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The Association Between Pri-Mir-34b/Crs4938723 Polymorphism and Risk of Hepatocellular Carcinoma in Egyptian Patients

Alyaa A. Abdelwahed [a], Naglaa A. A. Allam [a], Asmaa I. E. Gomaa [a], Sameera E. Aboelkheir [b], Heba S. M. Ghanem [c], Nehal H. Ibrahim [d,*]

[a] Department of Hepatology and Gastroenterology, National Liver Institute, Menoufia University, Menoufia, Egypt
[b] Department of Public Health Epidemiology and Preventive Medicine, National Liver Institute, Menoufia University, Menoufia, Egypt
[c] Department of Clinical Pathology, National Liver Institute, Menoufia University, Menoufia, Egypt
[d] Department of Hepatology and Gastroenterology, Sheheen El Qanater Hospital, Al-Qalyubia, Egypt

Abstract

Background: ***Hepatocellular carcinoma (HCC) is responsible for the fourth-highest mortality rate for both males and females.***

Aim of the work: To gain a better understanding of the relationship between the pri-miR-34b/crs4938723 genetic variation and the risk of stomach cancer in Egyptian people.

Patients and methods: ***This case control study, conducted on 100 patients attended the inpatient unit and the outpatient clinics of the Hepatology department, National Liver Institute and 100 healthy volunteers age, and gender matched enrolled as a control group.***

Results: ***The HCC group had a higher frequency of the variant C allele of the pri-miR-34b/c rs4938723 SNP than the healthy control group (p=0.015). Similar results were found for the genotypic distribution (p=0.041) and recessive genetic model (p=0.032). Different genotypes had significantly different focal lesion sizes and multiplicity. A small percentage of CC, TC, and TT genotype patients had focal lesion symptoms. Despite this, 66.7% of CC genotype patients, 43.1% of TC genotype patients, and 17.9% of TT genotype patients had small focal lesions (P 0.002). Patients with one focal lesion were 33.3% for the CC genotype, 49.0% for the TC genotype, and 78.6% for the TT genotype, while those with two or more lesions were 66.7%, 51.0%, and 21.4%, respectively (P 0.004).***

Conclusions: ***pr-miR-34b/crs4938723 hydrogel. The TT genotype has the potential to be a non-invasive diagnostic tool for predicting the development of HCC in the Egyptian population.***

Keywords: pri-miR-34b/crs4938723; polymorphism; Hepatocellular Carcinoma

1. Introduction

Of all the cancers in the world, hepatocellular carcinoma (HCC) ranks fourth in terms of mortality rate among both men and women.[1] Hormonal cell carcinoma (HCC) can develop due to a variety of environmental and lifestyle factors. Dietary deficits, aflatoxin exposure in food, chronic alcohol consumption, hepatitis C and B virus infections, and other similar conditions. [2]

Comparing individuals exposed to the same environmental and lifestyle risk factors for HCC reveals that susceptibility to the disease varies significantly.[3] Multiple genes have been found to play a role in the development and progression of HCC. These genes include interleukin-28B, let-7 family, glucose-6-phosphate isomerase, Glutathione S-Transferase Omega, P2X purinoceptor 7, miR-196a2 C > T, and miR-499 A > G. [4]

The 22-nucleotide noncoding RNA molecules called microRNAs (miRNAs) play a significant role in embryonic development, cell differentiation, and cancer, among other critical biological processes.[5]

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* Corresponding author at: Hepatology and Gastroenterology, Sheheen El Qanater Hospital, Al-Qalyubia, Egypt.
E-mail address: dr.nehalhamdi@gmail.com (N. H. Ibrahim).

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By controlling the production of oncogenes and tumor suppressors, several microRNAs are recognized to play a role in carcinogenesis.[6] As an example, microRNA-34 (miR-34) is a gene that P53 directly targets downstream. The expression and characteristics of miRNAs, as well as their cancer regulatory effects, can be affected by single-nucleotide polymorphisms (SNPs).[7] Apoptotic cycle and pathways in cells downstream of miR-34 are influenced by P53-mediated regulation, which alters miR-34, which in turn influences cancer pathogenesis and progression. Some recent research has shown that methylation of the CpG island can prevent p53 from regulating miR-34b/c, which in turn causes cell proliferation and, ultimately, cancer. Pri-miR-34b/c single-nucleotide polymorphisms (SNPs) may affect cancer risk in individuals by changing their expression.[8]

An essential function of microRNAs (miRNAs) in post-transcriptional gene regulation is their size and noncoding nature. Incorrect levels of microRNAs can cause degradation or inhibition of messenger RNA translation. The link between miRNA dysregulation and cancer and other human disorders is becoming increasingly apparent. The miR-34s, which include miR-34a, miR-34b, and miR-34c, have been the primary focus of studies investigating the tumor-suppressor effects of microRNAs. In this review, we will look at the main gene networks and signaling pathways regulated by miR-34s in various cancers, with an emphasis on their critical role as tumor suppressors.[9]

Examining the potential link between the pri-miR-34b/crs4938723 polymorphism and HCC risk in Egyptian patients was the primary objective of this study.

2. Patients and methods

This case control study was conducted on 100 patients who attended the inpatient unit and the outpatient clinics of the Hepatology department, National Liver Institute, and 100 age- and gender-matched healthy volunteers who were enrolled as a control group. All patients had signed a written informed consent. The study was approved by the local ethical Committee (IRP: 00681/2025).

Inclusion criteria: People of either sex who are 18 years old or older who have been diagnosed with HCC. The diagnosis of hepatocellular carcinoma (HCC) was established after an abdominal ultrasound revealed a hepatic focal lesion, which was later confirmed by CT or MRI scans.

Exclusion criteria: Patients with other malignancies and patients with uncontrolled cardiac, renal, or other chronic diseases, e.g., diabetes mellitus and hypertension.

Study Groups:

Group I: We used triphasic CT with contrast (demonstrating arterial enhancement and delayed venous washout) or MRI to identify HCC in 100 individuals at random.

Group II: One hundred apparently healthy people served as a control group. Those in the control group did not have a history of hepatic illness, hepatocellular carcinoma (HCC), diabetes, hypertension, or any other related conditions.

All patients were subjected to the following: Laboratory tests included a full blood count, liver profiles including serum transaminases (ALT and AST), liver function tests (serum albumin and serum bilirubin), prothrombin time, concentration with international normalize ratio, hepatitis markers (HCV Ab, HBs Ag), kidney function tests (blood urea and serum creatinine), and blood sugar analysis, accompanied by a thorough history taking and physical examination. Tests for serum AFP and imaging

DNA Extraction: DNA was extracted from whole blood samples by using Invitrogen DNA Blood Mini Kit (Pure Link ® 96 Genomic DNA Kit (K1821-04) as recommended by the manufacturer.

The tube contains purified genomic DNA and the extracted DNA was stored at -20°C until pri-miR-34b/c SNP genotyping by PCR.

TaqMan SNP Genotyping assay: Using a Rotor-Gene Q Real Time PCR System (Germany), the pri-miR-34b/c rs4938723 SNP was genotyped.

Principle of the procedure: The TaqMan assay employs sequence-specific oligonucleotides that contain a quencher and a fluorophore. The annealing stage is the process by which primers bind to the target sequence in a polymerase chain reaction (PCR). The reaction contains two TaqMan probes, one for each of the possible alleles (C or T), as the primer is extended by the Taq DNA polymerase. Upon reaching the TaqMan probe, the probe is physically separated from the quencher due to the 5'—3' exonuclease activity. The fluorescence intensity and the Rn values measured from the released fluorophore can be used to determine the alleles present in a sample.

Assay procedures and interpretation of results: Here are the materials you'll need for PCR cycling: In the first step, known as "pre-reading the plate," the background fluorescence is recorded. After that, the AB standard PCR protocol is followed, which includes a 10-minute run at 95°C, a 15-second run at 95°C, and an extra 1-minute extension at 60°C. The amplification step is repeated for 40 cycles. When PCR is finished, the next step is to

perform a post-read. Allelic discrimination analysis for PCR plates was performed: A scatter plot showing the results of the Allelic Discrimination Run compared to Allele 2 is shown by the software of the real-time PCR instrument. The plot was made up of 96-well reaction plates, with each point representing a well in the plate. Automatic or manual allele calls were employed. The program used pre- and post-experiment measurements of fluorescent levels to determine the normalized dye fluorescence (Δ Rn) for Allele1 (wild-type) or Allele2 (mutant) in relation to the cycle number. The program figures out if the person is homozygous (CC), heterozygous (TT), or CC automatically using this value, which is a relative count of the possible outcomes (TT).

Statistical analysis

An analysis of the results was conducted using SPSS 22.0, a statistical tool for the social sciences developed by IBM/SPSS Inc. of Chicago, IL .[10]

Mean (X), standard deviation (SD), median (Med), and interquartile range (IQR) are some of the ways quantitative data can be summarized using the estimates provided. For qualitative data, we offer counts and percentages. Median and range or IQ were used to represent data that did not adhere to a normal distribution, while mean ± SD was used for data that did adhere to a normal distribution. John Payne's work on the chi-square (x2) test allows for the comparison of one qualitative variable across various groups. Since we did not adhere to the assumption that 80% of the anticipated frequencies are greater than five, we opted for Fisher's Exact Test over the Chi-square (x2) test. A non-parametric Mann-Whitney test, comparable to Student's test, can be used if comparing two sets of skewed data reveals a violation of normalcy. A one-way analysis of variance test was used to examine continuous data for statistical significance when there were more than two normally distributed groups. After making sure the groups and variances followed normal distributions, the researchers used Shapiro-Wilk, Kolmogorov-Smirnov, and Levine's tests to confirm it. In cases where the assumptions of analysis of variance (ANOVA) were not satisfied or when comparing more than two groups of continuous skewed data, the non-parametric Kruskal-Wallis test was used instead. To handle multiple pairwise comparisons that occurred when a significant Kruskal-Wallis or Pearson chi-square test was run to find out which groups were significantly different, the Dunn-Sidak post hoc test was employed. Analysis using binary logistic regression: (unrelated factors). In order to evaluate the risk of HCC when smoking was taken into account, which was found to be a possible risk factor in univariable analysis, multivariable logistic regression analysis was performed.

3. Results

A total of two hundred patients who visited the hepatology and gastrointestinal clinics or inpatient unit at the National Liver Institute at Menoufia University were the subjects of this case control study. The research participants were split into two groups:

Group I: One hundred patients with HCC were chosen at random. Supposedly healthy 100 people serve as a control group in Group II.

With p-values of 0.711 for age and 0.243 for gender, there was no discernible difference between the healthy control group and those with HCC. But smoking separated the two groups significantly (P=0.023). Table 1

Table 1. Socio-demographic data of HCC patients and healthy controls

PARAMETERS	HCC PATIENTS (N= 100)	HEALTHY CONTROLS (N= 100)	TEST STATISTICS	P-VALUE
AGE (YEAR)			z= 0.37 [a]	0.711 [NS]
MEAN ± SD	58.54 ± 5.35	58.07 ± 4.66		
MEDIAN (IQR)	59.00 (8.00)	58.00 (6.00)		
RANGE (MIN-MAX)	44.00 - 70.00	46.00 - 68.00		
GENDER [N (%)]			χ^2= 1.36 [b]	0.243 [NS]
MALE	80 (80.0)	73 (73.0)		
FEMALE	20 (20.0)	27 (27.0)		
SMOKING [N (%)]			χ^2= 5.17 [b]	0.023 [S]
NO	37 (37.0)	53 (53.0)		
YES	63 (63.0)	47 (47.0)		

"IQR: Interquartile range (difference between 1st and 3rd quartiles), SD: Standard deviation, %: percent within groups a: Mann-Whitney test, b: Pearson Chi-square test, NS: Non-significant at P-value ≥0.05, S: Significant at P-value <0.05"

In the HCC group, 46.5% of individuals had the C variant of the pri-miR-34b/c rs4938723 SNP, compared to 34.5% in the healthy control group (p-value = 0.015). Genetic distribution (p=0.041) and the recessive genetic model (CC vs. TT+TC, p=0.032) both revealed evidence of a comparable pattern. Unfortunately, the most common genetic model (CC+TC vs. TT) was not statistically significant (p=0.053). as shown in Table 2.

Table 2. Genotypes distribution and allele frequencies of pri-miR-34b/c rs4938723 SNP of HCC patients and healthy controls

PRI-MIR-34B/C RS4938723 SNP	HCC PATIENTS (N= 100)	HEALTHY CONTROLS (N= 100)	TEST STATISTICS (X^2)	P-VALUE [A]
GENOTYPES			6.39	0.041 [S]
CC	21 (21.0)	10 (10.0)		
TC	51 (51.0)	49 (49.0)		
TT (REF)	28 (28.0)	41 (41.0)		
DOMINANT [C]			3.74	0.053 [NS]
CC + TC	72 (72.0)	59 (59.0)		
TT (REF)	28 (28.0)	41 (41.0)		
RECESSIVE [D]			4.62	0.032 [S]
CC	21 (21.0)	10 (10.0)		
TT + TC (REF)	79 (79.0)	90 (90.0)		
ALLELES			5.98	0.015 [S]
C	93 (46.5)	69 (34.5)		
T (REF)	107 (53.5)	131 (65.5)		
P_{HWE}	0.961	0.693		

"A: Pearson Chi-Square test, c: Dominant model; variant type + hetero type vs wild type, d:

Recessive model; variant type vs wild type + heterotyper P HWE: P-value for testing Hardy-Weinberg equilibrium, NS: Non-significant at P-value ≥0.05, S: Significant at P-value <0.05"

If you have the variant C allele instead of the wild T allele, your risk of having HCC is 1.65 times higher (95% CI: 1.10-2.47, with p=0.015). There was no significant difference between the CC and TT genotypes in either the recessive model (OR=2.39, 95% CI: 1.06 -5.39, with p=0.032) or the genotypic distribution (OR=3.08, 95% CI:1.26 -7.51, with p=0.012). The occurrence of HCC was not shown to be significantly related to either the CC+TC vs. TT genotype (OR=1.79, 95% CI: 0.99 -3.23, with p=0.053) or the TC genotype (OR=1.52, 95% CI:0.82 -2.83, with p=0.182). The use of regression analysis helped reduce the impact of smoking to a larger extent. A higher risk of HCC was observed in the CC genotype, recessive models, and allelic frequency analyses when comparing the C allele to the TT allele (OR=1.58, 95% CI: 1.05-2.37, with p=0.029; OR=2.82, 95% CI:1.14-6.97, with p=0.024; OR=2.27, 95% CI: 1.00-5.16, with p=0.049; respectively). A higher risk of HCC was estimated (OR=1.44, 95% CI: 0.77-2.69, with p=0.260; OR=1.67, 95% CI: 0.92-3.04, with p=0.094; respectively) in the codominant (TC vs. TT) and dominant (CC+TC vs. TT) models, but the C allele did not infer any significant association in either of these models prior to adjustment. As a risk factor for HCC susceptibility, the variation C allele of the pri-miR-34b/c rs4938723 SNP stood out when smoking's effects were taken into consideration. Table 3

Table 3. Association between pri-miR-34b/c rs4938723 SNP and the risk of HCC susceptibility

PRI-MIR-34B/C RS4938723 SNP	HCC PATIENTS (N= 100)	HEALTHY CONTROLS (N= 100)	OR (95% CI)	P-VALUE [A]	ADJUSTED OR (95% CI) [B]	P-VALUE [B]
GENOTYPES						
CC	21 (21.0)	10 (10.0)	3.08 (1.26 -7.51)	0.012 S	2.82 (1.14-6.97)	0.024 S
TC	51 (51.0)	49 (49.0)	1.52 (0.82 -2.83)	0.182 NS	1.44 (0.77-2.69)	0.260 NS
TT (REF)	28 (28.0)	41 (41.0)	Ref. (1.00)	-	Ref. (1.00)	-
DOMINANT [C]						
CC + TC	72 (72.0)	59 (59.0)	1.79 (0.99 -3.23)	0.053 NS	1.67 (0.92-3.04)	0.094 NS
TT (REF)	28 (28.0)	41 (41.0)	Ref. (1.00)	-	Ref. (1.00)	-
RECESSIVE [D]						
CC	21 (21.0)	10 (10.0)	2.39 (1.06 -5.39)	0.032 S	2.27 (1.00-5.16)	0.049 S
TT + TC (REF)	79 (79.0)	90 (90.0)	Ref. (1.00)	-	Ref. (1.00)	-
ALLELES						
C	93 (46.5)	69 (34.5)	1.65 (1.10 -2.47)	0.015 S	1.58 (1.05-2.37)	0.029 S
T (REF)	107 (53.5)	131 (65.5)	Ref. (1.00)	-	Ref. (1.00)	-
P HWE	0.961	0.693				

"A: Pearson Chi-Square test, b: Odds ratios, 95% confidence intervals, and P-values adjusted for smoking, c: Dominant model; variant type + hetero type vs wild type; d: Recessive model; variant type vs wild type + heterotype, P HWE: P-value for testing Hardy-Weinberg equilibrium, NS: Non-significant at P-value ≥0.05; S: Significant at P-value <0.05"

Differences in focal lesion size and multiplicity were found to be statistically significant across the various genotypes. Sporadic localized lesions (< 5 cm) were found in the skin of only 33.3% of patients with the CC genotype, 56.9% with the TC genotype, and 82.1% with the TT genotype. In contrast, significant focal lesions (> 5 cm) were present in 66.7% of CC genotype patients, 43.1% of TC genotype patients, and 17.9% of TT genotype patients (P = 0.003). Many lesions were seen in 66.7% of CC genotype patients, 51.0% of TC genotype patients, and 21.4% of TT genotype patients, whereas a single focal lesion was seen in 33.3%, 49.0%, and 78.6% of TC genotype patients, respectively (P = 0.004). In terms of imaging findings (spleen, liver, ascites, PVT) and child categorization, however, there was no statistically significant variation among the genotypes. Table 4

Table 4. Relation between pri-miR-34b/c rs4938723 genotypes and clinical data of HCC patients

CLINICAL PARAMETERS	PRI-MIR-34B/C RS4938723			TEST STATISTICS/ P-VALUES	PAIRWISE COMPARISONS*
	CC (n= 21)	TC (n= 51)	TT (n= 28)		
FL SIZE [N (%)]				χ^2= 12.02 [b]	P1=0.196 NS
SMALL (< 5 CM)	7 (33.3)	29 (56.9)	23 (82.1)	P =0.002 HS	P2=0.003 HS
LARGE (>5CM)	14 (66.7)	22 (43.1)	5 (17.9)		P3=0.067 NS
FL MULTIPLICITY [N (%)]				χ^2= 10.93 [b]	0.531 NS
SINGLE	7 (33.3)	25 (49.0)	22 (78.6)	P =0.004 HS	0.003 HS
TWO OR MORE	14 (66.7)	26 (51.0)	6 (21.4)		0.030 S
CHILD CLASSIFICATION [N (%)]				χ^2= 3.71 [c]	-----
A	9 (42.9)	32 (62.7)	17 (60.7)	P =0.439 NS	
B	11 (52.4)	15 (29.4)	10 (35.7)		
C	1 (4.8)	4 (7.8)	1 (3.6)		
ASCITES [N (%)]				χ^2= 1.55 [b]	----
NO	14 (66.7)	38 (74.5)	23 (82.1)	P =0.462 NS	
YES	7 (33.3)	13 (25.5)	5 (17.9)		
SPLENOMEGALY [N (%)]				χ^2= 2.29 [b]	----
NO	2 (9.5)	13 (25.5)	6 (21.4)	P =0.357 NS	
YES	19 (90.5)	38 (74.5)	22 (78.6)		
HEPATOMEGALY [N (%)]				χ^2= 3.16 [b]	----
NO	20 (95.2)	40 (78.4)	22 (78.6)	P =0.229 NS	
YES	1 (4.8)	11 (21.6)	6 (21.4)		
PVT [N (%)]				χ^2= 0.28 [c]	----
NO	19 (90.5)	44 (86.3)	25 (89.3)	P =1.000 NS	
YES	2 (9.5)	7 (13.7)	3 (10.7)		

"IQR: Interquartile range (difference between 1st and 3rd quartiles), SD: Standard deviation, b: Pearson Chi-square test, c: Fisher's Exact test, *: Multiple pairwise comparisons adjusted by Dunn-Sidak post hoc test: p1: comparison between CC and TC genotypic groups, p2: comparison between CC and TT genotypic groups, p3: comparison between TC and TT genotypic groups, NS: Non-significant at P-value ≥0.05; S: Significant at P-value <0.05; HS: Highly significant at P-value < 0.01; FL: (Focal lesion); PVT: (Portal vein thrombosis)"

4. Discussion

Cancer develops when microRNA-34 (miR-34) is controlled by P53, which modifies genes downstream of it, changes the apoptotic cycle and pathways of cells downstream of it, and so on .[11]

In this case control study, with respect to age (P=0.711) and gender (P=0.243), there was no statistically significant difference between the healthy control group and those with HCC. But smoking separated the two groups significantly (P=0.023).

There was a total of 60 participants in this case-control study, including 35 people with HCC, 35 people with HCV, and 30 healthy individuals who were matched for age and gender. The main objective was to discover possible indicators for the early detection and prognosis of hepatocellular cancer (HCC). Researchers in Egypt found a correlation between the results and variations in two genes: miR-146a rs2910164 (C>G) and pri-miR-34b/c rs4938723 (T>C). The HCV group's gender distribution differed significantly from that of the control and HCC groups. A variant C allele of the pri-miR-34b/c rs4938723 SNP was found in 46.5% of the HCC group and 34.5% of the healthy controls, a difference that was statistically significant (p = 0.015). Comparisons of the recessive genetic model (CC vs. TT+TC, p=0.032) and the genotypic distribution (p=0.041) also yielded similar results. Furthermore, the leading genetic model (CC+TC vs. TT) was only marginally unsuccessful in reaching statistical significance (p=0.053). [12]

It was identified that 58 (35.37%), 80 (46.78%), and 26 (15.85%) instances of HCC exhibited TT, TC, and CC genotypes, respectively. Out of a total of 142 controls, 142 (46.23%) had TT genotypes, while 22 (7.21%) did not. There was a notable disparity in the genotype distribution of pri-miR-34b/c rs493-8723 between the control group and HCC patients (x2 = 13.58, P = 0.001).

The current study found that an increased risk of HCC was associated with the variant C allele compared to the wild T allele (OR=1.65, 95% CI:1.10-2.47, and p=0.015). In both the recessive model (OR=2.39, 95% CI:1.06 -5.39, and p=0.032) and the random sample (OR=3.08, 95% CI:1.26 -7.51, and p=0.012), it was observed that the TT genotype was associated with the CC genotype. Unfortunately, the CC+TC genotype and TT were not linked to an increased risk of HCC in the dominant model (OR=1.79, 95% CI: 0.99 -3.23, and p=0.053). Both of these permutations were statistically unrelated. [13]

Just forty people have received a diagnosis of HCC. Researchers found that the miR34 b/c rs4938723 CC genotype was unique in all three groups they looked at. [14]

Similarly, it was amendment rs4938723 to miR-34b/c in comparison to the wild-type TT genotype, the TC/CC genotype was significantly associated with a significantly higher risk of HCC. Results for TC, CC, and TC/CC when controlled for confounding variables are as follows: 1.37 (95% CI = 1.06-1.78), 1.53 (95% CI = 1.02-2.31), and 1.40 (95% CI = 1.10-1.80), respectively. That TP53 Arg72Pro raised the risk of HCC was not found to be the case in this study. In terms of adjusted odds ratios, Arg/Pro came out at 1.03 and Pro/Pro at 0.95 with 95% CIs of 0.67-1.34 and 0.78-1.37, respectively. [15]

Moreover, it was concluded that the risk of HCC was increased by the combination of rs4938723 CC and TP53 Arg/Arg. [16]

Size and number of focal lesions showed a statistically significant difference between genotypes (P = 0.002 and 0.004, respectively). There was no notable variation (P ≥0.05) in the genotypes in either the kid classification or the imaging results (spleen, liver, ascites, PVT).

A massive dataset consisting of 33,325 individuals was used to determine that rs4938723 was linked to a higher risk of HCC, with the HBV mutations being the major contributor. Individuals with the pri-miR-34b/c rs4938723 variant genotype had an increased risk of HCC, according to multivariate regression analysis of the dominant genetic model. I. However, the chance of HCC was drastically decreased when it interacted with the C1730G mutation of HBV, which is inversely associated with HCC risk. Thus, HBV mutations can significantly alter the rs4938723 influence on the risk of liver cancer. [17]

Genotypes differed significantly in this study with respect to HCC aggressiveness, as measured by ALT and AST levels and the number and size of focal lesions. The clinical examinations and laboratory tests did not include the following: white blood cell and platelet counts; anti-fetal growth factor; total and direct bilirubin; albumin; international normalized ratio; serum creatinine; hemoglobin; and child categorization.

When we compared the pri-miR-34b/c rs4938723 genotype subgroups according to age (P=0.960) or gender (0.483), we did not find a different pattern. The opposite was true for smoking, where a statistically significant difference in genotype was observed (P=0.003). The pri-miR-34b/c rs4938723 SNP variation C allele was discovered to be an extra risk factor for HCC susceptibility in the smoking effect, alongside smoking directly.

It was no evidence of a gene-environment interaction was found for the primiR-34b/c rs4938723 polymorphism with respect to age (0.035, P = 0.25), gender (0.041, P = 0.21), alcohol consumption (0.037, P = 0.23), hepatitis B virus

(HBV) (0.052, P = 0.06), or hepatitis C virus infection (10.25).

Multiple focal lesions were more common in subjects with the CC genotype of pri-miR-34b/c rs4938723 compared to those with the TC and TT genotypes, according to the current study. It was observed that the rs11614913 genotype was linked to tumor size (p=0.046) but not tumor number in a follow-up study of the correlation between microRNA-196a2 and clinicopathological variables. [18]

Strength of the study: This is a case control study which relatively quick to perform, economical, and easy to design and implement, also this study has no funds which eliminate the effect of pharmaceutical manufacturers on the accuracy of the results. Presence of the control group which gave validation to the results of comparison.

Limitations of the study: There are numerous potential limitations to our case-control investigation. As an initial matter, the statistical efficacy of our investigation may be restricted by the sample size, particularly in the context of gene-environmental interaction and subgroup analyses. Secondly, the sample population was not representative of the general population, as the research subjects were selected from a single institution. The fact that the control samples' rs4938723 gene distributions matched the HWE suggests, however, that these samples might be typical of the population at large.

4. Conclusion

Based on our findings, the pri-miR-34b/crs4938723 TT genotype in Egyptians may serve as a non-invasive diagnostic marker for the risk of HCC. Further prospective studies involving a large number of cases and different comparison groups could evaluate the pri-miR-34b/crs4938723 polymorphism in different clinical contexts to better understand its position in HCC.

Disclosure

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