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***Case Control Study***

**Molecular evaluation of glutathione S transferase family genes in patients with sporadic colorectal cancer**

Rodrigues-Fleming GH *et al.* Glutathione S transferase family genes in CRC

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# Abstract

# *AIM*

To evaluate the association of polymorphisms in glutathione S transferases (GSTs) in the risk of sporadic colorectal cancer (SCRC), tumor progression and survival of patients.

# *METHODS*

A case-control study was conducted in 970 individuals from the Brazilian population (232 individuals from the case group with colorectal cancer and 738 individuals from the control group without a history of cancer). PCR multiplex and PCR-RFLP techniques were used for genotyping of the polymorphisms. The tumor was classified according to TNM: tumor extension (T), affected lymph nodes (N), and presence of metastasis (M). logistic regression, multiple logistic regression and survival analysis were used to analyze the data. The results were presented in terms of odds ratio (OR) and 95% confidence interval (CI). The level of significance was set at 5% (*P* ≤ 0.05).

# *RESULTS*

Age equal to or over 62 years (OR = 8.79; 95%CI: 5.90-13.09, *P* < 0.01) and female gender (OR = 2.91; 95%CI: 1.74-4.37; *P* < 0.01) were associated with increased risk of SCRC. The analysis of the polymorphisms revealed an association between the *GSTM1* polymorphisms and risk of SCRC (OR = 1.45; 95%CI: 1.06-2.00; *P* = 0.02), as well as between *GSTT1* and reduced risk of the disease (OR = 0.65; 95%CI: 0.43-0.98; *P* = 0.04). An interaction between the presence of the wild-type allele of *GSTP1* Ile105Val polymorphism and tobacco consumption on risk of SCRC (OR = 2.33; 95%CI: 1.34-4.05; *P* = 0.05) was observed. There was an association between the *GSTM1* null genotype and the presence of advanced tumors (OR = 2.33; 95%CI: 1.23-4.41; *P* = 0.009), as well as increased risk of SCRC in the presence of a combination of *GSTT1* non- null/*GSTM1* null genotypes (OR = 1.50; 95%CI: 1.03-2.19; *P* = 0.03) and *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (OR = 1.85; 95%CI: 1.01-3.36, *P* = 0.04). Combined *GSTT1* non-null/*GSTM1* null genotypes (OR = 2.40; 95%CI: 1.19-4.85; *P* = 0.01) and *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (OR = 2.92; 95%CI: 1.05-8.12; *P* = 0.04) were associated with tumor progression. Polymorphisms were not associated with the survival of patients with SCRC.

# *CONCLUSION*

Individuals aged 62 years or older and of the female gender are more susceptible to SCRC. Polymorphisms of *GSTT1* and *GSTM1* null genotypes modulate the susceptibility to SCRC in the population studied.

**Key words:** Genetic polymorphisms; Colorectal neoplasms; Smoking; Alcohol; Glutathione S transferase

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**Core tip:** Sporadic colorectal cancer (SCRC) is the third most common cancer in the world and includes malignancies that occur in the colon and rectum. Age above 60 years, smoking, and alcohol habits are some of the risk factors for SCRC. Detoxification and elimination of carcinogens contained in tobacco and alcohol requires metabolic activation mediated by enzymes that metabolize the xenobiotic (XME). Polymorphisms in genes such as *GSTP1*, *GSTT1*, and *GSTM1* that encode enzymes involved in XMEs may be related to important processes of colorectal carcinogenesis.

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# INTRODUCTION

Colorectal cancer is the third most frequent cancer in the world[1] and the fifth most frequent type in Brazil[2]. Estimates for the year 2018 in Brazil are 17380 new cases for men and 18980 new cases for women[2].

Sporadic colorectal cancer (SCRC) develops from polyps (adenoma) in the colon and rectum walls, of varying sizes, and can turn into dysplasia, triggering the development of cancer[2-4].

SCRC is a multifactorial disease, influenced by genetic factors, such as mutations or polymorphisms in genes that participate in pathways responsible for regulating cell growth, including tumor suppressor genes and proto-oncogenes[5,6]. Other related factors are age, gender, environmental factors, and lifestyle habits such as smoking and alcohol habits[7]. Genetic factors may influence the effect of the environment on predisposition to the disease. Therefore, the incidence of SCRC varies among populations[1,8,9].

There are many genes encoding enzymes responsible for the xenobiotics metabolism, in which occurs detoxification of the organism. Some of the major genes involved in phase II are the cytosolic glutathione S transferase (GST) superfamily, including GST mi (*GSTM1*), theta (*GSTT1*), and pi (*GSTP1*)[10,11]. They catalyze the conjugation of structurally diﬀerent by-products of oxidative stress and xenobiotics to glutathione (GSH), which leads to eliminate toxic substances from the cells and protecting important cellular components like nucleic acids and proteins[12]. GST gene expression varies between different tissues and cell types[13].

In addition to being very common in the general population, the complete absence of GSTT1 and/or GSTM1 may alter their expression or the activity of the protein itself[14]. And in general, GSTP1 appears to be highly expressed in proliferating cells than in differentiated cells. In addition, many of the GSTs are overexpressed in various neoplastic cells and higher levels are observed in aggressive cancer cells[15]. The change in the GSTP1 gene also significantly alters the enzymatic activity[16,17], influencing in the detoxification of carcinogens, causing DNA damage, exerting an indirect effect on the risk of cancer development[18].

Therefore, the objectives of this study were to evaluate the association of epidemiological risk factors and these polymorphisms with the development of SCRC, the interaction between these polymorphisms with smoking and alcohol habits, and the association between the polymorphisms and clinical- histopathological parameters and survival among patients with SCRC.

# MATERIALs AND METHODS

## Approval and consent

The study was approved by the Ethics Committee-Medical School of Sao Jose do Rio Preto – FAMERP (no. 012/2012). The 970 individuals who agreed to participate in the study signed the consent form. The variables analyzed included gender, age, ethnicity, profession, smoking, alcohol, and personal and familial history of cancer.

## Study populations

The case group consisted of 232 (112 men and 120 women) patients from the Department of Coloproctology of the Base Hospital of Sao Jose do Rio Preto who received the clinical and/or histopathological diagnosis of SCRC between 2010 and 2016. The exclusion criterion was previous treatment with chemotherapy and/or radiotherapy. The control group included 738 (370 men and 368 women) blood donors from the Blood Center of Sao Jose do Rio Preto. The exclusion criterion for controls was personal and family history of cancer in at least three previous generations. Individuals who had smoked at least 100 cigarettes throughout their lives were considered smokers, and those who drank more than four servings of alcohol per week (one serving corresponds to 30 mL of liquor, a 102-mL glass of wine containing 12% alcohol, or a 340-mL can of beer) were considered alcohol consumers[19,20]. SCRC was classified according to TNM: tumor extension (T), affected lymph nodes (N), and presence of metastasis (M)[21].

## Molecular analysis

The analysis of the *GSTT1* and *GSTM1* polymorphisms was performed using the polymerase chain reaction (PCR) multiplex technique, with the *CYP1A1* gene as the internal positive control of amplification[22]. PCR products were analyzed on 1.5% agarose gel stained with red gel.

The analysis of this *GSTP1* A313G polymorphism was performed using the polymerase chain reaction-polymorphism restriction fragment chain reaction (PCR-RFLP) technique with primers described by Harries *et al*[23]. The 176 base pair (bp) PCR products were analyzed by electrophoresis in 1.5% agarose gel stained with red gel. The restriction enzyme digestion was performed using B*sma*I. The results and genotyping were performed after 2.0% agarose gel electrophoresis stained with red gel. The presence of 91 and 85 bp bands corresponds to the GG polymorphic genotype; the 176, 91, and 85 bp bands correspond to the heterozygous genotype AG; and the 176 bp band corresponds to the wild-type AA genotype.

## Statistical analysis

Descriptive statistics included mean values, standard deviation for continuous data, and percentage for categorical data. The Hardy-Weinberg equilibrium (HWE) was evaluated using the chi-square test through the BioEstat Program version 5.0. The binary logistic regression model, using the Minitab/Windows-Version 12.22 program, was used to evaluate the association of age, gender, smoking, and drinking habits with SCRC, as well as to evaluate the association of SCRC and clinical-histopathological parameters. Binary multiple logistic regression, adjusted for age, gender, and smoking and drinking habits, was used to evaluate the association between the genetic models of the polymorphisms and the development of SCRC using the SNPStats program (available at: <http://bioinfo.iconcologia.net/SNPstats_web).> The effect of the polymorphisms was evaluated in the models as (1) codominant (heterozygous versus wild-type homozygous and polymorphic homozygous versus wild-type homozygous); (2) dominant (heterozygous + polymorphic homozygous versus wild-type homozygous); (3) recessive (homozygous polymorphic versus wild- type homozygous + heterozygous); (4) overdominant (heterozygous versus wild-type homozygous + polymorphic homozygous); or (5) additive (polymorphic homozygous with 2 + heterozygous versus wild-type homozygous). The SNPStats program was used to evaluate the interaction between the polymorphisms and smoking habit, adjusted for age, gender, and alcohol consumption, as well as to evaluate the interaction between polymorphisms and alcohol consumption, adjusted for age, gender, and smoking, in the SCRC risk. The effect of the polymorphisms on the overall survival time of SCRC patients was analyzed using the Kaplan-Meier curve and log rank test using the StatsDirect version 2.7.2 program. The results were presented in terms of odds ratio (OR) and 95% confidence interval (CI). For all statistical analasys the level of significance was set at 5% (*P* < 0.05).

# RESULTS

# *Sociodemographic data*

Table 1 presents the demographic data of SCRC patients and controls. Age equal to or above 62 years (OR = 8.79; 95%CI: 5.90-13.09; *P* < 0.01) and female gender (OR = 2.91; 95%CI: 1.74-4.37; *P* < 0.01) were associated with risk of SCRC. The genotypic frequencies of *GSTP1* Ile105Val polymorphism were in HWE in both groups (Case: *P* = 1, Control: *P* = 0.29).

***Individual polymorphism analysis***

*GSTM1* null genotype carriers presented a higher risk of developing the disease (OR = 1.45; 95%CI: 1.06-2.00; *P* = 0.022). On the other hand, the *GSTT1* polymorphism was associated with a reduced risk of SCRC (OR = 0.65; 95%CI: 0.43-0.98; *P* = 0.037; Table 1).

In the present study, there was a significant interaction between the presence of the wild-type allele of the *GSTP1* Ile105Val polymorphism and smoking habit in the risk of SCRC (OR = 2.33; 95%CI: 1.34-4.05; *P* = 0.049). However, there was no interaction between the other polymorphisms and smoking or drinking habits in the risk of the disease (Table 2).

Regarding the clinical-histopathological parameters of the SCRC samples, the rectum was the most frequent primary site (60%), in addition to aggressive tumors (69.65%; Table 3). There was only association between the *GSTM1* null genotype and the presence of aggressive tumors (OR = 2.33, 95%CI: 1.23-4.41; *P* = 0.0087).

***Analysis of the combined polymorphisms***

An increased risk of SCRC was observed in the presence of the combination of the *GSTT1* non-null/*GSTM1* null genotypes (OR = 1.50; 95%CI: 1.03-2.19; *P* = 0.033) and the *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (\*with the presence of at least one polymorphic allele) (OR = 1.85; 95%CI: 1.01-3.36; *P* = 0.045). The combined *GSTT1* non-null/*GSTM1* null genotypes (OR = 2.40; 95%CI: 1.19-4.85; *P* = 0.015) and *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (OR = 2.92; 95%CI: 1.05-8.12; *P* = 0.040) were associated with tumor progression (Table 4).

***Survival analysis***

Kaplan-Meier curve analysis showed that the survival time of carriers of the polymorphic allele *GSTP1* Ile105Val, and the *GSTM1* and *GSTT1* null genotypes, were not significantly different from the survival time of non- carriers of these polymorphisms (Table 5).

# DISCUSSION

In the present study, it was observed that individuals with advanced age (≥ 62 years) are more susceptible to SCRC, which corroborates with the literature that considers old age to be an etiological factor for this tumor type[2,24]. In terms of gender, women are more susceptible to SCRC. Other studies have observed a similar proportion of genders among patients with SCRC and the control group[25-27]. It is possible to observe an increase in the number of cases among women due to the increase in cigarette and alcohol consumption[28,29]. It is important to note that the group of women with SCRC evaluated in this study had a mean age of 62 ± 13 years, which could suggest that the hormonal factor may contribute to SCRC. Some studies have associated postmenopausal state with the incidence of colorectal cancer in women[30-32]. In addition, hormone replacement therapy proved to be a protective factor for SCRC[33-36]. A meta-analysis associated protective effect of soy estrogen in women with SCRC and postmenopause[37].

Smoking and drinking habits were not associated with SCRC in the present study. On the other hand, Koh *et al*[38] observed a threefold increased risk of colorectal cancer among smokers compared to those who had never smoked. Some data on the risk of SCRC due to alcohol consumption are inconsistent, which can be explained by the variation in the amount of alcohol consumption analyzed in the different studies[39,40]. The analysis of HWE revealed that the *GSTP1* Ile105Val polymorphism was in equilibrium in both the case and control groups. This result was similar to that observed by other studies in SCRC[26,41]. Regarding the *GSTT1* and *GSTM1* polymorphisms, the HWE test was not possible because the molecular analysis did not distinguish wild-type homozygous and heterozygous individuals[25].

In the present study, the *GSTP1* gene polymorphism showed no association with SCRC, corroborating with other investigations in Bulgarian and Chinese populations[3,25,27,42]. However, one study in the Tunisian population observed a significant difference in the frequency of polymorphisms between case and control groups and was associated with the risk of SCRC[26]. A single study observed a reduced risk of SCRC in the presence of the *GSTP1* Ile105Val polymorphism; however, there are no consistent data to explain the biological relevance of this finding[16].

The *GSTP1* gene polymorphism results in alteration of the amino acid sequence of the protein and consequent reduction of enzymatic activity and inefficient detoxification[43]. However, although the *GSTP1* Ile105Val polymorphism was not associated with SCRC in this study, the level of expression of this gene may be an important factor, which is not dependent on this genetic change. A hepatocellular carcinoma (HCC) study found that increased *GSTP1* gene expression in vivo and in vitro resulted in reduced cell proliferation in tumor cells, inhibition of Akt phosphorylation, and cell cycle disruption in G1/S by increasing p21 and p27 cell cycle inhibitors[44]. High *GSTP1* expression was also associated with better prognosis in patients with HCC[44]. In addition, hypermethylation of *GSTP1* has been observed in several types of cancers, such as prostate, breast, lung, and liver cancers[45].

In relation to the *GSTT1* and *GSTM1* gene polymorphisms, the *GSTT1* null genotype was associated with a reduced risk of the development of SCRC, whereas the presence of the *GSTM1* null genotype was associated with increased risk of SCRC. The absence of some of the GST isoenzymes in normal colorectal mucosa resulting from null genotypes such as the presence of the *GSTM1* polymorphism may alter the major detoxification function of GSTs in the metabolism of xenobiotics[4]. In Chinese and Iranian populations, an increased risk of SCRC in the presence of *GSTT1* and *GSTM1* null genotypes was shown[25,46]*.* On the other hand, other studies did not find an association between *GSTT1* and *GSTM1* null genotypes with SCRC[3,26,16,46-49]. In their case control study, Vlaykova *et al*[4] found no association between *GSTM1* null genotype and risk of SCRC, but the *GSTT1* null genotype was associated with increased risk of SCRC. These different results may be related to the time of exposure to environmental factors and the population heterogeneity.

It has been observed that the effect of GST polymorphisms, when combined, may increase the risk of SCRC two- or threefold[41]. The present study demonstrated that combinations of *GSTT1* non-null/*GSTM1* null genotypes and *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (presence of at least one polymorphic allele) are associated with increased risk of SCRC and tumor progression. These findings corroborate the results of individual analyses of polymorphisms, which suggest the influence of the *GSTT1* non-null genotype on SCRC because the null genotype was associated with reduced risk of the disease.

In the Indian population, an association between the *GSTM1* null/*GSTT1* null genotypes and the combination of *GSTM1* null/*GSTT1* null/*GSTP1* Val\* and the risk of SCRC was observed[41]. This result was also observed in a study by Vlaykova *et al*[4] in the Bulgarian population. A study in the Turkish population found an association between the *GSTT1* null/*GSTM1* non-null genotypes and *GSTT1* null/*GSTM1* non-null/*GSTP1* Ile (wild-type homozygote) and SCRC[3]. Cong *et al*[25] observed an increased risk in the presence of *GSTT1*/*GSTM1* genotypes, whereas the combination of *GSTT1* non- null/*GSTM1* null genotypes resulted in a significant reduced risk of SCRC, differing from the findings of this and other studies. On the other hand, other studies that analyzed the effect of the combined genotypes *GSTT1*/*GSTM1* did not find an association with the risk of SCRC[26,47,48]. Several studies have evaluated the potential association between SCRC and the combined genotypes of these polymorphisms. The observed results vary, evidencing the importance of studying the effects of the genotypic combination in SCRC.

In the present study, a significant interaction between the presence of the wild-type allele of *GSTP1* Ile105Val polymorphism and smoking habit in the risk of SCRC was evidenced. Differing from the results of the present study, a study in the Chinese population found no interaction between the *GSTP1* Ile105Val and smoking habit or drinking habit in the risk of SCRC[38]. The literature is sparse in terms of studies evaluating the interaction of risk factors with the *GSTP1* Ile105Val polymorphism in the development of SCRC. The biological relevance of this finding is unclear because the presence of at least one polymorphic allele of the *GSTP1* gene combined with the nullity of *GSTM1* and the presence of the *GSTT1* allele were associated with increased risk of SCRC. In addition, smoking habit was not associated with this tumor type in the present study.

For the *GSTT1* and *GSTM1* polymorphisms, this study did not show interaction with smoking or drinking habits in the risk of SCRC. These results corroborate with two other studies in Korean and Japanese populations that also did not find these interactions[46,48]. Analyzing the interaction between drinking habit and the *GSTT1* and *GSTM1* null genotypes for the risk of SCRC, the study by Piao *et al*[49] did not show this relationship. However, a study in Singapore found an increased risk for smokers carrying at least two null genotypes that cause low enzyme activity[38].

The controversial results regarding the polymorphisms may suggest that other genes involved in the metabolism of xenobiotics may be more relevant for the development of SCRC, such as polymorphisms in genes acting on phase I xenobiotic metabolism[27,50]. Although the polymorphisms studied change in order to reduce or eliminate the enzymatic activity, other genes can act, compensating for the detoxification of the substances present in tobacco and alcohol.

Regarding the clinical-histopathological parameters of SCRC, some studies have been showed that low activity GST genotypes can be associated with more aggressive tumour and survival in colorectal cancer patients[51,52]. It is possible to observe an association between the *GSTM1* null genotype and the presence of advanced tumors. One study demonstrated an association between aggressive tumors with the presence of the *GSTT1* null genotype[47]. However, other studies that evaluated the same polymorphisms did not find an association between the polymorphic genotypes and the clinical- histopathological parameters of SCRC[3,27,42,49].

This biological relationship between GST and progression is still not well described. But the possible explanation would because GSTs have play important roles in regulation of genes related with activating cellular maintenance, proliferation and apoptosis evasion. Thus, GSTs plays interacting with TNF receptor associated factor 2 (TRAF2) and decreasing signal transduction from receptors in the tumour necrosis factor alpha-like (TNF-α) and c-Jun NH2-terminal kinase (JNK kinase) pathways[53-55].

When investigating the association between polymorphisms and the primary sites of SCRC, no association was evidenced. Corroborating these findings, a study by Vlaykova *et al*[4] did not correlate polymorphisms of *GSTT1* and *GSTM1* null genotypes with the primary site. However, Wang *et al[*41], observed increased risk of rectal cancer in the presence of the *GSTM1* null genotype, while the *GSTT1* null genotype was associated with the risk of colon cancer.

It is worth noting that predisposition to SCRC is multifactorial and results from the interaction between allelic variants of low-penetrance genes and environmental factors such as advanced age, eating habits, and smoking and drinking habits[3,56,57]. Therefore, the findings regarding the modulation of susceptibility to SCRC in the presence of the polymorphisms analyzed, regardless of smoking or drinking habit, reinforces the influence of these polymorphisms on the etiology of SCRC, even though they do not influence patient survival. These results may contribute to the understanding of the mechanisms involved in colorectal carcinogenesis.

In conclusion, individuals with advanced age and of the female gender are more susceptible to SCRC. The presence of the *GSTM1* null genotype is associated with increased risk of SCRC. The *GSTM1* null genotype is associated with the tumor progression. The combination of *GSTT1*/*GSTM1* and *GSTT1*/*GSTM1*/*GSTP1* genotypes are associated with increased risk of SCRC and tumor progression. Polymorphisms are not associated with the overall survival rate of SCRC patients.

**Article Highlights**

***Research background***

Colorectal cancer is the third most common cancer in the world and develops on the inner walls of the colon and rectum. Genetic and environmental factors may increase the risk of colorectal cancer through the metabolism of carcinogens. Therefore, the evaluation of polymorphisms in genes involved in this process may help to modulate the development of colorectal cancer. Polymorphisms in genes encoding GSTP1, GSTT1, and GSTM1 may alter enzymatic activity. This change can lead to DNA damage and deregulation of the mechanisms involved in colorectal cancer.

***Research motivation***

Polymorphisms in the coding genes *GSTP1*, *GSTT1*, and *GSTM1* have been studied in terms of susceptibility to diseases such as cancer. However, the literature presents conflicting results. Therefore, several studies are needed to assess and confirm the real role among factors that influence changes in metabolic processes related to colorectal cancer.

***Research objectives***

The main objective of this study was to evaluate the influence of polymorphisms in the *GSTP1*, *GSTT1* and *GSTM1* genes on the risk for colorectal cancer. The data showed that carriers of polymorphisms in the *GSTM1* genes and the combination of *GSTT1* non-null/*GSTM1* null genotypes and *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (\*with the presence of at least one polymorphic allele) constitute a risk group for sporadic colorectal cancer (SCRC), and polymorphisms in the *GSTM1* gene and the *GSTT1* non-null/*GSTM1* null combinations, *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* increase the aggressiveness of the tumor. Thus, considering the high incidence of this cancer, it is important to understand the factors that lead to carcinogenesis for the development of preventive and therapeutic strategies for the management of cancer.

***Research methods***

This case-control study evaluated 970 individuals, 232 case and 738 control, through multiplex polymerase chain reaction (PCR) and polymerase chain reaction-restriction fragment chain reaction (PCR-RFLP) polymorphism, Demographics were tabulated by percentage. The binary logistic regression model was used to evaluate the association of age, gender, smoking and eating habits with SCRC, as well as to evaluate the association of Hardy-Weinberg (HWE) with the Chi-square test. The multiple binary logistic regression, adjusted for age, gender and smoking and alcohol habits, was also used to evaluate the association between the genetic models of the polymorphisms and the development of the SCRC. the dominant genotypic model to assess the interaction of polymorphisms and smoking habits, adjusted for age, gender, and ethnicity, as well as to evaluate the interaction of polymorphism and alcoholic habit, adjusted for age, gender and smoking, on the risk of SCRC. And Kapla-Meier was used to assess the overall survival of patients with SCRC.

***Research results***

The data showed that carriers of polymorphisms in the *GSTM1* genes and the combination of *GSTT1* non-null/*GSTM1* null genotypes and *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* (\*with the presence of at least one polymorphic allele) constitute a risk group for SCRC, and polymorphisms in the *GSTM1* gene and the *GSTT1* non-null/*GSTM1* null combinations, *GSTT1* non-null/*GSTM1* null/*GSTP1* Val\* increase the aggressiveness of the tumor. Thus, considering the high incidence of this cancer, it is important to understand the factors that lead to carcinogenesis for the development of preventive and therapeutic strategies for the management of cancer.

***Research conclusions***

A similar study was not previously performed in the Brazilian population. Therefore, it is unprecedented in this studied population. In addition, we emphasize the importance of the association of the female gender and the susceptibility to SCRC as well as the survival analysis associated to the polymorphisms studied, which is not well explored in the literature. Polymorphisms in the *GSTP1*, *GSTT1* and *GSTM1* genes were involved in carcinogenesis and poor proginostic of SCRC. In the brazilian population we could observe that individuals with advanced age and of the female gender are more susceptible to SCRC. The presence of the *GSTM1* null genotype, the combination of *GSTT1*/*GSTM1* and *GSTT1*/*GSTM1*/*GSTP1* genotypes are associated with increased risk of SCRC and tumor progression.

This study provides a perspective on biomarkers of GSTs related to the prognosis of SCRC that has not been extensively studied in others population, especially in Brazilian population. These data may contribute to clinical practice. Another interesting fact was the association of individuals of the female gender, aged over 60 years with the risk for SCRC, in which the association of menopausal women (estrogen reduction) was shown to be more susceptible in SCRC. Polymorphisms in the genes involved in xenobiotic metabolism pathway can be associated with development and poor proginostic of SCRC

In this study, statistical analysis was widely used, unlike other studies, using multiple logistic regression, to evaluated the interactions between polymorphisms studied and variables. As well as survival analysis using the Kaplan Meyer test. Such data analyzes are extremely relevant in studies involving population genetic polymorphisms.

It was possible to observe an association between the some polymorphisms of xenobiotic metabolism and development and tumor progression of SCRC. Advanced age and female gender was associated with development of SCRC and polymorphisms in the genes involved in xenobiotic metabolism pathway was associated with development and poor proginostic of SCRC. This study may contribute as a diagnostic and prognostic biomarker for SCRC. These data associated with other studies may contribute to the development of strategies against SCRC.

***Research perspectives***

This study showed us the importance of population studies with a larger sample when studies were carried out with polymorphisms. Thus, we intend to expand the sample number to better validate the results and further include more polymorphisms related to the xenobiotics pathways in order to better understand this pathway as an important factor in carcinogenesis of the SCRC. These methods are suitable for research, however methods such as real-time PCR, can be an important tool to accurately quantify the presence of polymorphisms studied.

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**Table 1 Sociodemographic characteristics, risk factors, and polymorphisms**

***GSTT1*, *GSTM1*, *GSTP1* A313G in patients with colorectal cancer and controls *n* (%)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variables** |  | **Case (*n* = 232)** | **Control (*n* = 738)** | **OR1** |
|  |  |  |  | **(95%CI)** |
| Gender |  |  |  |  |
| Female |  | 120 (52) | 368 (50) | 1.00 |
| Male |  | 112 (48) | 370 (50) | 2.91 (1.94-4.37)a |
| Age [(Mean) ± SD] |  | (62) ± 12 | (48) ±12 |  |
| < 62 |  | 112 (49) | 621 (84) | 1.00 |
| ≥ 62 |  | 120 (51) | 117 (16) | 8.79 (5.90-13.09)a |
| Smoking Habit |  |  |  |  |
| Non-smoke |  | 130 (56) | 465 (63) | 1.00 |
| Smoke |  | 102 (44) | 273 (37) | 1.45 (0.98-2.14) |
| Alcoholic Habit |  |  |  |  |
| Non-alcoholic |  | 132 (57) | 395 (54) | 1.00 |
| Alcoholic |  | 100 (43) | 343 (46) | 1.28 (0.85-1.91) |
| *GSTP1* |  |  |  |  |
| Codominant | A/A | 227 (43.7) | 107 (46.1) | 1.00 |
|  | A/G | 224 (43.2) | 102 (44) | 1.06 (0.73-1.54) |
|  | G/G | 68 (13.1) | 23 (9.9) | 0.88 (0.48-1.59) |
| Dominant | A/A | 227 (43.7) | 107 (46.1) | 1.00 |
|  | A/G-G/G | 292 (56.3) | 125 (53.9) | 1.02 (0.71-1.45) |
| Recessive | A/A-A/G | 451 (86.9) | 209 (90.1) | 1.00 |
|  | G/G | 68 (13.1) | 23 (9.9) | 0.85 (0.48-1.50) |
| Overdominant | A/A-G/G | 295 (56.8) | 130 (56) | 1.00 |
|  | A/G | 224 (43.2) | 102 (44) | 1.09 (0.76-1.55) |
| Additive |  | --- | --- | 0.97 (0.75-1.27) |
| *GSTT1* |  |  |  |  |
|  | +/+ | 573 (77.6) | 192 (82.8) | 1.00 |
|  | 0/0 | 165 (22.4) | 40 (17.2) | 0.65 (0.43-0.98)a |
| *GSTM1* |  |  |  |  |
|  | +/+ | 385 (52.2) | 100 (43.1) | 1.00 |
|  | 0/0 | 353 (47.8) | 132 (56.9) | 1.45 (1.06-2.00)a |

1OR adjusted for age, gender, and alcohol and smoking habits and polymorphisms; a*P* < 0.05 *vs* control. OR: Odds Ratio.

**Table 2 Interaction between polymorphisms in the genes *GSTP1*, *GSTT1,* and *GSTM1* and smoking or alcoholic habit in the risk of** **sporadic colorectal cancer**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Tobacco consumption** | | | | | | |
| **Non-smoker** | | | **Smoker** | | | |
|  | **Case** | **Control** | **OR1 (95%CI)** | **Case** | | **Control** | **OR1 (95%CI)** |
| *GSTP1* |  |  |  | |  |  |  |
| A/A | 50 | 136 | 1,00 | | 57 | 91 | 2.33 (1.34-4.05)a |
| A/G-G/G | 80 | 177 | 1.40 (0.87-2.27) | | 45 | 115 | 1.59 (0.91-2.77) |
| *GSTT1* |  |  |  | |  |  |  |
| +/+ | 110 | 362 | 1,00 | | 82 | 211 | 1.42 (0.98-2.08) |
| 0/0 | 20 | 103 | 0.60 (0.34-1.04) | | 20 | 62 | 1.03 (0.57-1.88) |
| *GSTM1* |  |  |  | |  |  |  |
| +/+ | 52 | 231 | 1.00 | | 48 | 154 | 1.40 (0.86-2.28) |
| 0/0 | 78 | 234 | 1.38 (0.90-2.10) | | 54 | 119 | 2.19 (1.34-3.57) |
|  | **Alcohol consumption** | | | | | | |
|  | **Non-drinker** | | | | **Drinker** | | |
|  | **Case** | **Control** | **OR1 (95%CI)** | | **Case** | **Control** | **OR1 (95%CI)** |
| *GSTP1* |  |  |  | |  |  |  |
| A/A | 59 | 116 | 1,00 | | 48 | 111 | 1.31 (0.74-2.31) |
| A/G-G/G | 73 | 147 | 1.12 (0.69-1.81) | | 52 | 145 | 1.19 (0.70-2.04) |
| *GSTT1* |  |  |  | |  |  |  |
| +/+ | 108 | 300 | 1.00 | | 84 | 273 | 0.76 (0.52-1.12) |
| 0/0 | 24 | 95 | 0.63 (0.37-1.07) | | 16 | 70 | 0.53 (0.28-1.01) |
| *GSTM1* |  |  |  | |  |  |  |
| +/+ | 56 | 206 | 1.00 | | 44 | 179 | 0.76 (0.46-1.26) |
| 0/0 | 76 | 189 | 1.42 (0.93-2.18) | | 56 | 164 | 1.14 (0.72-1.82) |
|  |  |  |  | |  |  |  |

1OR adjusted for age, gender, and alcohol and smoking habits and polymorphisms; a*P* < 0.05 *vs* control. OR: Odds Ratio.

**Table 3 Distribution of the clinical-histopathological parameters in relation to the polymorphisms in the genes *GSTP1*, *GSTT1,* and *GSTM1* in patients with colorectal cancer *n* (%)**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Tumor progression (TNM) (*n* = 201)** | | | |  | **Primary site** | | | |
| **Models** | **Genotypes** | **Non- advanced** | **Advanced** | **OR1** | **95%CI** |  | **Colon** | **Rectum** | **OR1** | **95%CI** |
|  |  | **61 (31)** | **140 (69)** |  |  |  |  |  |  |  |
| *GSTP1* |  |  |  |  |  |  |  |  |  |  |
| Codominant | A/A | 31 (51) | 62 (44) | 1.00 |  |  | 42 (46) | 65 (46) | 1.00 |  |
|  | A/G | 23 (38) | 65 (47) | 1.37 | (0.70-2.66) |  | 38 (41) | 64 (45) | 0.96 | (0.54-1.72) |
|  | G/G | 6 (10) | 11 (8) | 1.14 | (0.37-3.50) |  | 11 (12) | 12 (8) | 0.73 | (0.29-1.85) |
| Dominant | A/A | 31 (51) | 62 (44) | 1.00 |  |  | 42 (46) | 65 (46) | 1.00 |  |
|  | A/G-G/G | 29 (48) | 76 (55) | 1.32 | (0.71-2.48) |  | 49 (53) | 76 (53) | 0.91 | (0.53-1.57) |
| Recessive | A/A-A/G | 54 (90) | 127 (92) | 1.00 |  |  | 80 (87) | 129 (91) | 1.00 |  |
|  | G/G | 6 (10) | 11 (8) | 1.00 | (0.34-2.95) |  | 11 (12) | 12 (8) | 0.74 | (0.31-1.81) |
| Overdominant | A/A-G/G | 37 (61) | 73 (52) | 1.00 |  |  | 53 (58) | 77 (54) | 1.00 |  |
|  | A/G | 23 (38) | 65 (47) | 1.34 | (0.70-2.56) |  | 38 (41) | 64 (45) | 1.02 | (0.59-1.77) |
| Aditivo | - | - | - | 1.18 | (0.73-1.92) |  | - | - | 0.89 | (0.59-1.34) |
| *GSTT1* |  |  |  |  |  |  |  |  |  |  |
|  | +/+ | 47 (78) | 47 (78) | 1.00 |  |  | 78 (85) | 114 (80) | 1.00 |  |
|  | 0/0 | 13 (22) | 20 (14) | 0.57 | (0.26-1.27) |  | 13 (14) | 27 (19) | 1.47 | (0.71-3.06) |
| *GSTM1* |  |  |  |  |  |  |  |  |  |  |
|  | +/+ | 34 (56) | 53 (38) | 1.00 |  |  | 45 (49.5) | 55 (39) | 1.00 |  |
|  | 0/0 | 26 (43) | 85 (61) | 2.33 | (1.23-4.41)a |  | 46 (50.5) | 86 (61) | 1.49 | (0.87-2.57) |

1OR adjusted for age, gender, and alcohol and smoking habits and polymorphisms; a*P* < 0.05 *vs* control. OR: Odds ratio.

**Table 4** **Association of the double combined *GSTT1*/*GSTM* genotypes and triple combined *GSTT1*/*GSTM*/*GSTP1*, colorectal cancer, tumor progression, and primary site, adjusted for gender, age, smoking, and alcohol consumption**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | | **Colorectal Cancer** | | | |  | **Tumor progression (TNM) (*n* = 198)** | | | |  | **Primary site** | | | |
| **Double combination of genotypes** | | | **Case**  **(*n* = 19)** | **Control**  **(*n* = 738)** | **OR1** | **95%CI** |  | **Non- advanced (*n* = 60)** | **Advanced (*n* = 138)** | **OR1** | **95%CI** |  | **Colon**  **(*n* = 81)** | **Rectum**  **(*n* = 117)** | **OR1** | **95%CI** |
| *GSTT1* | GTM1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| (+) | (+) |  | 68 | 303 | 1 |  |  | 26 | 42 | 1 |  |  | 34 | 34 | 1 |  |
| (+) | (-) |  | 97 | 270 | 1.50 | (1.03-2.19)a |  | 21 | 76 | 2.40 | (1.19-4.85)a |  | 36 | 61 | 1.67 | (0.88-3.18) |
| (-) | (+) |  | 19 | 82 | 1.00 | (0.55-1.84) |  | 8 | 11 | 0.74 | (0.26-2.15) |  | 7 | 12 | 1.70 | (0.59-4.94) |
| (-) | (-) |  | 14 | 83 | 0.61 | (0.32-1.19) |  | 5 | 9 | 1.20 | (0.35-4.10) |  | 4 | 10 | 2.60 | (0.72-9.46) |
| **Triple combination of genotypes** | | | **Case**  **(*n* = 19)** | **Control**  **(*n* = 519)** | **OR1** | **95%CI** |  | **Non- advanced (*n* = 60)** | **Advanced (*n* = 138)** | **OR1** | **95%CI** |  | **Colon**  **(*n* = 81)** | **Rectum**  **(*n* = 117)** | **OR1** | **95%CI** |
| *GSTT1* | *GSTM1* | *GSTP1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| (+) | (+) | Ile/Ile | 32 | 96 | 1 |  |  | 12 | 20 | 1 |  |  | 16 | 10 | 1 |  |
| (+) | (+) | Val\* | 36 | 126 | 1.13 | (0.61-2.10) |  | 14 | 22 | 0.93 | (0.34-2.56) |  | 12 | 17 | 1.81 | (0.67-4.92) |
| (-) | (+) | Ile/Ile | 10 | 22 | 1.45 | (0.56-3.77) |  | 5 | 5 | 0.50 | (0.12-2.18) |  | 18 | 22 | 1.41 | (0.33-5.98) |
| (-) | (+) | Val\* | 9 | 34 | 0.90 | (0.36-2.25) |  | 3 | 6 | 1.07 | (0.21-5.31) |  | 2 | 7 | 4.57 | (0.80-26.24) |
| (+) | (-) | Ile/Ile | 42 | 86 | 1.52 | (0.81-2.83) |  | 8 | 22 | 1.78 | (0.65-4.86) |  | 11 | 19 | 2.58 | (0.99-6.75) |
| (+) | (-) | Val\* | 55 | 98 | 1.85 | (1.01-3.36)a |  | 10 | 42 | 2.92 | (1.05-8.12)a |  | 19 | 33 | 2.06 | (0.83-5.15) |
| (-) | (-) | Ile/Ile | 9 | 23 | 1.27 | (0.48-3.40) |  | 3 | 5 | 1.25 | (0.25-6.19) |  | 1 | 7 | 5.47 | (0.92-32.60) |
| (-) | (-) | Val\* | 5 | 34 | 1.27 | (0.11-1.08) |  | 1 | 3 | 1.01 | (0.14-7.42) |  | 2 | 2 | 1.88 | (0.27-13.33) |

1OR adjusted for age, gender, and alcohol and smoking habits and polymorphisms; a*P* < 0.05 *vs* control; \*Ile/Val ou Val / Ile. OR: Odds Ratio.

**Table 5 Polymorphisms *GSTT1*, *GSTM1*, and *GSTP1* in relation to overall survival of colorectal cancer patients**

|  |  |
| --- | --- |
| **Polymorphisms** | **Survival**  **(5 yr)** |
| *GSTT1* |  |
| Positive | 64 |
| Negative | 68 |
| *GSTM1* |  |
| Positive | 67 |
| Negative | 63 |
| *GSTP1* A313G |  |
| AA | 61 |
| AG | 70 |
| GG | 63 |

a*P* < 0.05 *vs* control.