

Association study of genetic variation of lncRNA MALAT1 with carcinogenesis of colorectal cancer

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Introduction: Colorectal cancer (CRC) remains a major public health concern worldwide. However, the detailed molecular mechanisms of CRC remain poorly understood.

Methods: In the current study, we evaluated associations of four genetic variants located in the promoter and gene region of long noncoding RNAs metastasis-associated lung adenocarcinoma transcript 1 (lncRNA MALAT1) with CRC susceptibility among a Chinese population with 966 CRC cases and 988 healthy controls, using a two-stage, case-control study design (400 CRC cases and 400 controls in stage 1, and 566 CRC cases and 588 controls in stage 2).

Results: We found that the minor alleles of rs619586 (OR=0.73; 95% CI=0.60–0.88; $P=0.001$) and rs1194338 (OR=0.80; 95% CI=0.70–0.92; $P=0.001$) were significantly associated with decreased CRC susceptibility. Compared with those with rs619586 –AA genotype, the risk of CRC was significantly lower in individuals with AG genotype (OR=0.76; 95% CI=0.61–0.95) and GG genotype (OR=0.46; 95% CI=0.23–0.90). Compared with those with rs1194338 –CC genotype, the risk of CRC was significantly lower in individuals with AC genotype (OR=0.79; 95% CI=0.65–0.95) and AA genotype (OR=0.68; 95% CI=0.51–0.89).

Conclusion: Taken together, our findings provided strong evidence for the hypothesis that genetic variants in lncRNA MALAT1 might contribute to the carcinogenesis of CRC.

Keywords: colorectal cancer, genetic, lncRNA, susceptibility, MALAT1

Introduction

Colorectal cancer (CRC) ranks the third most prevalent cancer type in both men and women worldwide.¹ According to the Colorectal Cancer Statistics in 2017, there were about 135,430 newly diagnosed CRC cases and 50,260 deaths from the disease in United States in 2017.² It was reported that 376,300 new CRC cases and 191,000 CRC death occurred per year in China.³ CRC has a complicated carcinogenesis involving multiple risk factors for its initiation, promotion, and progression, as well as its relapse and metastasis.^{2,4} In addition to some well-known risk factors, such as older age, male gender, obesity, lack of physical exercise, adenomas, and smoking, genetic factors also play an important role in CRC carcinogenesis.^{2,4–7} In spite of great effort for the research of CRC carcinogenesis, the detailed molecular mechanisms of CRC remain poorly understood.^{8,9}

Recently, the long noncoding RNAs (lncRNAs), which are defined as transcripts longer than 200 nucleotides that are not translated into protein, have gradually been reported to be an important class of RNAs with pivotal roles in regulation of gene expression, and involved in multitudinous human complex diseases.^{10,11} However, the biological functions and precise mechanisms of the majority of lncRNAs are still poorly understood. lncRNA-

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metastasis-associated lung adenocarcinoma transcript 1 (*MALAT1*), originally identified as a marker for predicting metastasis and prognosis of early-stage non-small-cell lung cancer patients, was reported to be dysregulated in multiple human cancer types,¹² diabetic retinopathy,¹³ thoracic aortic aneurysm,¹⁴ etc. Studies also found that *MALAT1* contributed to the cell proliferation/migration/invasion, malignancy, tumor growth, metastasis, and poor prognosis of CRC.^{15–19} Additionally, many epidemiologic studies have explored the link between genetic variants in *MALAT1* and disease susceptibility.^{20–25} Meta-analyses showed that *MALAT1* rs619586 was associated with overall cancer risk.²⁶ However, the associations between genetic variants of lncRNA *MALAT1* and carcinogenesis of CRC were less investigated. Only Li et al found rs1194338 in the promoter region of *MALAT1* was significantly associated with decreased CRC risk.²⁴ In this study, we genotyped the tag single-nucleotide polymorphisms (tagSNPs) located in lncRNA *MALAT1* gene, as well as an SNP located in the promoter region of *MALAT1*, and aimed to investigate their associations with the CRC susceptibility among a Chinese population.

Patients and methods

Study subjects

In the current study, we adopted a two-stage, case–control study design, which aims to reduce the false discovery rate, and the subjects were divided into two groups according the recruitment time. A total of 966 CRC cases and 988 healthy controls were included in this study. The inclusion criterion for patients was histopathologically confirmed CRC without previous chemotherapy or radiotherapy. Cancer-free controls came from health check-up programs at the same hospital during the same time, which were matched to cases by gender and age group (± 5 years). Face-to-face interviews were conducted by trained interviewers, who administered a structured questionnaire relating to demographic characteristics and lifestyle-related factors. Meanwhile, 5 mL peripheral blood from each individual was collected and stored in tubes containing sodium citrate anticoagulant, at -80°C , for DNA isolation. This study was approved by the Medical Ethical Committee of Liyuan Hospital, and all subjects enrolled were heritably unrelated ethnic Han Chinese. Written informed consent was signed by each participant.

SNP selection, DNA extraction, and genotyping

TagSNPs of lncRNA *MALAT1* were selected using GVS online server (<http://gvs.gs.washington.edu/GVS150/index.jsp>).

Linkage disequilibrium value r^2 should be less than 0.8, and the minor allele frequency of the selected SNP should be above 0.05 in Chinese Han Beijing population. As a result three tagSNPs (rs11227209, rs619586, and rs3200401) were selected. Another SNP (rs1194338) in the promoter region of *MALAT1*, which was reported to be associated with CRC susceptibility,²⁴ was also included. DNA was extracted from peripheral blood leukocytes with RelaxGene Blood System DP319-02 (Tiangen, Beijing, People's Republic of China). A260/A280 ratio of the purified DNA samples was assessed to ensure purity. DNA samples were then stored at -80°C for further genotyping. Candidate SNPs were genotyped by the TaqMan SNP Genotyping Assay on an ABI PRISM 7900HT Fast Real-Time PCR platform (Applied Biosystems, Waltham, MA, USA). For quality control, we randomly selected 10% of these DNA samples for further validation, which were 100% consistent. Two researchers performed genotyping independently to cross-validate the results.

Statistical analysis

Categorical data were expressed as number (percentage) and analyzed using chi-squared test.

Continuous data were expressed as mean $\pm$ SD and analyzed using Student's *t*-test. Hardy–Weinberg equilibrium (HWE) was tested by using a chi-squared goodness-of-fit test. ORs and 95% CIs were selected to estimate the strength of association between SNPs and risk of CRC adjusted for age, gender, alcohol drinking and smoking status, and family history of cancer. The analyses were done first per allele and then per genotype. All statistics were performed using SPSS software 19.0 (IBM Corporation, Armonk, NY, USA), and $P < 0.05$ was considered as statistically significant.

Results

Characteristics of study population

The descriptive characteristics of the study participants are provided in Table 1. No significant differences were found between the CRC patients and controls with regard to the distribution of age, gender, and smoking and drinking status in the discovery set and validation set, yet the distribution of family history of cancer in CRC patients was significantly higher than that in the controls in both stages ($P < 0.001$). Overall, 52.5% of the tumor site was located at colon.

Associations of candidate SNPs and CRC risk in stage I

Table 2 shows the effects of four SNPs (rs11227209, rs619586, rs3200401, and rs1194338) on CRC susceptibility

Table 1 The demographic characteristics between the colorectal cancer cases and controls

Variables	Stage 1			Stage 2		
	Cases (n=400)	Controls (n=400)	P-value	Cases (n=566)	Controls (n=588)	P-value
Age group						
≥55	250 (62.5%)	256 (64.0%)	0.660	371 (65.6%)	383 (65.2%)	0.883
<55	150 (37.5%)	144 (36.0%)		195 (34.4%)	205 (34.8%)	
Gender						
Male	240 (60.0%)	244 (61.0%)	0.772	334 (59.0%)	341 (58.0%)	0.726
Female	160 (40.0%)	156 (39.0%)		232 (41.0%)	247 (42.0%)	
Smoking, n (%)						
Yes	120 (30.0%)	114 (28.5%)	0.641	164 (29.0%)	162 (27.5%)	0.591
No	280 (70.0%)	286 (71.5%)		402 (71.0%)	426 (72.5%)	
Alcohol drinking, n (%)						
Yes	132 (33.0%)	120 (30.0%)	0.361	198 (35.0%)	200 (34.0%)	0.729
No	268 (67.0%)	280 (70.0%)		368 (65.0%)	388 (66.0%)	
Family history of cancer						
Yes	80 (20.0%)	44 (11.0%)	0.0004	113 (20.0%)	59 (10.0%)	<0.001
No	320 (80.0%)	356 (89.0%)		453 (80.0%)	529 (90.0%)	
Tumor site						
Colon	206 (51.5%)			301 (53.2%)		
Rectum	194 (48.5%)			265 (46.8%)		

Table 2 Association of the selected SNPs with colorectal cancer risk in stage 1

Genotypes	Cases	Controls	OR (95% CI) ^a	P-value
rs11227209				
CC	301	316	1.00 (reference)	
CG	88	76	1.21 (0.86–1.72)	0.267
GG	11	8	1.44 (0.57–3.62)	0.434
G vs C			1.23 (0.91–1.65)	0.175
rs619586				
AA	330	308	1.00 (reference)	
AG	65	82	0.74 (0.52–1.06)	0.101
GG	5	10	0.47 (0.16–1.34)	0.159
G vs A			0.71 (0.52–0.97)	0.031
rs3200401				
CC	283	294	1.00 (reference)	
CT	102	96	1.10 (0.80–1.52)	0.549
TT	15	10	1.56 (0.69–3.50)	0.284
T vs C			1.16 (0.89–1.53)	0.269
rs1194338				
CC	194	164	1.00 (reference)	
CA	156	172	0.77 (0.57–1.03)	0.083
AA	50	64	0.66 (0.43–1.01)	0.055
A vs C			0.78 (0.64–0.96)	0.021

Notes: ^aAdjusted by age, gender, alcohol drinking and smoking status, and family history of cancer. Statistically significant values are shown in bold.

Abbreviation: SNP, single-nucleotide polymorphism. Bold means statistically significant.

in stage 1. The genotypic distributions of four SNPs among the controls were in accordance with HWE ($P>0.05$). In the four loci, the per allele association of rs619586 (OR=0.71; 95% CI=0.52–0.97; $P=0.031$) and rs1194338 (OR=0.78; 95% CI=0.64–0.96; $P=0.021$) was statistically significant, after being adjusted for age, gender, alcohol drinking and smoking status, and family history of cancer. However, the

genotypic distribution for rs11227209 and rs3200401 was not statistically significant, indicating no evidence of association with CRC risk.

Associations of candidate SNPs and CRC risk in stage 2

Further, we replicated the above finding in an independent stage II samples (Table 3). Both rs619586 and rs1194338 were validated for significant association ($P<0.05$). When pooled together, the minor alleles of rs619586 (OR=0.73; 95% CI=0.60–0.88; $P=0.001$) and rs1194338 (OR=0.80; 95% CI=0.70–0.92; $P=0.001$) were significantly associated with CRC susceptibility. Compared with those with rs619586–AA genotype, the risk of CRC was significantly lower in individuals with AG genotype (OR=0.76; 95% CI=0.61–0.95) and GG genotype (OR=0.46; 95% CI=0.23–0.90). Compared with those with rs1194338–CC genotype, the risk of CRC was significantly lower in individuals with AC genotype (OR=0.79; 95% CI=0.65–0.95) and AA genotype (OR=0.68; 95% CI=0.51–0.89).

Discussion

Up to date, CRC remains a major public health concern worldwide. The current study explored the associations between genetic variants located in the promoter and gene region of lncRNA MALAT1 and CRC susceptibility among a Chinese population, using a two-stage, case–control study design. We detected that minor alleles of both MALAT1 rs619586 and rs1194338 were significantly associated with decreased CRC susceptibility in two stages.

Table 3 Association of MALAT1 variants with colorectal cancer risk in stage 2 and combined stage

Genotypes	Cases	Controls	OR (95% CI) ^a	P-value
rs619586				
Stage 2				
AA	454	442	1.00 (reference)	
AG	105	131	0.78 (0.58–1.04)	0.091
GG	7	15	0.45 (0.19–1.10)	0.081
G vs A			0.74 (0.57–0.95)	0.019
Pooled results				
AA	784	750	1.00 (reference)	
AG	170	213	0.76 (0.61–0.95)	0.019
GG	12	25	0.46 (0.23–0.90)	0.025
G vs A			0.73 (0.60–0.88)	0.001
rs1194338				
Stage 2				
CC	267	241	1.00 (reference)	
CA	235	263	0.80 (0.63–1.03)	0.088
AA	64	84	0.69 (0.48–0.99)	0.046
A vs C			0.81 (0.69–0.97)	0.021
Pooled results				
CC	461	405	1.00 (reference)	
CA	391	435	0.79 (0.65–0.95)	0.015
AA	114	148	0.68 (0.51–0.89)	0.006
A vs C			0.80 (0.70–0.92)	0.001

Notes: ^aAdjusted by age, gender, alcohol drinking and smoking status, and family history of cancer.

Increasing evidence shows that lncRNAs can be used as biomarkers for the prediction of susceptibility, prognosis, or as tumor therapeutic targets in human cancers.^{27–29} MALAT1, also known as NEAT2 (noncoding nuclear-enriched abundant transcript 2), was located at 11q13.1. Tripathi et al first identified that MALAT1 could regulate alternative splicing by modulating serine/arginine splicing factor phosphorylation.³⁰ It was also found to be involved in multiple types of physiological processes, such as alternative splicing, nuclear organization, epigenetic modulating of gene expression, and various pathological processes, ranging from diabetes complications to cancers.^{12,31–33} Functional investigations indicated that G allele of rs619586 could trigger higher expression of MALAT1 in multiple tissues, which might affect the physiological processes consequently.^{3,29} Function of MALAT1 rs1194338 was only studied in 71 CRC tissues samples; however, no statistically significant difference of MALAT1 expression between CC genotype and AA genotype was detected.⁶

Genetic variants in lncRNA MALAT1 have also been linked to various kinds of diseases. Li et al found rs1194338 was significantly associated with decreased CRC risk.²⁴ Wang et al identified that rs3200401 was associated with survival for advanced lung adenocarcinoma patients.²³ Peng et al showed that individuals with genotype AG of rs619586 have a decreased risk of breast cancer.²⁵ Additionally, Wang et al found that rs619586AG/GG genotypes might protect against the

occurrence of coronary atherosclerotic heart disease.³⁴ Li et al identified that MALAT1 rs619586 was significantly associated with lower risk of congenital heart disease.²⁰ Zhuo et al showed rs619586 was associated with a decreased risk of pulmonary arterial hypertension.²¹ All the above findings were consistent with our results, which showed rs619586 and rs1194338 were significantly associated with decreased CRC susceptibility.

Strengths and limitations

A relatively small sample size for the stratification and interaction analyses is the limitation of this study that should be pointed out. However, for the main effect, the statistical power for rs619586 was 88.2%, and the statistical power for rs1194338 was 91.1%. The strength of this study is that we used a two-stage investigation to validate the association between the genetic variants and CRC susceptibility.

Conclusion

Conclusively, the current findings indicate that genetic variants in lncRNA MALAT1 may influence the risk of CRC. However, since the exact mechanism and function of these gene variants have not yet been fully defined, the present findings need to be confirmed in further studies with other populations in order to clarify the association between these polymorphisms and the risk of CRC.

Disclosure

The authors report no conflicts of interest in this work.

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