Research Article

The Genetic Polymorphisms in the MIR17HG Gene Are Associated with the Risk of Head and Neck Squamous Cell Carcinoma in the Chinese Han Population

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1. Introduction

Head and neck squamous cell carcinoma (HNSCC) is the most common malignant tumors in the world. Genetic variants have an important role in HNSCC progression. Our study is aimed at exploring the relationship between MIR17HG polymorphisms and HNSCC risk in the Chinese Han population.

Purpose. Head and neck squamous cell carcinoma (HNSCC) is the most common malignant tumors in the world. Genetic variants have an important role in HNSCC progression. Our study is aimed at exploring the relationship between MIR17HG polymorphisms and HNSCC risk in the Chinese Han population. Methods. We recruited 537 HNSCC cases and 533 healthy subjects to detect the correlation of six polymorphisms in MIR17HG with HNSCC susceptibility. The associations were evaluated by computing odds ratios (ORs) and 95% confidence intervals (CIs) using logistic regression analysis. Results. Our study revealed that rs7336610 (OR 1.77, 95% CI = 1.09–2.86, and p = 0.021) and rs1428 (OR 1.73, 95% CI = 1.07–2.81, and p = 0.025) are strongly associated with increased susceptibility to HNSCC in men. Besides, rs17735387 played a crucial protective role in stage III/IV HNSCC patients (OR 0.34, 95% CI = 0.12–0.95, and p = 0.040) compared with stage I/II. Conclusion. Our study firstly indicated that MIR17HG polymorphisms are significantly associated with HNSCC susceptibility, which suggests that MIR17HG has a potential role in the occurrence of HNSCC.

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17-92 gene cluster miR-17 and therefore contributes to the development of human tumors [13]. Wang et al. found that the silencing of miR-17 can promote cell apoptosis and inhibit cell proliferation in laryngeal squamous cell carcinoma [14]. MIR17HG acted as a tumor suppressor lncRNA in HPV-positive HNSCC tumors compared to HPV-negative tumors, which plays a distinct role in HPV-related HNSCC [15]. Genetic variants within genes can affect the expression or structure of the genes, which may result in the progression of cancers. Moreover, previous studies have revealed that the polymorphisms of MIR17HG are markedly related to the occurrence of cancers [13, 16, 17]. Taken together, we speculate that the MIR17HG genetic variant may have a potential role in the HNSCC progression. To our knowledge, there is no study on the association between the MIR17HG polymorphisms and HNSCC susceptibility.

To better know the effect of MIR17HG genetic variant on the risk of HNSCC in the Chinese population. In this case-control study, we selected six (single nucleotide polymorphisms) SNPs (rs75267932, rs7336610, rs72640334, rs7318578, and rs1428) in MIR17HG from 1000 Genomes Project with minor allele frequencies > 5%, r² < 0.8, and Hardy–Weinberg equilibrium > 0.05. MassARRAY platform was performed to detect the SNP genotyping. We then studied the association of MIR17HG SNPs with the susceptibility of HNSCC. Finally, we evaluated the relationship of MIR17HG variants with the risk of HNSCC stratified by age, gender, and pathological grade. Our present work will give new scientific evidence for the molecular mechanism of HNSCC development in the Chinese population.

### 2. Materials and Methods

#### 2.1. Study Population

A total of 1070 participants included in 537 unrelated Chinese HNSCC patients (43 laryngeal SCC, 77 nasopharyngeal SCC, 398 thyroid SCC, and 19 parotid SCC) and 533 age-sex matched healthy controls were recruited from the First Affiliated Hospital of Xi’an Jiaotong University in this case-control study. All patients were newly diagnosed by clinical manifestations and confirmed to be HNSCC based on histopathological examination. The controls were selected from healthy individuals with a physical examination in the same hospital. All participants with other types of cancers and familial history of any cancers included HNSCC must be excluded. The basic characteristic of each individual was obtained from the medical records included in age, gender, lymph node metastasis status, clinical stage, BMI (body mass index), and smoking/drinking status. Each participant was told the research purpose, and informed consent was obtained from them. Our study was approved by the ethics committee of the First Affiliated Hospital of Xi’an Jiaotong University. All experiments were carried out based on the guideline of Helsinki’s declaration.

#### 2.2. SNP Selection and Genotyping

In our study, six SNPs (rs75267932, rs7336610, rs72640334, rs17735387, rs7318578, and rs1428) of the MIR17HG gene were selected by 1000 Genomes Project with MAF > 5% and r² (the measure value of linkage disequilibrium (LD)) < 0.8 and for further genotyp-

| Characteristics | Cases (n = 537) | Controls (n = 533) | P |
|-----------------|----------------|--------------------|---|
| Age, years (mean ± SD) | 46.87 ± 15.05 | 46.62 ± 13.67 | 0.782 |
| >46 | 299 (56.0%) | 282 (53.0%) | |
| ≤46 | 238 (44.0%) | 251 (47.0%) | |
| Gender | | | 0.950 |
| Male | 207 (39.0%) | 204 (38.0%) | |
| Female | 330 (61.0%) | 329 (62.0%) | |
| LN metastasis | | | |
| Node positive | 103 (19.0%) | | |
| Missed | 352 (66%) | | |
| Clinical stage | | | |
| III/IV | 38 (7%) | | |
| I/II | 140 (26%) | | |
| Missing | 359 (67%) | | |
| Nasopharyngeal carcinoma | 77 (14%) | | |
| Thyroid cancer | 398 (74%) | | |
| Laryngeal carcinoma | 43 (8%) | | |
| Parotid gland carcinoma | 19 (4%) | | |
| BMI, kg/m² (mean ± SD) | | | |
| <24 | 12 (6%) | 247 (46%) | |
| >24 | 1 (0.2%) | 158 (30%) | |
| Missing | 515 (93.8%) | 128 (24%) | |
| Smoking | 90 (17%) | 365 (69%) | |
| Drinking | 46 (9%) | 344 (65%) | |

*aStudent’s t-test is used. bPearson’s χ² test is used. p < 0.05 indicates statistical significance. HNSCC: head and neck squamous cell carcinoma; LN: lymph node; BMI: body mass index.*

The genomic DNA from each peripheral blood sample was extracted by a whole-blood genomic DNA extraction kit (GoldMag, Xi’an, China). The NanoDrop 2000C spectrophotometer (Thermo Scientific, Waltham, USA) was performed to test the concentration and purity of the genomic DNA. PCR primers used for genotyping were designed by the Agena Bioscience Assay Design Suite software (V2.0, https://agenacx.com/online-tools/). We further identified the SNP genotyping via the Agena MassARRAY iPLEX version 4.0 platform, and the data was organized and analyzed by the Agena Bioscience TYPER version 4.0 software.

#### 2.3. Statistical Analysis

All variables were examined for normal distributions using the Kolmogorov-Smirnov test. Comparisons of age and clinical characteristics between the cases and controls were, respectively, analyzed by the t-test. The difference of gender between the cases and controls was analyzed by the χ² test. A chi-squared test was used to evaluate the Hardy-Weinberg equilibrium (HWE) of each SNP in the control group. Distributions of allele and genotype of SNPs in the cases and controls were analyzed by the χ² test or exact test. The association between the MIR17HG
Table 2: The distribution of allele frequencies of MIR17HG SNPs in case and control.

| SNP ID    | Chromosome position | Function | Alleles (minor/major) | MAF Case | MAF Control | O Case (HET) | E Control (HET) | p^a HWE | OR (95% CI)        | p^b |
|-----------|---------------------|----------|-----------------------|----------|-------------|--------------|-----------------|---------|-------------------|-----|
| rs75267932 | chr13: 91351812     | Exon     | G/A                   | 0.104    | 0.115       | 0.205        | 0.204           | 1.000   | 0.89 (0.68-1.17) | 0.412 |
| rs72640334 | chr13: 91352674     | Intronic | A/C                   | 0.100    | 0.086       | 0.164        | 0.156           | 0.411   | 1.19 (0.89-1.60) | 0.238 |
| rs7336610  | chr13: 91352883     | Intronic | C/T                   | 0.493    | 0.489       | 0.485        | 0.500           | 0.489   | 1.02 (0.86-1.21) | 0.826 |
| rs7318578  | chr13: 91353215     | Intronic | C/A                   | 0.289    | 0.277       | 0.400        | 0.401           | 1.000   | 1.06 (0.88-1.28) | 0.559 |
| rs17735387 | chr13: 91353800     | Intronic | A/G                   | 0.201    | 0.197       | 0.311        | 0.316           | 0.683   | 1.03 (0.83-1.27) | 0.811 |
| rs1428     | chr13: 91354516     | Exon     | C/A                   | 0.490    | 0.488       | 0.484        | 0.500           | 0.488   | 1.01 (0.85-1.19) | 0.929 |

HNSCC: head and neck squamous cell carcinoma; SNP: single nucleotide polymorphisms; MAF: minor allele frequency; HWE: Hardy-Weinberg equilibrium. p^a values were calculated by exact test, and p^a < 0.05 are excluded; p^b values were calculated by two-sided χ^2, and p^b < 0.05 indicates statistical significance.

Table 3: Association of MIR17HG polymorphism with HNSCC risk.

| SNP ID    | Model | Allele/genotype | Case n | Control n | With adjusted OR (95% CI) | p |
|-----------|-------|-----------------|--------|-----------|----------------------------|----|
| rs75267932 | Allele | A               | 962    | 943       | 1                          |    |
|           |       | G               | 112    | 123       | 0.89 (0.68-1.17)           | 0.412 |
|           |       | AA              | 433    | 417       | 1                          |    |
|           | Codominant | GA            | 96     | 109       | 0.85 (0.63-1.15)           | 0.297 |
|           |       | GG              | 8      | 7         | 1.10 (0.39-3.06)           | 0.859 |
|           | Dominant | AA              | 433    | 417       | 1                          |    |
|           | Recessive | AG-GG          | 104    | 116       | 0.86 (0.64-1.16)           | 0.338 |
|           |       | AA-AG           | 529    | 526       | 1                          |    |
|           | Log-additive | –             | –      | –         | 0.90 (0.68-1.17)           | 0.421 |
| rs72640334 | Allele | C               | 959    | 973       | 1                          |    |
|           |       | A               | 107    | 91        | 1.19 (0.89-1.60)           | 0.238 |
|           |       | CC              | 432    | 443       | 1                          |    |
|           | Codominant | CA            | 95     | 87        | 1.12 (0.81-1.54)           | 0.490 |
|           |       | AA              | 6      | 2         | 3.09 (0.62-15.44)          | 0.169 |
|           | Dominant | CC              | 432    | 443       | 1                          |    |
|           | Recessive | CA-AA          | 101    | 89        | 1.16 (0.85-1.59)           | 0.344 |
|           |       | CC-CA           | 527    | 530       | 1                          |    |
|           | Log-additive | –             | –      | –         | 1.20 (0.89-1.61)           | 0.235 |
| rs7336610  | Allele | T               | 544    | 544       | 1                          |    |
|           |       | C               | 530    | 520       | 1.02 (0.86-1.21)           | 0.826 |
|           |       | TT              | 133    | 143       | 1                          |    |
|           | Codominant | TC            | 278    | 258       | 1.16 (0.87-1.55)           | 0.316 |
|           |       | CC              | 126    | 131       | 1.03 (0.73-1.45)           | 0.856 |
|           | Dominant | TT              | 133    | 143       | 1                          |    |
|           | TC-CC  | 404              | 389    | 1.12 (0.85-1.47) | 0.429 |
gene and HNSCC susceptibility was detected by calculating ORs and 95% CIs under five inheritance models using logistic regression analysis. In addition, we investigated the correlation of the SNPs with HNSCC risk under subgroups such as age, gender, clinical stage, and HNSCC types. What is more, we also carried out a false-positive report probability (FPRP) analysis to further detect whether the significant findings were just chance or noteworthy observations [18].

Statistical analyses in this study were performed using the SPSS version 17.0 software. All statistical tests were two-tailed and p value <0.05 indicates statistically significant.

## 3. Results

### 3.1. Basic Characteristics of Study Participants

The basic characteristics of all participants were summarized in Table 1. This study consisted of 537 cases (207 men and 330 women) and 533 controls (204 men and 329 women).
The average ages were $46.62 \pm 13.67$ years in controls and $46.87 \pm 15.05$ years in cases. There were no significant differences in age and gender between the case and control participants ($p = 0.782; p = 0.950$, respectively).

3.2. Association Analysis between MIR17HG Genetic Variants and HNSCC Susceptibility. The basic information of the candidate SNPs in this study was presented in Table 2. A total of six SNPs were successfully genotyped in our study. The distributions of the genotype of all SNPs in controls were in accordance with HWE ($p > 0.05$). We then investigate the association of SNPs in the MIR17HG gene with the risk of HNSCC under allele, codominant, dominant, recessive, and log-additive models (Table 3). It was shown that significant associations were not observed in SNPs.

3.3. Correlation of SNPs with HNSCC Risk Stratified by Demographic and Clinical Characteristics. We further carried out the correlation of SNPs with HNSCC risk stratified by age and gender. The relationship of MIR17HG variants with HNSCC stratified by age and gender is shown in Table 4.
out stratification analyses by age, gender, and pathological grade. When stratified by age, we found that there is no strong significant association with the risk of HNSCC (Table 4). After stratifying by gender, our result indicated that rs7336610 (TC vs. TT, OR 1.77, 95% CI = 1.09-2.86, and $p = 0.021$; TC-CC vs. TT, OR 1.64, 95%CI = 1.04-2.57, and $p = 0.030$) and rs1428 (AC vs. AA, OR 1.73, 95%CI = 1.07-2.81, and $p = 0.025$; AC-CC vs. AA, OR 1.63, 95%CI = 1.04-2.56, and $p = 0.035$) polymorphisms are strongly associated with an increased risk of HNSCC in men (Table 4). We further evaluated the relationship of the $MIR17HG$ genetic variants with pathological grade of HNSCC (Table 5). rs17735387 SNP played a crucial protective role in stage III/IV HNSCC patients (GA vs. GG, OR 0.34, 95%CI = 0.12-0.95, and $p = 0.040$; GA-AA vs. GG, OR 0.59, 95%CI = 0.29-1.23, and $p = 0.154$) compared with stage I/II.

We finally detected the impacts of $MIR17HG$ SNPs on nasopharyngeal SCC and thyroid SCC susceptibilities

### Table 5: The relationship of $MIR17HG$ polymorphisms with HNSCC stratified by pathological grade.

| SNP ID    | Allele/genotype | III-IV (n) | I-II (n) | OR (95% CI)     | $p$  |
|-----------|-----------------|------------|----------|-----------------|------|
| rs75267932| A 70            | 253        | 1        |                 |      |
|           | G 6             | 27         | 0.80 (0.32-2.02) | 0.641 |
|           | AA 32           | 113        | 1        |                 |      |
|           | GA 6            | 27         | /        | /               |      |
|           | GG 0            | 0          | /        | /               |      |
|           | AG-GG 6         | 27         | 0.65 (0.23-1.86) | 0.420 |
| rs72640334| C 66            | 251        | 1        |                 |      |
|           | A 10            | 29         | 1.31 (0.61-2.83) | 0.488 |
|           | CC 28           | 112        | 1        |                 |      |
|           | CA 10           | 27         | 1.90 (0.76-4.71) | 0.169 |
|           | AA 0            | 1          | /        | /               |      |
|           | CA-AA 10        | 28         | 1.84 (0.74-4.55) | 0.189 |
| rs7336610 | T 33            | 144        | 1        |                 |      |
|           | C 43            | 136        | 1.38 (0.83-2.30) | 0.216 |
|           | TT 8            | 36         | 1        |                 |      |
|           | TC 17           | 72         | 0.98 (0.37-2.60) | 0.963 |
|           | CC 13           | 32         | 1.67 (0.58-4.81) | 0.342 |
|           | TC-CC 30        | 104        | 1.19 (0.48-2.97) | 0.706 |
| rs7318578 | A 53            | 195        | 1        |                 |      |
|           | C 23            | 85         | 1.00 (0.57-1.73) | 0.987 |
|           | AA 20           | 65         | 1        |                 |      |
|           | CA 13           | 65         | 0.84 (0.36-1.93) | 0.676 |
|           | CC 5            | 10         | 2.25 (0.62-8.16) | 0.218 |
|           | AC-CC 18        | 75         | 1.01 (0.47-2.20) | 0.973 |
| rs17735387| G 66            | 223        | 1        |                 |      |
|           | A 10            | 57         | 0.59 (0.29-1.23) | 0.154 |
|           | GG 30           | 92         | 1        |                 |      |
|           | GA 6            | 39         | 0.34 (0.12-0.95) | 0.040 |
|           | AA 2            | 9          | 0.60 (0.11-3.16) | 0.549 |
|           | GA-AA 8         | 48         | 0.38 (0.15-0.97) | 0.042 |
| rs1428    | A 33            | 143        | 1        |                 |      |
|           | C 43            | 135        | 1.38 (0.83-2.30) | 0.215 |
|           | AA 8            | 36         | 1        |                 |      |
|           | CA 17           | 71         | 0.99 (0.37-2.64) | 0.980 |
|           | CC 13           | 32         | 1.69 (0.59-4.87) | 0.330 |
|           | AC-CC 30        | 103        | 1.21 (0.48-3.02) | 0.684 |

$\text{p}$ values were calculated by unconditional logistic regression analysis with adjustment for age and gender. $\text{p} < 0.05$ indicates statistical significance. Highlighted in bold indicates the significant association between SNPs and HNSCC risk.
(Table 6). No significant associations were found between the SNPs and nasopharyngeal SCC and thyroid SCC susceptibilities.

3.4. FPRP Analysis. FPRP and statistical power were calculated for the positive findings for the samples. As was shown in Table 7, the association of the MIR17HG rs17735387 polymorphism (GA vs. GG) with the risk of stage III/IV HNSCC remained noteworthy (FPRP = 0.192), while the association of rs17735387 (GA-AA vs. GG) was not noteworthy at the prior probability level of 0.25 and FPRP threshold of 0.2 (FPRP = 0.192, FPRP = 0.192, FPRP = 0.192, and FPRP = 0.192, respectively).

### Table 6: The relationship of MIR17HG variants with nasopharyngeal SCC and thyroid SCC risk.

| SNP ID   | Allele/genotype | Nasopharyngeal SCC | Thyroid SCC |
|----------|-----------------|--------------------|-------------|
|          |                 | Case Control OR (95% CI) | p | Case Control OR (95% CI) | p |
| rs75267932 | A 135 943 1 1.08 (0.64-1.81) 0.773 714 943 1 0.88 (0.66-1.18) 0.399 |
|          | G 19 123 1 1.24 (0.68-2.24) 0.485 68 109 0.79 (0.56-1.11) 0.173 |
|          | AA 59 417 1 1.24 (0.68-2.24) 0.485 68 109 0.79 (0.56-1.11) 0.173 |
|          | AG-GG 18 116 1 1.21 (0.68-2.16) 0.524 75 116 0.82 (0.59-1.14) 0.247 |
|          | C 132 973 1 1.24 (0.68-2.24) 0.485 68 109 0.79 (0.56-1.11) 0.173 |
|          | A 19 91 1 1.24 (0.68-2.24) 0.485 68 109 0.79 (0.56-1.11) 0.173 |
|          | CC 58 443 1 1.24 (0.68-2.24) 0.485 68 109 0.79 (0.56-1.11) 0.173 |
| rs72640334 | CA 16 87 1 1.29 (0.70-2.37) 0.419 71 87 1.15 (0.81-1.63) 0.435 |
|          | AA 1 2 3.65 (0.29-46.40) 0.318 5 2 3.09 (0.58-16.38) 0.184 |
|          | CA-AA 17 89 1 1.34 (0.73-2.43) 0.342 76 89 1.20 (0.85-1.68) 0.306 |
|          | C 84 520 1 1.26 (0.89-1.76) 0.188 388 520 0.99 (0.83-1.20) 0.956 |
|          | TT 14 143 1 1 102 143 1.02 (0.83-1.25) 0.890 |
| rs7336610 | TC 42 258 1 1.72 (0.90-3.29) 0.102 204 258 1.09 (0.79-1.50) 0.594 |
|          | CC 21 131 1 1.45 (0.70-3.01) 0.319 92 131 1.00 (0.69-1.46) 0.986 |
|          | TC-CC 63 389 1 1.62 (0.87-3.01) 0.127 296 389 1.06 (0.79-1.43) 0.697 |
|          | A 102 769 1 1 573 769 1 0.121 223 295 1.02 (0.83-1.25) 0.890 |
|          | C 52 295 1 1.33 (0.93-1.91) 0.121 223 295 1.02 (0.83-1.25) 0.890 |
| rs7318578 | AA 32 278 1 1 202 278 1 0.121 223 295 1.02 (0.83-1.25) 0.890 |
|          | CA 38 213 1 1.46 (0.88-2.44) 0.147 169 213 1.10 (0.84-1.45) 0.494 |
|          | CC 7 41 1 1.36 (0.55-3.35) 0.503 27 41 0.89 (0.53-1.50) 0.664 |
|          | AC-CC 45 254 1 1.45 (0.88-2.37) 0.144 196 254 1.07 (0.82-1.39) 0.632 |
|          | G 122 856 1 1 634 856 1 0.121 223 295 1.02 (0.83-1.25) 0.890 |
| rs17735387 | A 32 210 1 1.07 (0.70-1.62) 0.754 162 210 1.04 (0.83-1.31) 0.728 |
|          | GG 48 345 1 1 253 345 1 0.121 223 295 1.02 (0.83-1.25) 0.890 |
|          | GA 26 166 1 1.14 (0.68-1.93) 0.621 128 166 1.06 (0.79-1.40) 0.708 |
|          | AA 3 22 0.88 (0.25-3.10) 0.843 17 22 1.11 (0.57-2.14) 0.762 |
|          | GA-AA 29 188 1 1.11 (0.67-1.83) 0.692 145 188 1.06 (0.81-1.40) 0.667 |
|          | A 70 546 1 1 412 546 1 0.121 223 295 1.02 (0.83-1.25) 0.890 |
|          | C 84 520 1 1.26 (0.90-1.77) 0.181 384 520 0.98 (0.81-1.18) 0.818 |
| rs1428   | AA 14 144 1 1 106 144 1 0.121 223 295 1.02 (0.83-1.25) 0.890 |
|          | CA 42 258 1 1.73 (0.90-3.31) 0.099 200 258 1.03 (0.75-1.42) 0.838 |
|          | CC 21 131 1 1.46 (0.70-3.02) 0.314 92 131 0.97 (0.67-1.41) 0.878 |
|          | AC-CC 63 389 1 1.63 (0.88-3.02) 0.123 292 389 1.01 (0.75-1.36) 0.933 |

Nasopharyngeal SCC: nasopharyngeal squamous cell carcinoma; thyroid SCC: thyroid squamous cell carcinoma. \( p \) values were calculated by unconditional logistic regression analysis with adjustment for age and gender. \( p < 0.05 \) indicates statistical significance. Highlighted in bold indicates the significant association between SNPs and HNSCC risk.
### 4. Discussion

In this study, we assessed the association of the MIR17HG genetic variants (rs75267932, rs7318578, rs72640334, rs17735387, rs7336610, and rs1428) with HNSCC risk in a Chinese population. We observed that MIR17HG SNPs are strongly associated with HNSCC susceptibility, especially rs7336610, rs17735387, and rs1428. To our knowledge, our study is the first to investigate the correlation between MIR17HG variants and HNSCC risk, which suggests that MIR17HG genetic variants have a potential role in HNSCC progression.

MIR17HG is a member of lncRNAs located in a region of human chromosome 13q31, which was shown to play an important role in the development and progression of several human cancers through regulating tumor growth and apoptosis [19–21]. Jiang et al. showed that the higher expression level of the MIR17HG gene can inhibit the growth and metastasis of colon tumors [22]. The overexpression of MIR17HG resulted in the evasion of apoptosis in Burkitt lymphoma cells [23]. Another study found that overexpression of MIR17HG was involved in a negatively regulating proapoptotic gene in the occurrence of lung cancer [21]. MIR17HG could affect the abnormal expression of the miR-17-92 gene. The silencing of miR-17 has a crucial role in laryngeal squamous cell carcinoma progression. MIR17HG plays a distinct role in HPV-related HNSCC [15]. In addition, we observed that the expression level of the MIR17HG

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**Table 7: False-positive report probability analysis for the significant findings between MIR17HG variants and HNSCC risk.**

| Genotype and variables | OR (95% CI) | $p$ value | Statistical power | Prior probability | 0.25 | 0.10 | 0.01 | 0.001 | 0.0001 |
|-----------------------|------------|-----------|-----------------|-----------------|------|------|------|------|-------|
| III-IV                |            |           |                 |                 |      |      |      |      |       |
| rs17735387 G>A        |            |           |                 |                 |      |      |      |      |       |
| GA vs. GG             | 0.34 (0.12-0.95) | 0.040    | 0.308           | 0.192           | 0.416| 0.887| 0.988| 0.999 |
| GA-AA vs. GG          | 0.38 (0.15-0.97) | 0.042    | 0.329           | 0.205           | 0.436| 0.895| 0.988| 0.999 |
| rs7336610 T>C         |            |           |                 |                 |      |      |      |      |       |
| TC vs. TT             | 1.77 (1.09-2.86) | 0.021    | 0.487           | 0.106           | 0.262| 0.796| 0.975| 0.997 |
| TC-CC vs. TT          | 1.64 (1.04-2.57) | 0.032    | 0.031           | 0.156           | 0.357| 0.859| 0.984| 0.998 |
| rs1428 A>C            |            |           |                 |                 |      |      |      |      |       |
| CA vs. AA             | 1.73 (1.07-2.81) | 0.025    | 0.410           | 0.138           | 0.325| 0.841| 0.982| 0.998 |
| AC-CC vs. AA          | 1.63 (1.04-2.56) | 0.035    | 0.034           | 0.169           | 0.379| 0.870| 0.985| 0.999 |

HNSCC: head and neck squamous cell carcinoma. $p$ value was calculated by unconditional logistic regression analysis with adjustment for age and gender. Statistical power was calculated using the number of observations in the subgroup and the OR and $p$ values in this table. The level of false-positive report probability threshold was set at 0.2, and noteworthy findings are presented.

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**Figure 1:** The expression of the MIR17HG gene between HNSCC and normal tissues from the UALCAN database. HNSCC: head and neck squamous cell carcinoma.
gene in tumors is much higher than in normal tissues based on the UALCAN database (http://ualcan.path.uab.edu/cgi-bin/TCGAExResultNew2.pl?genenam=MIR17HG&ctype=HNSC) (Figure 1) [24]. We guess that the abnormal expression of MIR17HG also plays a vital role in the progression of HNSCC. As we all know, SNPs can affect the expression of genes. Thus, the study of the association between MIR17HG SNPs and HNSCC may help to understand whether they have a potential molecular role in the development of HNSCC.

rs7336610 and rs1428 have been identified in the correlation with human cancers at previous researches. The study of Chen et al. showed that there is a strongly increased association between rs7336610 and rs1428 and colorectal cancer susceptibility in the Chinese population in men [16]. Our study also exhibited the same association in HNSCC risk. However, Chacon-Cortes et al. found that rs7336610 is related to breast cancer susceptibility in females of Northern European [17]. In addition, it was shown that rs17735387 SNP played a crucial protective role in stage III/IV HNSCC patients compared with stage I/II. A recent study indicated that the mutation of SNP can influence the stability of lncRNA by changing its folding structure [25]. We speculate that SNPs in the MIR17HG gene contribute to HNSCC progression through influencing the stability.

Our study has some limitations. First, we have not detected the association of SNPs with HNSCC stratified by smoking and drinking status due to the very limited information from the medical records of participants. Next, we will collect more basic characteristics to study the associations. Second, whether the polymorphisms in the MIR17HG gene involved in the progression of HNSCC through affecting its functions, which is needed to explore in the subsequent work. Despite the limitations, our study supplied some scientific evidence for finding a new biomarker in the diagnosis and management of HNSCC.

5. Conclusions

In summary, our study showed that there is a strong association between MIR17HG genetic variants and HNSCC susceptibility in a Chinese population, which will provide available information for the molecular mechanism of HNSCC in the Chinese population.

Data Availability

Participant informed consent statements did not seek consent for data to be made publicly available; however, data will be made available to individual researchers upon reasonable request.

Ethical Approval

All procedures performed in studies involving human participants were in accordance with the ethical standards of the First Affiliated Hospital of Xi’an Jiaotong University and the 1964 Helsinki declaration.

Conflicts of Interest

All authors declare that they have no competing interests.

Authors’ Contributions

Yuan Shao and Baiya Li designed the study. Yuan Shao revised the manuscript. Chongwen Xu performed the data and wrote the manuscript. Wanli Ren, Hao Dai, Yanxia Bai, and Zhen Shen recruited and collected study samples. Peng Han analyzed the data. Chongwen Xu and Peng Han contributed equally to this work.

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