectum Division's clinical practice guideline requires enrolees to return once every 3 mo in the first year after surgical resection and once every 3–6 mo thereafter. Written informed consent was obtained from all patients before participation in the study. The TSGH Institutional Review Board approved this study (TSGHIRB approval number: 098-05-292 and 2-105-05-129). Data regarding registered patients—including sex, surgical age (permanent variable), adjuvant chemotherapy, histologic grade and location of the tumour, and survival—were collected from the TSGH’s cancer registry database and analyzed to investigate the association with *MTNR1B* genotyping. All methods were performed in accordance with the relevant guidelines and regulations. OS was defined as the time from the date of surgery to the date of death from any cause or the last follow-up date before December 31, 2010. Cellulose-coated magnetic beads were employed to extract genomic DNA from the tumour tissues stored at −80 °C in a liquid nitrogen tank by using the MagCore Compact Automated Nucleic Acid Extractor (catalogue no. MCA0801; RBC Bioscience, Taipei, Taiwan) and Genomic DNA Tissue Kit (catalogue no. 69504; Qiagen, Taipei, Taiwan).

***MTNR1B genotyping***

The *MTNR1B* gene polymorphisms rs1387153, rs2166706, rs10830963, and rs1447352 were screened using the Agena MassARRAY platform with iPLEX gold chemistry (Agena, San Diego, CA, United States). The detailed genotyping protocols have been reported elsewhere[28,29]. Following the manufacturer guide, the specific polymerase chain reaction (PCR) primer and extension primer sequences were designed using the Assay Designer software package (v.4.0). A 1-μL genomic DNA sample (10 ng/μL) was employed in multiplex PCR in 5-μL volumes containing 1 unit of Taq polymerase, 500 nmol of each PCR primer mix, and 2.5 mmol/L of each dNTP (Agena, PCR accessory and Enzyme kit). Thermocycling was performed at 94 °C for 4 min, which was followed by 45 cycles at 94 °C for 20 s, 56 °C for 30 s, 72 °C for 1 min, and then 72 °C for 3 min. Unincorporated dNTPs were deactivated using 0.3 U of shrimp alkaline phosphatase. Single-base extension reaction was performed using iPLEX enzyme, terminator mix, and extension primer mix; this was followed by 94 °C for 30 s, 40 cycles at 94 °C for 5 s, 5 inner-cycles at 56 °C for 5 s, 80 °C for 5 s, and finally 72 °C for 3 min (Agena, iPLEX gold kit). After cation exchange resin was added to remove residual salt from the reaction, 7 nL of the purified primer extension reaction was loaded onto the matrix pad of a SpectroCHIP (Agena). The SpectroCHIPs were analysed using a MassARRAY Analyzer 4, and clustering analysis was performed using TYPER 4.0 software.

***Methylation-specific-PCR***

We analyzed *CDKN2A*, *hMLH1*, and *MGMT* DNA methylation in the promoter regions through methylation-specific polymerase chain reaction (MS-PCR), as described in our earlier study[25]. Perform MS-PCR with 1.2-μL aliquots of forward and reverse primers, with 12.5 μL HotStart Taq Premix (RBC Bioscience) and bisulfite-converted DNA according to the manufacturer's protocol. The sequences, annealing temperature of individual primer used for ampliﬁcation, and MS-PCR product sizes are illustrated in Table 1. The MS-PCR procedures were in accordance with the previous study[25]: first, 10 min at 95 °C; then, 35 cycles of 30-s denaturation at 95 °C, 30-s annealing, and 48-s extension at 72 °C; finally, 4-min extension at 72 °C. After the amplification, MS-PCR products were mixed with a loading buffer, electrophoresed on 2% agarose gel by using 0.2-μL gel-stained dye for 25 min, and visualized using an ultraviolet transilluminator.

***Statistical analysis***

Student's *t*-tests were performed to analyse continuous variables, and *χ*2 tests were performed for statistical analyses of categorical variables (IBM SPSS Statistics 22). The existence of a Hardy–Weinberg equilibrium per single-nucleotide polymorphism (SNP) was assessed using two goodness-of-fit tests. Linkage disequilibrium (LD) among genotyped SNPs was obtained using the Haploview 4.2 programme. The minor allele frequencies of four *MTNR1B* gene polymorphisms (rs1387153, rs2166706, rs10830963, and rs1447352) are higher than 5% in an ethnic Chinese population according to data in the dbSNP database.

The relationships between the *MTNR1B* SNPs and 5-year OS of patients with CRC and between the cumulative effect of *MTNR1B* SNPs and 5-year OS of CRC were assessed using adjusted hazard ratios (aHRs) with 95%CIs, calculated using Cox proportional-hazards analyses and adjusted for all the aforementioned patient-level and hospital-level characteristics.

Haplotype frequencies for these SNPs combinations were first estimated using haplo.stats (version 12.1) for the R statistical package and then verified using Haploview 4.2. These software programmes employ expectation–maximisation algorithms when constructing the haplotypes. All statistical tests were two-sided, and *P* < 0.05 was considered statistically significant.

**RESULTS**

In this study, 94 CRC tumor samples from the TSGH tumor bank were analyzed. LD was evaluated for all *MTNR1B* SNP pairs. The Lewontin’s D’ values of the pairs were 1.00 (rs1387153: rs2166706), 0.90 (rs1387153: rs10830963), and 0.88 (rs1387153: rs1447352); and the R2 values were 0.98, 1.00, and 1.00, respectively. Four haplotypes with frequencies of 0.034 (T-C-G-A), 0.011 (C-T-C-A), 0.011 (C-T-C-G), and 0.472 (C-T-G-A) were selected for the haplotype association analysis. The relationship between the *MTNR1B* genotype and the demographic and clinicopathological features of patients with CRC was evaluated. Among the patients with CRC, 41.5% were men; the mean age at surgery was 64.2 ± 13.8 years; 51.0% were at stage III–IV; and 19.1% of the patients died during the study period. Table 2 and Table 3 show that certain possible CRC risk factors, such as age, sex, tumor-node-metastasis stage, and *CDKN2A*, *MLH1* and *MGMT* genes methylation status, were not significantly associated with the *MTNR1B* genotype. However, tumor location and survival were associated with a *MTNR1B* polymorphism. The relationships between each *MTNR1B* genotype were analyzed to determine their association with 5-year OS in patients with CRC using Cox proportional-hazards models adjusted for age, sex, stage, adjuvant chemotherapy, tumor location, and the methylation status of the *CDKN2A,* *MLH1* and *MGMT* genes (Table 4). All SNPs were associated with lower 5-year OS. The variant types of rs1387153 (TT *vs* CC + CT: aHR = 6.23, 95%CI = 2.01–19.3), rs2166706 (CC *vs* TT + TC: aHR = 6.40, 95%CI = 2.21–18.6), rs10830963 (GG *vs* CC + CG: aHR = 7.43, 95%CI = 2.63–21.1), and rs1447352 (AA *vs* GG + GA: aHR = 4.28, 95%CI = 1.32–13.9) decreased the 5-year OS in patients with CRC.

We further examined the relationship between each SNP and the 5-year OS, with data stratified by the methylation status of the *CDKN2A* and *MGMT* genes (Table 5). Particularly, 5-year OS was significantly reduced in the rs1387153 and rs1447352 polymorphism subgroups of unmethylation of the *MGMT* gene (aHR = 8.57, 95%CI = 1.67–44.1; aHR = 19.4, 95%CI = 2.94–128, respectively) compared with the opposite subgroups. In contrast, we determined that the rs1447352 polymorphism was related to a higher risk of mortality in the subjects with methylation of the *CDKN2A* gene (aHR = 9.40, 95%CI = 1.02 –86.8). Besides, rs10830963 exhibited a significant association with 5-year OS in the subgroups with hypermethylation of the *CDKN2A* gene (aHR = 27.2, 95%CI = 3.12–233). According to the small number of hypermethylation *MLH1* gene, we could not perform the *MLH1* gene methylation-stratified analysis.

The cumulative effects of four SNPs were then evaluated. We selected polymorphism to classify the risk based on genotypes, in accordance with the findings summarised in Table 4: TT *vs* CC + CT for rs1387153, CC *vs* TT + TC for rs2166706, GG *vs* CC + CG for rs10830963, and AA *vs* GG + GA for rs1447352. The subjects were classified into five groups on the basis of their genotypical risk score (0, 1, 2, 3, and 4), and the significance of the linear trend was then evaluated. The risk of poor CRC prognosis significantly increased with an increase in the SNP risk genotypes (*P*trend < 0.001, Table 6). Furthermore, patients were divided into two groups on the basis of the number of risk genotypes, forming the < 2 and ≥ 2 SNP risk genotypes groups. The 5-year OS was significantly different between the group with two or more SNP risk genotypes and the comparison group (aHR = 5.81, 95%CI = 2.03–16.6).

Haplotype analysis was performed to determine the relationship between haplotypes of the studied SNPs (rs1387153, rs2166706, rs10830963, and rs1447352) and the 5-year OS. Four haplotypes were screened and two demonstrated significance. The T-C-G-A haplotype contributed to reduced 5-year OS (aHR = 2.75, 95%CI = 1.82–11.2), whereas the C-T-C-G haplotype reduced the risk of mortality (aHR = 0.21, 95%CI = 0.06–0.71, Table 7). No significant relationship with the 5-year OS was evident for the C-T-G-A haplotype (aHR = 1.96, 95%CI = 0.44–8.66) or the C-T-C-A haplotype (aHR = 0.70, 95%CI = 0.28–1.72).

**DISCUSSION**

In this retrospective cohort study, we examined the associations between four *MTNR1B* gene polymorphisms (rs1387153, rs2166706, rs10830963, and rs1447352) and CRC outcomes in terms of OS. Correlations between all SNPs and the 5-year OS were identified. In stratified analysis, the rs1387153 and rs1447352 risk genotypes were determined to be associated with 5-year OS in the unmethylation *MGMT* gene subgroup. In contrast, the rs10830963 and rs1447352 risk genotypes with hypermethylation *CDKN2A* gene had a higher risk of death in five years. Four haplotypes of *MTNR1B* SNPs were also determined to be associated with increased risk of mortality. This study is one of a few that has reported an association between *MTNR1B* SNPs and the 5-year OS in patients with CRC. The *MTNR1B* gene location of both rs1387153 and rs2166706 is > 11 kb upstream. The variant rs10830963 is located in an intronic region, whereas the variant rs1447352 is located at approximately 4.5 kb from the *MTNR1B* gene[30]. Qiu *et al*[31] indicated that these SNPs may influence the *MTNR1B* expression, causing a functional deficiency of melatonin. De Luis *et al*[32] demonstrated that rs10830963 was associated with an increased *MTNR1B* mRNA expression and the expression of other genes that may affect the energy balance role of melatonin[33]. However, the potential role and regulation of the other three SNPs in the *MTNR1B* expression are poorly understood[34].

Mechanisms involving the oncostatic effect of melatonin binding to MT1 and MT2 receptors in CRC have been reported in numerous studies. An *in vitro* study conducted by Karasek *et al*[35] determined that both MT1 and MT2 were part of the oncostatic action of melatonin on Colon 38 adenocarcinoma cells. Furthermore, activation of the tumour suppressor *p53* gene by melatonin is reportedly directly controlled by MT1 and MT2. Melatonin’s suppression of cell proliferation and clonogenic activity is impaired because of the lack of either receptor[18]. León *et al*[16] demonstrated an association between reduced MT1 and MT2 expression and increased malignancy in CRC in 54 Spanish patients with CRC. Moreover, expression of the tumour markers CD44 and CD133 was negatively correlated with MT1 and MT2 expression in patients with CRC[17]. Furthermore, the role of the MT1 receptor in gastric adenocarcinoma was demonstrated in patients over the age of 50 years[36]. In the present study, we determined that four *MTNR1B* gene polymorphisms were significantly associated with the 5-year OS of patients with CRC, with a cumulative effect on prediction for poorer prognosis. Few studies have assessed the relationship between *MTNR1B* gene polymorphisms and CRC prognosis. However, some type 2 diabetes susceptibility genes are correlated with metastasis development[37]. Nasrabadi *et al*[38] indicated that high expression of MT2 was associated with gastric adenocarcinoma, because MT2 receptors enhance the secretion of bicarbonate by stimulating calcium release into the mucosa of enterochromaffin cells. Numerous reports have indicated that *MTNR1B* SNPs are associated with fasting glucose level, obesity, carbohydrate disorders, and type 2 diabetes, which are crucial metabolic risk factors for CRC[39,40]. Indeed, Johnson *et al*[41] reviewed the association between colorectal cancer and type 2 diabetes and indicated that there is a positive and observational correlation. Besides, the GG genotype of the variant rs10830963 was discovered to significantly increase the risk of breast cancer than the CC genotype[39,42]. Moreover, the AA genotype of the variant rs10765576 was correlated with lower risk of breast cancer compared with the GG or GA major allele among Chinese women[13].

Data concerning the effect of gene methylation modification on the association between *MTNR1B* gene polymorphisms and CRC prognosis are scarce. The case-only analysis performed by Das *et al*[43] assessed the potential interactions and associations between epigenetics, genetics, and the risk of oesophageal cancer. Das *et al*[43] determined that *CDKN2A* methylation and the *p53* polymorphism were significantly associated with oesophageal cancer risk. DNA methylation can regulate gene expression by modifying chromatin complexes and recruiting methyl-CpG domain-binding proteins around CpG islands, and this is the most common epigenetic alteration. There was a clinical study had revealed the feasibility of using specific gene methylation statuses as biomarkers for CRC prognosis[44]. For instance, the hypermethylation of *CDKN2A* and *MGMT* promoters has been suggested to be independently correlated with poorer prognosis (including metastasis, recurrence, and mortality) in patients with CRC[45,46]. Our findings demonstrated that the risk of mortality in *CDKN2A* hypermethylation patients with rs10830963 or rs1447352 risk genotype was higher than that in the opposing subgroups. However, SNPs−rs1387153 and rs1447352 with unmethylation of the *MGMT* gene were associated with poorer CRC prognosis. All these findings regarding the correlation with gene promoter methylation status and polymorphisms suggest an overlap and crosstalk between the involved pathways, adversely affecting cancer prognosis, and indicate a strong correlation between genetic and epigenetic factors in the Taiwanese population. Therefore, *CDKN2A* and *MGMT* methylation status and *MTNR1B* SNPs may be used as molecular targets for predicting CRC prognosis. The efficiency of any single polymorphic site for risk detection is usually limited because of the multistep model of colorectal carcinogenesis. The benefits of using a combination of several SNPs are well-documented[47]. Our analysis revealed a significant cumulative effect, which was observed as *MTNR1B* SNPs correlating with the 5-year OS, which indicates that using more risk genotypes may improve the accuracy of CRC prognoses. Furthermore, the risk of mortality in individuals with the TT genotype rs1387153, CC genotype rs2166706, and GG genotype rs10830963 may be 2.75-fold higher than that in other haplotypes.

Certain limitations to the present study should be considered. First, limitations are inherent in any retrospective cohort study. Second, our sample size was not sufficiently large enough to provide a more precise estimate of the association between *MTNR1B* SNPs and CRC prognosis. Third, our preliminary retrospective cohort study was not designed to clarify the pathophysiology of how the risk genotype of the *MTNR1B* gene reduces postoperative survival. In addition, data regarding registered patients were collected from the TSGH's cancer registry database. Other potential risk factors, such as dietary habits, obesity, and combined primary diseases were unavailable from the database. Furthermore, this study did not include normal colorectal tissues, *i.e.* we could not describe *MTNR1B* polymorphic variants in normal colorectal tissues. The results of the present study should be verified using a large-scale study that controls for confounding variables, such as lifestyle, carcinogen exposure, and diet, among others.

**CONCLUSION**

In summary, we conducted a retrospective cohort study to investigate the association between *MTNR1B* SNPs and CRC prognosis in those with different gene methylation statuses. All polymorphisms were correlated with 5-year OS. Three SNPs (rs1387153, rs10830963, and rs1447352) were associated with enhanced mortality risk when combined with different *CDKN2A* or *MGMT* gene methylation status. Furthermore, we observed a strong cumulative effect of *MTNR1B* SNPs on the 5-year OS of patients with CRC. Our findings indicate that *MTNR1B* SNPs combined with *CDKN2A* and *MGMT* gene methylation statuses may be predictive biomarkers for CRC prognosis. This study offers insights into novel genetic and epigenetic biomarkers for the prediction of CRC prognosis, and the findings could be used to individualise the treatment of patients with CRC.

**ARTICLE HIGHLIGHTS**

***Research background***

Melatonin plays a central role in the management of circadian rhythm and was identified in the gastrointestinal tract. Epidemiological studies demonstrated that melatonin has oncostatic effects including induction of epigenetic alteration on different types of tumours. The melatonin receptor MT2 encoded by *MTNR1B* is generally responsible for mediating the downstream effects of melatonin. The expression of MT2 in tumour mucosa is lower than the normal mucosa in patients with colorectal cancer (CRC).

***Research motivation***

Growing studies have investigated the association between melatonin and CRC carcinogenesis. However, the relationship between *MTNR1B* gene polymorphisms and CRC sensitivity is not clear. To analyze the effects of *MTNR1B* gene polymorphisms on CRC prognosis and evaluate the interactions with aberrant promoter methylation of the *CDKN2A* and *MGMT* genes will be of great significance.

***Research objectives***

In our study, we aimed to explore the association between *MTNR1B* single-nucleotide polymorphism (SNPs) and the 5-year overall survival (OS) of CRC patients. To further assess the interaction between *MTNR1B* SNPs and *CDKN2A* and *MGMT* gene methylation, we examined the relationship between each SNP and the 5-year OS, with data stratified by the methylation status of the *CDKN2A* and *MGMT* gene.

***Research methods***

Ninety four CRC patients from Taiwan were enrolled to evaluate the association between *MTNR1B* SNPs, *CDKN2A*, *MGMT* gene hypermethylation and 5-year OS. The *MTNR1B* gene polymorphisms were screened using the Agena MassARRAY platform with iPLEX gold chemistry. The promoter methylation status of *CDKN2A* and *MGMT* was assessed using methylation-specific polymerase chain reaction. Associations of the genetic and epigenetic effect and 5-year OS were assessed using the Cox proportional hazards regression model.

***Research results***

In this retrospective cohort study, we found that *MTNR1B* SNPs was associated with a significantly increased risk of CRC 5-year OS. A strong cumulative effect of the four polymorphisms on CRC prognosis was observed. In stratified analysis, rs1387153, and rs1447352 risk genotype were determined to be associated with 5-year OS in the unmethylation *MGMT* gene subgroup. In contrast, rs10830963 and rs1447352 risk genotype with hypermethylation *CDKN2A* gene had a higher risk of death in five years. Four haplotypes of MTNR1B SNPs were also determined to be associated with increased risk of mortality.

***Research conclusions***

This study is one of few reports which demonstrated the association between MTNR1B SNPs and the 5-year OS in patients with CRC. Our data identified these novel genetic biomarkers combined with *CDKN2A* and *MGMT* methylation status for the prediction of CRC prognosis, and the findings could be used to individualise the treatment of patients with CRC.

***Research perspectives***

Based on our findings, the novel genetic biomarkers, *MTNR1B*, combined with *CDKN2A* and *MGMT* gene methylation statuses could be a predictive tool for CRC prognosis. The new set of markers may help physicians make treatment decisions based on the prognostic information and would improve the OS of patients with CRC. This study warrant further investigation of the underlying mechanisms related to oncostatic effects of *MTNR1B* on CRC.

**REFERENCES**

1 **Bray F**, Ferlay J, Soerjomataram I, Siegel RL, Torre LA, Jemal A. Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA Cancer J Clin* 2018; **68**: 394-424 [PMID: 30207593 DOI: 10.3322/caac.21492]

2 **Tseng CH**. Diabetes, metformin use, and colon cancer: a population-based cohort study in Taiwan. *Eur J Endocrinol* 2012; **167**: 409-416 [PMID: 22778198 DOI: 10.1530/EJE-12-0369]

3 **Lv Z**, Xu Q, Sun L, Wen J, Fang X, Xing C, Yuan Y. Four novel polymorphisms in long non-coding RNA HOTTIP are associated with the risk and prognosis of colorectal cancer. *Biosci Rep* 2019; **39** [PMID: 30940774 DOI: 10.1042/BSR20180573]

4 **Lam K**, Pan K, Linnekamp JF, Medema JP, Kandimalla R. DNA methylation based biomarkers in colorectal cancer: A systematic review. *Biochim Biophys Acta* 2016; **1866**: 106-120 [PMID: 27385266 DOI: 10.1016/j.bbcan.2016.07.001]

5 **Kim TO**, Park J, Kang MJ, Lee SH, Jee SR, Ryu DY, Yang K, Yi JM. DNA hypermethylation of a selective gene panel as a risk marker for colon cancer in patients with ulcerative colitis. *Int J Mol Med* 2013; **31**: 1255-1261 [PMID: 23546389 DOI: 10.3892/ijmm.2013.1317]

6 **Lech G**, Słotwiński R, Słodkowski M, Krasnodębski IW. Colorectal cancer tumour markers and biomarkers: Recent therapeutic advances. *World J Gastroenterol* 2016; **22**: 1745-1755 [PMID: 26855534 DOI: 10.3748/wjg.v22.i5.1745]

7 **Acuña-Castroviejo D**, Escames G, Venegas C, Díaz-Casado ME, Lima-Cabello E, López LC, Rosales-Corral S, Tan DX, Reiter RJ. Extrapineal melatonin: sources, regulation, and potential functions. *Cell Mol Life Sci* 2014; **71**: 2997-3025 [PMID: 24554058 DOI: 10.1007/s00018-014-1579-2]

8 **Li Y**, Li S, Zhou Y, Meng X, Zhang JJ, Xu DP, Li HB. Melatonin for the prevention and treatment of cancer. *Oncotarget* 2017; **8**: 39896-39921 [PMID: 28415828 DOI: 10.18632/oncotarget.16379]

9 **Seely D**, Wu P, Fritz H, Kennedy DA, Tsui T, Seely AJ, Mills E. Melatonin as adjuvant cancer care with and without chemotherapy: a systematic review and meta-analysis of randomized trials. *Integr Cancer Ther* 2012; **11**: 293-303 [PMID: 22019490 DOI: 10.1177/1534735411425484]

10 **Zhao M**, Wan J, Zeng K, Tong M, Lee AC, Ding J, Chen Q. The Reduction in Circulating Melatonin Level May Contribute to the Pathogenesis of Ovarian Cancer: A Retrospective Study. *J Cancer* 2016; **7**: 831-836 [PMID: 27162542 DOI: 10.7150/jca.14573]

11 **Brown SB**, Hankinson SE, Eliassen AH, Reeves KW, Qian J, Arcaro KF, Wegrzyn LR, Willett WC, Schernhammer ES. Urinary melatonin concentration and the risk of breast cancer in Nurses' Health Study II. *Am J Epidemiol* 2015; **181**: 155-162 [PMID: 25587174 DOI: 10.1093/aje/kwu261]

12 **Gil-Martín E**, Egea J, Reiter RJ, Romero A. The emergence of melatonin in oncology: Focus on colorectal cancer. *Med Res Rev* 2019; **39**: 2239-2285 [PMID: 30950095 DOI: 10.1002/med.21582]

13 **Deming SL**, Lu W, Beeghly-Fadiel A, Zheng Y, Cai Q, Long J, Shu XO, Gao YT, Zheng W. Melatonin pathway genes and breast cancer risk among Chinese women. *Breast Cancer Res Treat* 2012; **132**: 693-699 [PMID: 22138747 DOI: 10.1007/s10549-011-1884-5]

14 **Ekmekcioglu C**. Melatonin receptors in humans: biological role and clinical relevance. *Biomed Pharmacother* 2006; **60**: 97-108 [PMID: 16527442 DOI: 10.1016/j.biopha.2006.01.002]

15 **Slominski RM**, Reiter RJ, Schlabritz-Loutsevitch N, Ostrom RS, Slominski AT. Melatonin membrane receptors in peripheral tissues: distribution and functions. *Mol Cell Endocrinol* 2012; **351**: 152-166 [PMID: 22245784 DOI: 10.1016/j.mce.2012.01.004]

16 **León J**, Casado J, Carazo A, Sanjuán L, Maté A, Muñoz de Rueda P, de la Cueva P, Quiles R, Ruíz S, Ruíz-Extremera A, Salmerón J. Gender-related invasion differences associated with mRNA expression levels of melatonin membrane receptors in colorectal cancer. *Mol Carcinog* 2012; **51**: 608-618 [PMID: 21809392 DOI: 10.1002/mc.20832]

17 **Casado J**, Iñigo-Chaves A, Jiménez-Ruiz SM, Ríos-Arrabal S, Carazo-Gallego Á, González-Puga C, Núñez MI, Ruíz-Extremera Á, Salmerón J, León J. AA-NAT, MT1 and MT2 Correlates with Cancer Stem-Like Cell Markers in Colorectal Cancer: Study of the Influence of Stage and p53 Status of Tumors. *Int J Mol Sci* 2017; **18** [PMID: 28604612 DOI: 10.3390/ijms18061251]

18 **Santoro R**, Mori F, Marani M, Grasso G, Cambria MA, Blandino G, Muti P, Strano S. Blockage of melatonin receptors impairs p53-mediated prevention of DNA damage accumulation. *Carcinogenesis* 2013; **34**: 1051-1061 [PMID: 23354312 DOI: 10.1093/carcin/bgt025]

19 **Tarnowski M**, Malinowski D, Safranow K, Dziedziejko V, Pawlik A. MTNR1A and MTNR1B gene polymorphisms in women with gestational diabetes. *Gynecol Endocrinol* 2017; **33**: 395-398 [PMID: 28084098 DOI: 10.1080/09513590.2016.1276556]

20 **Patel R**, Rathwa N, Palit SP, Ramachandran AV, Begum R. Association of melatonin &MTNR1B variants with type 2 diabetes in Gujarat population. *Biomed Pharmacother* 2018; **103**: 429-434 [PMID: 29674279 DOI: 10.1016/j.biopha.2018.04.058]

21 **Kim MS**, Lee J, Sidransky D. DNA methylation markers in colorectal cancer. *Cancer Metastasis Rev* 2010; **29**: 181-206 [PMID: 20135198 DOI: 10.1007/s10555-010-9207-6]

22 **Hiraoka S**, Kato J, Horii J, Saito S, Harada K, Fujita H, Kuriyama M, Takemoto K, Uraoka T, Yamamoto K. Methylation status of normal background mucosa is correlated with occurrence and development of neoplasia in the distal colon. *Hum Pathol* 2010; **41**: 38-47 [PMID: 19733896 DOI: 10.1016/j.humpath.2009.06.002]

23 **Imperiale TF**, Ransohoff DF, Itzkowitz SH, Levin TR, Lavin P, Lidgard GP, Ahlquist DA, Berger BM. Multitarget stool DNA testing for colorectal-cancer screening. *N Engl J Med* 2014; **370**: 1287-1297 [PMID: 24645800 DOI: 10.1056/NEJMoa1311194]

24 **Chang HF**, Wu CC, Sun CA, Chu CM, Lin FG, Hsieh JF, Hsu CH, Huang CH, Yang T, Tsai YM, Kuan JC, Chou YC. Clinical stage and risk of recurrence and mortality: interaction of DNA methylation factors in patients with colorectal cancer. *J Investig Med* 2016; **64**: 1200-1207 [PMID: 27296458 DOI: 10.1136/jim-2016-000086]

25 **Kuan JC**, Wu CC, Sun CA, Chu CM, Lin FG, Hsu CH, Kan PC, Lin SC, Yang T, Chou YC. DNA methylation combinations in adjacent normal colon tissue predict cancer recurrence: evidence from a clinical cohort study. *PLoS One* 2015; **10**: e0123396 [PMID: 25815725 DOI: 10.1371/journal.pone.0123396]

26 **Hsu CH**, Hsiao CW, Sun CA, Wu WC, Yang T, Hu JM, Huang CH, Liao YC, Chen CY, Lin FH, Chou YC. Novel methylation gene panel in adjacent normal tissues predicts poor prognosis of colorectal cancer in Taiwan. *World J Gastroenterol* 2020; **26**: 154-167 [PMID: 31988582 DOI: 10.3748/wjg.v26.i2.154]

27 **Hsu CH**, Hsiao CW, Sun CA, Wu WC, Yang T, Hu JM, Liao YC, Huang CH, Chen CY, Lin FH, Chou YC. Multiple gene promoter methylation and clinical stage in adjacent normal tissues: Effect on prognosis of colorectal cancer in Taiwan. *Sci Rep* 2020; **10**: 145 [PMID: 31924802 DOI: 10.1038/s41598-019-56691-6]

28 **Zou M**, Li R, Wang JY, Wang K, Wang YN, Li Y, Ji FX, Sun SN, Huang SS, Fan HH, Huang CP, Zhang X, Zhu JH. Association analyses of variants of SIPA1L2, MIR4697, GCH1, VPS13C, and DDRGK1 with Parkinson's disease in East Asians. *Neurobiol Aging* 2018; **68**: 159.e7-159.e14 [PMID: 29622492 DOI: 10.1016/j.neurobiolaging.2018.03.005]

29 **Huang CY**, Lin YC, Shiue HS, Chen WJ, Su CT, Pu YS, Ao PL, Hsueh YM. Comparison of arsenic methylation capacity and polymorphisms of arsenic methylation genes between bladder cancer and upper tract urothelial carcinoma. *Toxicol Lett* 2018; **295**: 64-73 [PMID: 29859237 DOI: 10.1016/j.toxlet.2018.05.035]

30 **Liao S**, Liu Y, Tan Y, Gan L, Mei J, Song W, Chi S, Dong X, Chen X, Deng S. Association of genetic variants of melatonin receptor 1B with gestational plasma glucose level and risk of glucose intolerance in pregnant Chinese women. *PLoS One* 2012; **7**: e40113 [PMID: 22768333 DOI: 10.1371/journal.pone.0040113]

31 **Qiu XS**, Tang NL, Yeung HY, Lee KM, Hung VW, Ng BK, Ma SL, Kwok RH, Qin L, Qiu Y, Cheng JC. Melatonin receptor 1B (MTNR1B) gene polymorphism is associated with the occurrence of adolescent idiopathic scoliosis. *Spine (Phila Pa 1976)* 2007; **32**: 1748-1753 [PMID: 17632395 DOI: 10.1097/BRS.0b013e3180b9f0ff]

32 **Lyssenko V**, Nagorny CL, Erdos MR, Wierup N, Jonsson A, Spégel P, Bugliani M, Saxena R, Fex M, Pulizzi N, Isomaa B, Tuomi T, Nilsson P, Kuusisto J, Tuomilehto J, Boehnke M, Altshuler D, Sundler F, Eriksson JG, Jackson AU, Laakso M, Marchetti P, Watanabe RM, Mulder H, Groop L. Common variant in MTNR1B associated with increased risk of type 2 diabetes and impaired early insulin secretion. *Nat Genet* 2009; **41**: 82-88 [PMID: 19060908 DOI: 10.1038/ng.288]

33 **de Luis DA**, Izaola O, Primo D, Aller R. Association of the rs10830963 polymorphism in melatonin receptor type 1B (MTNR1B) with metabolic response after weight loss secondary to a hypocaloric diet based in Mediterranean style. *Clin Nutr* 2018; **37**: 1563-1568 [PMID: 28869073 DOI: 10.1016/j.clnu.2017.08.015]

34 **Wang T**, Wang XT, Lai R, Ling HW, Zhang F, Lu Q, Lv DM, Yin XX. *MTNR1B* Gene Polymorphisms Are Associated With the Therapeutic Responses to Repaglinide in Chinese Patients With Type 2 Diabetes Mellitus. *Front Pharmacol* 2019; **10**: 1318 [PMID: 31787898 DOI: 10.3389/fphar.2019.01318]

35 **Karasek M**, Carrillo-Vico A, Guerrero JM, Winczyk K, Pawlikowski M. Expression of melatonin MT(1) and MT(2) receptors, and ROR alpha(1) receptor in transplantable murine Colon 38 cancer. *Neuro Endocrinol Lett* 2002; **23 Suppl 1**: 55-60 [PMID: 12019353]

36 **Nasrabadi NN**, Sargazi F, Shokrzadeh M, Abediankenari S, Hoseini SV, Najafi M, Haghi-Aminjan H, Mirmajidi SH, Ataee R. Expression of MT1 receptor in patients with gastric adenocarcinoma and its relationship with clinicopathological features. *Neuro Endocrinol Lett* 2018; **39**: 111-118 [PMID: 30183205]

37 **Vincent EE**, Yaghootkar H. Using genetics to decipher the link between type 2 diabetes and cancer: shared aetiology or downstream consequence? *Diabetologia* 2020; **63**: 1706-1717 [PMID: 32705315 DOI: 10.1007/s00125-020-05228-y]

38 **Nasrabadi NN**, Ataee R, Abediankenari S, Shokrzadeh M, Najafi M, Hoseini SV, Jan HH. Expression of MT2 receptor in patients with gastric adenocarcinoma and its relationship with clinicopathological features. *J Gastrointest Cancer* 2014; **45**: 54-60 [PMID: 24142542 DOI: 10.1007/s12029-013-9552-0]

39 **Ziółko E**, Kokot T, Skubis A, Sikora B, Szota-Czyż J, Kruszniewska-Rajs C, Wierzgoń J, Mazurek U, Grochowska-Niedworok E, Muc-Wierzgoń M. The profile of melatonin receptors gene expression and genes associated with their activity in colorectal cancer: a preliminary report. *J Biol Regul Homeost Agents* 2015; **29**: 823-828 [PMID: 26753642]

40 **Lopez-Minguez J**, Saxena R, Bandín C, Scheer FA, Garaulet M. Late dinner impairs glucose tolerance in MTNR1B risk allele carriers: A randomized, cross-over study. *Clin Nutr* 2018; **37**: 1133-1140 [PMID: 28455106 DOI: 10.1016/j.clnu.2017.04.003]

41 **Johnson JA**, Carstensen B, Witte D, Bowker SL, Lipscombe L, Renehan AG; Diabetes and Cancer Research Consortium. Diabetes and cancer (1): evaluating the temporal relationship between type 2 diabetes and cancer incidence. *Diabetologia* 2012; **55**: 1607-1618 [PMID: 22476947 DOI: 10.1007/s00125-012-2525-1]

42 **Zienolddiny S**, Haugen A, Lie JA, Kjuus H, Anmarkrud KH, Kjærheim K. Analysis of polymorphisms in the circadian-related genes and breast cancer risk in Norwegian nurses working night shifts. *Breast Cancer Res* 2013; **15**: R53 [PMID: 23822714 DOI: 10.1186/bcr3445]

43 **Das M**, Sharma SK, Sekhon GS, Mahanta J, Phukan RK, Jalan BK. p16 gene silencing along with p53 single-nucleotide polymorphism and risk of esophageal cancer in Northeast India. *Tumour Biol* 2017; **39**: 1010428317698384 [PMID: 28459370 DOI: 10.1177/1010428317698384]

44 **Okugawa Y**, Grady WM, Goel A. Epigenetic Alterations in Colorectal Cancer: Emerging Biomarkers. *Gastroenterology* 2015; **149**: 1204-1225.e12 [PMID: 26216839 DOI: 10.1053/j.gastro.2015.07.011]

45 **Bihl MP**, Foerster A, Lugli A, Zlobec I. Characterization of CDKN2A(p16) methylation and impact in colorectal cancer: systematic analysis using pyrosequencing. *J Transl Med* 2012; **10**: 173 [PMID: 22925370 DOI: 10.1186/1479-5876-10-173]

46 **Konishi K**, Watanabe Y, Shen L, Guo Y, Castoro RJ, Kondo K, Chung W, Ahmed S, Jelinek J, Boumber YA, Estecio MR, Maegawa S, Kondo Y, Itoh F, Imawari M, Hamilton SR, Issa JP. DNA methylation profiles of primary colorectal carcinoma and matched liver metastasis. *PLoS One* 2011; **6**: e27889 [PMID: 22132162 DOI: 10.1371/journal.pone.0027889]

47 **Li X**, Liu W, Feng F, Hu X, Yuan P, Yan J, Yang Y. [Association between adiponectin rs2241766, rs1501299 polymorphisms and the risk of colorectal cancer]. *Zhonghua Liu Xing Bing Xue Za Zhi* 2014; **35**: 195-199 [PMID: 24739564]

**Footnotes**

**Institutional review board statement:** This study was approved by the TSGH Institutional Review Board (TSGHIRB approval number: 098-05-292 and 2-105-05-129).

**Informed consent statement:** Written informed consent was obtained from all patients before enrollment into the study to evaluate their prognosis.

**Conflict-of-interest statement:** We have no financial relationships to disclose.

**Data sharing statement:** No additional data are available.

**Open-Access:** This article is an open-access article that was selected by an in-house editor and fully peer-reviewed by external reviewers. It is distributed in accordance with the Creative Commons Attribution NonCommercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/Licenses/by-nc/4.0/

**Manuscript source:** Invited manuscript

**Peer-review started:** April 15, 2021

**First decision:** June 23, 2021

**Article in press:** August 23, 2021

**Specialty type:** Oncology

**Country/Territory of origin:** Taiwan

**Peer-review report’s scientific quality classification**

Grade A (Excellent): 0

Grade B (Very good): B

Grade C (Good): C, C

Grade D (Fair): 0

Grade E (Poor): 0

**P-Reviewer:** Ji G, Mogulkoc R, Xie M **S-Editor:** Zhang H **L-Editor:** A **P-Editor:** Liu JH

**Table 1 Primer sequences, annealing temperature and product size for methylation-specific polymerase of target genes**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Genes** | | **Forward primer (5’→3’)** | **Annealing temperature (oC)** | **Product size (bp)** |
| *CDKN2A* | M | F: TTATTAGAGGGTGGGGCGGATCGC | 62 | 150 |
| R: GACCCCGAACCGCGACCGTAA |
| U | F: TTATTAGAGGGTGGGGTGGATTGT | 62 | 151 |
| R: CAACCCCAAACCACAACCATAA |
| *MLH1* | M | F: ACGTAGACGTTTTATTAGGGTCGC | 60 | 118 |
| R: CCTCATCGTAACTACCCGCG |
| U | F: TTTTGATGTAGATGTTTTATTAGGGTTGT | 60 | 124 |
| R: ACCACCTCATCATAACTACCCACA |
| *MGMT* | M | F: TTTCGACGTTCGTAGGTTTTCGC | 53 | 81 |
| R: GCACTCTTCCGAAAACGAAACG |
| U | F: TTTGTGTTTTGATGTTTGTAGGTTTTTGT | 53 | 93 |
| R: AACTCCACACTCTTCCAAAAACAAAACA |

MSP: Methylation-specific polymerase chain reaction;M: Methylation; U: Unmethylation.

**Table 2 Clinical characteristics of colorectal cancer patients and *MTNR1B* genotypes (rs1387153 and rs2166706)**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No of subjects** | **Total** | **rs1387153 (C>T)** | | | | | | **rs2166706 (T>C)** | | | | | |
| **CC (%)** | **CT (%)** | **TT (%)** | ***P* value** | **CC + CT (%)** | ***P* value** | **TT (%)** | **TC (%)** | **CC (%)** | ***P* value** | **TT + TC (%)** | ***P* value** |
| Sex |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Male | 39 (41.5) | 8 (34.8) | 20 (41.7) | 10 (47.6) | 0.69 | 28 (39.4) | 0.62 | 8 (36.4) | 20 (40.8) | 11 (47.8) | 0.73 | 28 (39.4) | 0.63 |
| Female | 55 (58.5) | 15 (65.2) | 28 (58.3) | 11 (52.4) |  | 43 (60.6) |  | 14 (63.6) | 29 (59.2) | 12 (52.2) |  | 43 (60.6) |  |
| Age at surgery |  |  |  |  |  |  |  |  |  |  |  |  |  |
| mean ± SD (yr) | 64.2 ± 13.8 | 66.8 ± 13.8 | 61.7 ± 13.8 | 67.0 ± 13.3 | 0.20 | 63.3 ± 13.9 | 0.29 | 67.4 ± 13.8 | 61.8 ± 13.8 | 65.6 ± 13.5 | 0.24 | 63.6 ± 13.9 | 0.54 |
| < 65 | 50 (53.2) | 12 (52.2) | 27 (56.2) | 10 (47.6) | 0.80 | 39 (54.9) | 0.62 | 11 (50.0) | 27 (55.1) | 12 (52.2) | 0.92 | 38 (53.5) | 1.00 |
| ≥ 65 | 44 (46.8) | 11 (47.8) | 21 (43.8) | 11 (52.4) |  | 32 (45.1) |  | 11 (50.0) | 22 (44.9) | 11 (47.8) |  | 33 (46.5) |  |
| Stage |  |  |  |  |  |  |  |  |  |  |  |  |  |
| I | 12 (12.8) | 2 (8.7) | 6 (12.5) | 4 (19.0) | 0.31 | 8 (11.3) | 0.12 | 2 (9.1) | 6.1 (2.2) | 4 (17.4) | 0.24 | 8 (11.3) | 0.08 |
| II | 34 (36.2) | 9 (39.1) | 18 (37.5) | 6 (28.6) |  | 27 (38.0) |  | 8 (36.4) | 19 (38.8) | 7 (30.4) |  | 27 (38.0) |  |
| III | 30 (31.9) | 10 (43.5) | 16 (33.3) | 4 (19.0) |  | 26 (36.6) |  | 10 (45.5) | 16 (32.7) | 4 (17.4) |  | 26 (36.6) |  |
| IV | 18 (19.1) | 2 (8.7) | 8 (16.7) | 7 (33.3) |  | 10 (14.1) |  | 2 (9.1) | 8 (16.3) | 8 (34.8) |  | 10 (14.1) |  |
| Adjuvant chemotherapya |  |  |  |  |  |  |  |  |  |  |  |  |  |
| No | 23 (24.5) | 5 (22.7) | 12 (25.5) | 6 (33.3) | 0.74 | 17 (24.6) | 0.55 | 5 (23.8) | 12 (25.5) | 6 (30.0) | 0.90 | 17 (25.0) | 0.77 |
| Yes | 65 (69.1) | 17 (77.3) | 35 (74.5) | 12 (66.7) |  | 52 (75.4) |  | 16 (76.2) | 35 (74.5) | 4 (70.0) |  | 51 (75.0) |  |
| Tumor locationa |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Colon | 74 (78.7) | 21 (95.5) | 41 (87.2) | 11 (61.1) | < 0.001 | 62 (89.9) | < 0.001 | 20 (95.2) | 41 (87.2) | 13 (65.0) | 0.02 | 61 (89.7) | 0.01 |
| Rectum | 14 (14.9) | 1 (4.5) | 6 (12.5) | 7 (38.9) |  | 7 (10.1) |  | 1 (4.8) | 6 (12.8) | 7 (35.0) |  | 7 (10.3) |  |
| *CDKN2A* gene |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Unmethylation | 43 (45.7) | 13 (56.5) | 19 (39.6) | 10 (47.6) | 0.40 | 32 (45.1) | 1.00 | 12 (54.5) | 21 (42.9) | 10 (43.5) | 0.64 | 33 (46.5) | 0.99 |
| Methylation | 51 (54.3) | 10 (43.5) | 29 (60.4) | 11 (52.4) |  | 39 (54.9) |  | 10 (45.5) | 28 (57.1) | 13 (56.5) |  | 38 (53.5) |  |
| *MLH1* gene |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Unmethylation | 77 (81.9) | 20 (87.0) | 38 (79.2) | 17 (81.0) | 0.73 | 58 (81.7) | 1.00 | 19 (86.4) | 39 (79.6) | 19 (82.6) | 0.79 | 58 (81.7) | 1.00 |
| Methylation | 17 (18.1) | 3 (13.0) | 10 (20.8) | 4 (19.0) |  | 13 (18.3) |  | 3 (13.6) | 10 (20.4) | 4 (17.4) |  | 13 (18.3) |  |
| *MGMT* gene |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Unmethylation | 46 (48.9) | 8 (34.8) | 26 (54.2) | 12 (57.1) | 0.24 | 34 (47.9) | 0.62 | 8 (36.4) | 25 (51.0) | 13 (56.5) | 0.37 | 33 (46.5) | 0.55 |
| Methylation | 48 (51.1) | 15 (65.2) | 22 (45.8) | 9 (42.9) |  | 37 (52.1) |  | 14 (63.6) | 24 (49.0) | 10 (43.5) |  | 38 (53.5) |  |
| Death in 5 yr |  |  |  |  |  |  |  |  |  |  |  |  |  |
| No | 76 (80.9) | 21 (91.3) | 41 (85.4) | 13 (61.9) | 0.03 | 62 (87.3) | 0.02 | 20 (90.9) | 42 (85.7) | 14 (60.9) | 0.02 | 62 (87.3) | 0.01 |
| Yes | 18 (19.1) | 2 (8.7) | 7 (14.6) | 8 (38.1) |  | 9 (12.7) |  | 2 (9.1) | 7 (14.3) | 9 (39.1) |  | 9 (12.7) |  |

aThe total number of patients with colorectal cancer does not correspond because of missing data. CRC: Colorectal cancer.

**Table 3 Clinical characteristics of colorectal cancer patients and *MTNR1B* genotypes (rs10830963 and rs1447352)**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Variables** | **Total** | **rs10830963 (C>G)** | | | | | | **rs1447352 (A>G)** | | | | | |
| **CC (%)** | **CG (%)** | **GG (%)** | ***P* value** | **CC + CG (%)** | ***P* value** | **GG (%)** | **GA (%)** | **AA (%)** | ***P* value** | **GG + GA (%)** | ***P* value** |
| Sex |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Male | 39 (41.5) | 7 (33.3) | 22 (44.9) | 10 (43.5) | 0.66 | 29 (41.4) | 1.00 | 4 (66.7) | 16 (43.2) | 19 (38.0) | 0.40 | 20 (46.5) | 0.53 |
| Female | 55 (58.5) | 14 (66.7) | 27 (55.1) | 13 (56.5) |  | 41 (58.6) |  | 2 (33.3) | 21 (56.8) | 31 (62.0) |  | 23 (53.5) |  |
| Age at surgery |  |  |  |  |  |  |  |  |  |  |  |  |  |
| mean ± SD (yr) | 64.2 ± 13.8 | 67.0 ± 14.0 | 61.4 ± 13.9 | 66.8 ± 13.1 | 0.16 | 63.1 ± 14.0 | 0.26 | 69.7 ± 14.1 | 64.4 ± 14.0 | 63.0 ± 13.8 | 0.53 | 65.1 ± 14.0 | 0.47 |
| < 65 | 50 (53.2) | 11 (52.4) | 28 (57.1) | 11 (47.8) | 0.75 | 39 (55.7) | 0.63 | 3 (50.0) | 18 (48.6) | 29 (58.0) | 0.68 | 21 (48.8) | 0.41 |
| ≥ 65 | 44 (46.8) | 10 (47.6) | 21 (42.9) | 12 (52.2) |  | 31 (44.3) |  | 3 (50.0) | 19 (51.4) | 21 (42.0) |  | 22 (51.2) |  |
| Stage |  |  |  |  |  |  |  |  |  |  |  |  |  |
| I | 12 (12.8) | 2 (9.5) | 6 (12.2) | 4 (17.4) | 0.56 | 8 (11.4) | 0.30 | 0 (0) | 4 (10.8) | 8 (16.0) | 0.54 | 4 (9.3) | 0.60 |
| II | 34 (36.2) | 8 (38.1) | 18 (36.7) | 7 (30.4) |  | 26 (37.1) |  | 1 (16.7) | 15 (40.5) | 17 (34.0) |  | 16 (37.2) |  |
| III | 30 (31.9) | 9 (42.9) | 16 (32.7) | 5 (21.7) |  | 25 (35.7) |  | 4 (66.7) | 12 (32.4) | 14 (28.0) |  | 16 (37.2) |  |
| IV | 18 (19.1) | 2 (9.5) | 9 (18.4) | 7 (30.4) |  | 11 (15.7) |  | 1 (16.7) | 6 (16.2) | 11 (22.0) |  | 7 (16.3) |  |
| Adjuvant chemotherapya |  |  |  |  |  |  |  |  |  |  |  |  |  |
| No | 23 (24.5) | 5 (23.8) | 12 (25.5) | 6 (30.0) | 0.90 | 17 (25.0) | 0.77 | 1 (16.7) | 8 (22.2) | 14 (30.4) | 0.61 | 9 (21.4) | 0.47 |
| Yes | 65 (69.1) | 16 (76.2) | 35 (74.5) | 14 (70.0) |  | 51 (75.0) |  | 5 (83.3) | 28 (77.8) | 32 (69.6) |  | 33 (78.6) |  |
| Tumor locationa |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Colon | 74 (78.7) | 20 (95.2) | 41 (87.2) | 13 (65.0) | 0.02 | 61 (89.7) | 0.01 | 6 (100) | 34 (94.4) | 34 (73.9) | 0.02 | 40 (95.2) | < 0.001 |
| Rectum | 14 (14.9) | 1 (4.85) | 6 (12.8) | 7 (35.0) |  | 7 (10.3) |  | 0 (0) | 2 (5.6) | 12 (26.1) |  | 2 (4.8) |  |
| *CDKN2A* gene |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Unmethylation | 43 (45.7) | 12 (57.1) | 17 (34.7) | 13 (56.5) | 0.10 | 29 (41.4) | 0.31 | 4 (66.7) | 16 (43.2) | 22 (44.0) | 0.55 | 20 (46.5) | 0.97 |
| Methylation | 51 (54.3) | 9 (42.9) | 32 (65.3) | 10 (43.5) |  | 41 (58.6) |  | 2 (33.3) | 21 (56.8) | 28 (56.0) |  | 23 (53.5) |  |
| *MLH1* gene |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Unmethylation | 77 (81.9) | 18 (85.7) | 39 (79.6) | 19 (82.6) | 0.83 | 57 (81.4) | 1.00 | 5 (83.3) | 31 (83.8) | 40 (80.0) | 0.90 | 36 (83.7) | 0.79 |
| Methylation | 17 (18.1) | 3 (14.3) | 10 (20.4) | 4 (17.4) |  | 13 (18.6) |  | 1 (16.7) | 6 (16.2) | 10 (20.0) |  | 7 (16.3) |  |
| *MGMT* gene |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Unmethylation | 46 (48.9) | 8 (38.1) | 26 (53.1) | 12 (52.2) | 0.50 | 34 (48.6) | 0.95 | 4 (66.7) | 18 (48.6) | 24 (48.0) | 0.68 | 22 (51.2) | 0.92 |
| Methylation | 48 (51.1) | 13 (61.9) | 23 (46.9) | 11 (47.8) |  | 36 (51.4) |  | 2 (33.3) | 19 (51.4) | 26 (52.0) |  | 21 (48.8) |  |
| Death in 5 yr |  |  |  |  |  |  |  |  |  |  |  |  |  |
| No | 76 (80.9) | 19 (90.5) | 43 (87.8) | 13 (56.5) | < 0.001 | 62 (88.6) | < 0.001 | 6 (100) | 33 (89.2) | 36 (72.0) | 0.06 | 39 (90.7) | 0.03 |
| Yes | 18 (19.1) | 2 (9.5) | 6 (12.2) | 10 (43.5) |  | 8 (11.4) |  | 0 (0) | 4 (10.8) | 14 (28.0) |  | 4 (9.3) |  |

aThe total number of patients with colorectal cancer does not correspond because of missing data. CRC: Colorectal cancer.

**Table 4 Relationship between *MTNR1B* single-nucleotide polymorphism and 5-year overall survival of colorectal cancer patients**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **No. of subjects** | **No. of cases (%)** | **Crude** | | **Adjusteda** | |
| **HR** | **95%CI** | **HR** | **95%CI** |
| rs1387153 (C>T) |  |  |  |  |  |  |
| CC | 23 | 2 (11.8) | 1.00 | Referent | 1.00 | Referent |
| CT | 48 | 7 (41.2) | 1.65 | (0.34 to 7.95) | 1.98 | (0.40 to 9.82) |
| TT | 21 | 8 (47.1) | 6.03 | (1.28 to 28.4) | 10.6 | (1.87 to 59.5) |
| TT *vs* CC + CT |  |  | 4.18 | (1.61 to 10.9) | 6.23 | (2.01 to 19.3) |
| rs2166706 (T>C) |  |  |  |  |  |  |
| TT | 22 | 2 (11.1) | 1.00 | Referent | 1.00 | Referent |
| TC | 49 | 7 (38.9) | 1.55 | (0.32 to 7.47) | 1.91 | (0.39 to 9.45) |
| CC | 23 | 9 (50.0) | 5.74 | (1.24 to 26.6) | 10.5 | (1.96 to 56.4) |
| CC *vs* TT + TC |  |  | 4.15 | (1.65 to 10.5) | 6.40 | (2.21 to 18.6) |
| rs10830963 (C>G) |  |  |  |  |  |  |
| CC | 21 | 2 (11.1) | 1.00 | Referent | 1.00 | Referent |
| CG | 49 | 6 (33.3) | 1.19 | (0.24 to 5.91) | 1.40 | (0.27 to 7.22) |
| GG | 23 | 10 (55.6) | 5.79 | (1.27 to 26.5) | 9.46 | (1.90 to 47.1) |
| GG *vs* CC +  CG |  |  | 5.09 | (2.01 to 12.9) | 7.43 | (2.63 to 21.1) |
| rs1447352 (A>G) |  |  |  |  |  |  |
| AA | 50 | 14 (77.8) | 1.00 | Referent | 1.00 | Referent |
| GA | 37 | 4 (22.2) | 0.36 | (0.12 to 1.08) | 0.31 | (0.10 to 0.99) |
| GG | 6 | 0 (0) | N/A | N/A | N/A | N/A |
| AA *vs* GG + GA |  |  | 3.37 | (1.11 to 10.2) | 4.28 | (1.32 to 13.9) |

aAdjusted for age, sex, stage, adjuvant chemotherapy, tumor location and the methylation status of *CDKN2A, MLH1* and *MGMT* gene. HR: Hazard ratio; N/A: Not applicable.

**Table 5 Stratified effect between gene promoter region methylation and *MTNR1B* genotypes for 5-year overall survival of** **colorectal cancer patients**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | | **No. of subjects** | **No. of cases (%)** | **Crude** | | **Adjusteda** | |
| **HR** | **95%CI** | **HR** | **95%CI** |
| rs1387153 (C>T) | |  |  |  |  |  |  |
| TT *vs* CC + CT | CDKN2A |  |  |  |  |  |  |
| U | 10 | 4 (40.0) | 5.01 | (1.33 to 18.9) | 10.4 | (1.17 to 92.4) |
| M | 11 | 4 (36.4) | 3.83 | (0.96 to 15.3) | 8.86 | (1.08 to 72.8) |
| MGMT |  |  |  |  |  |  |
| U | 12 | 5 (41.7) | 3.63 | (1.05 to 12.6) | 8.57 | (1.67 to 44.1) |
| M | 9 | 3 (33.3) | 4.93 | (1.10 to 22.1) | 3.05 | (0.33 to 28.0) |
| rs2166706 (T>C) | |  |  |  |  |  |  |
| CC *vs* TT + TC | CDKN2A |  |  |  |  |  |  |
| U | 10 | 4 (40.0) | 5.02 | (1.33 to 19.0) | 10.4 | (1.17 to 92.4) |
| M | 13 | 5 (38.5) | 3.96 | (1.06 to 14.7) | 10.1 | (1.49 to 68.0) |
| MGMT |  |  |  |  |  |  |
| U | 13 | 5 (38.5) | 3.07 | (0.89 to 10.7) | 6.28 | (1.54 to 25.7) |
| M | 23 | 9 (39.1) | 6.25 | (1.56 to 25.1) | 8.28 | (0.95 to 72.3) |
| rs10830963 (C>G) | |  |  |  |  |  |  |
| GG *vs* CC + CG | CDKN2A |  |  |  |  |  |  |
| U | 13 | 5 (38.5) | 4.63 | (1.24 to 17.3) | 8.47 | (1.57 to 45.6) |
| M | 10 | 5 (50.0) | 5.61 | (1.51 to 20.9) | 27.2 | (3.12 to 233) |
| MGMT |  |  |  |  |  |  |
| U | 12 | 5 (41.7) | 3.47 | (1.00 to 12.0) | 8.50 | (1.98 to 36.5) |
| M | 11 | 5 (45.5) | 7.91 | (1.89 to 33.2) | 9.80 | (1.42 to 67.5) |
| rs1447352 (A>G) | |  |  |  |  |  |  |
| AA *vs* GG + GA | CDKN2A |  |  |  |  |  |  |
| U | 22 | 6 (27.3) | 2.05 | (0.51 to 8.22) | 2.28 | (0.51 to 10.2) |
| M | 28 | 8 (28.6) | 7.34 | (0.92 to 58.7) | 9.40 | (1.02 to 86.8) |
| MGMT |  |  |  |  |  |  |
| U | 24 | 8 (33.3) | 3.94 | (0.84 to 18.6) | 19.4 | (2.94 to 128) |
| M | 26 | 6 (23.1) | 2.77 | (0.56 to 13.7) | 2.04 | (0.35 to 12.0) |

aAdjusted for age, sex, stage, adjuvant chemotherapy, tumor location and the methylation status of *CDKN2A* and *MLH1* or *MGMT* and *MLH1* gene. U: Unmethylation; M: Methylation; HR: Hazard ratio.

**Table 6 Cumulative effect of *MTNR1B* single-nucleotide polymorphism associated with 5-year overall survival of** **colorectal cancer patients**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **No. of subjects** | **No. of cases (%)** | **Crude** | | **Adjusted**a | |
| **HR** | **95%CI** | **HR** | **95%CI** |
| No. of SNP risk genotypes |  |  |  |  |  |  |
| 0 | 41 | 3 (7.3) | 1.00 | Referent | 1.00 | Referent |
| 1 | 25 | 4 (16.0) | 2.27 | (0.51 to 10.1) | 2.60 | (0.55 to 12.2) |
| 2 | 7 | 3 (42.9) | 6.40 | (1.29 to 317) | 6.89 | (1.16 to 41.0) |
| 3 | 1 | 0 (0) | N/A | N/A | N/A | N/A |
| 4 | 18 | 7 (38.9) | 7.60 | (1.96 to 29.5) | 14.0 | (2.94 to 66.3) |
| *P* for trend |  |  |  | < 0.001 |  | < 0.001 |
| ≥ 2 of SNP risk genotypes | 26 | 10 (38.5) | 4.00 | (1.58 to 10.1) | 5.81 | (2.03 to 16.6) |

aAdjusted for age, sex, stage, adjuvant chemotherapy, tumor location and the methylation status of *CDKN2A*, *MLH1* and *MGMT* gene. SNP: Single-nucleotide polymorphism; U: Unmethylation; M: Methylation; HR: Hazard ratio; N/A: Not applicable.

**Table 7 Relationship between haplotypes of *MTNR1B* single-nucleotide polymorphism and 5-year overall survival of colorectal cancer patients**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Haplotypes** | **Survival group (%)** | **Death group (%)** | **Crude** | | **Adjusted**a | |
| **HR** | **95%CI** | **HR** | **95%CI** |
| T-C-G-A | 42.0 | 68.4 | 2.58 | (1.27 to 5.28) | 2.75 | (1.82 to 11.2) |
| C-T-G-A | 2.7 | 5.3 | 1.74 | (0.42 to 7.26) | 1.96 | (0.44 to 8.66) |
| C-T-C-G | 30.0 | 7.9 | 0.23 | (0.07 to 0.76) | 0.21 | (0.06 to 0.71) |
| C-T-C-A | 22.0 | 15.8 | 0.73 | (0.30 to 1.76) | 0.70 | (0.28 to 1.72) |

aAdjusted for age, sex, stage, adjuvant chemotherapy, tumor location. The reference is the set of all the other haplotypes when one haplotype is regarded as an analyzed item. HR: Hazard ratio.



Published by **Baishideng Publishing Group Inc**

7041 Koll Center Parkway, Suite 160, Pleasanton, CA 94566, USA

**Telephone:** +1-925-3991568

**E-mail:** bpgoffice@wjgnet.com

**Help Desk:** https://www.f6publishing.com/helpdesk

https://www.wjgnet.com



**© 2021 Baishideng Publishing Group Inc. All rights reserved.**