Interleukin-18 promoter genotype is associated with the risk of nasopharyngeal carcinoma in Taiwan

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Introduction

Nasopharyngeal carcinoma (NPC) is a rapidly growing squamous cell carcinoma that is manifested by distant metastasis and affects both adults and children.1 It has been reported that infection caused by the Epstein–Barr virus is a major risk factor for NPC.2 Furthermore, studies have shown that cigarette smoking and alcohol consumption constitute the environmental risk factors for NPC.3,4 Mounting evidence indicates that the variant genotypes of the genes related to inflammatory cytokines could modulate the susceptibility of individuals to cancers.5,6 Polymorphisms of these genes may affect the cellular responses to inflammation and the secretion of cytokines by altering the expression and function of the genes. In NPC-endemic areas, although every individual is exposed to the same environment, only a few develop the disease, suggesting that genetic differences such as single-nucleotide polymorphisms (SNPs) contribute to the risk of NPC.
carcinogenesis of NPC. However, the molecular mechanism by which these factors induce NPC still remains unknown. Increasing knowledge of NPC at the genomic level could indicate the novel biomarkers for the early detection and prediction of not only NPC susceptibility but also prognosis.

Interleukin-18 (IL-18), initially known as interferon-γ (IFN-γ)-inducing factor, is a cytokine with a proinflammatory biofunction and produced by activated macrophages, epithelial cells, osteoblasts, keratinocytes, and also cancer cells. Studies using animal models have demonstrated that administration of additional IL-18 resulted in the suppression of tumor growth, thus suggesting an important role of IL-18 in the host defense against cancer. Nevertheless, the role of IL-18 still remains incompletely understood. IL-18 is molecularly regulated and modulated under extremely complicated mechanisms in carcinogenesis, which is of great interest for oncologists. First, IL-18 may exert its tumor-suppressive effects by augmenting IFN-γ production, particularly in the presence of IL-12, promoting Th1 differentiation, enhancing the cytotoxic activities of natural killer cells and CD8+ lymphocytes, inducing cancer cell apoptosis, and inhibiting angiogenesis. Second, the activities of IL-18 have been reported to be effected by the microenvironmental milieu status; for instance, IL-18 could enhance the differentiation of Th2 based on the presence of IL-4. Moreover, IL-18 has the ability to suppress the recognition of cancer cells by immune cells, thereby enhancing the ability of cancer cells to adhere to the walls of the vascular cells, inducing the production of angiogenic and growth factors, and promoting a pro-metastatic microenvironment.

IL-18 levels were found to be much higher in the blood of patients with metastatic cancer than in patients without metastasis and in healthy people, thus deducing the reasonable hypothesis that serum IL-18 concentrations may be used as a noninvasive marker for detecting metastasis in breast cancer. All the abovementioned findings indicate that the pleiotropic cytokine IL-18 has the ability to biphasically perform its anticancerous and procancerous functions.

From the viewpoints of the genome, the expression of IL-18 appears to be regulated by at least two SNPs at the -607 (A/C) and -137 (G/C) positions of its promoter sequences. The former SNP may cause a change from A to C at position -607, which disrupts a potential cAMP-responsive element-binding protein site, and the latter may cause a change at position -137 from G to C, which may block the human histone H4 gene-specific transcription factor-1 nuclear factor-binding site. These differences in interaction between the sequences with related transcription factors are suggestive of the mechanisms through which the two promoter polymorphisms affect the overall IL-18 gene activity. Another well-known polymorphic site in the IL-18 promoter region is -656 (A/C) whose biofunction has not yet been clearly elucidated. In other words, the promoter polymorphism of IL-18 gene has been examined in autoimmune diseases but not frequently among cancers.

The majority of genomic studies published in the literature have focused on investigating the association between IL-18-607 and -137 polymorphisms and various types of cancers. Some of them have reported positive results, whereas others have reported negative findings. For instance, Pratesi et al showed that IL-18-607 or -137 polymorphism was not associated with NPC susceptibility. Similarly, Farhat et al also demonstrated a negative finding. However, Nong et al reported that the -137C/607A haplotype of IL-18 was associated with a significantly increased risk of NPC compared with its counterpart, the -137G/607C haplotype. In 2013, a meta-analysis investigating the contribution of IL-18 genotypes to cancer risk proposed that the C-607A polymorphism is significantly associated with overall cancer risk, especially in NPC and gastrointestinal cancer, and the G-137C polymorphism is associated with an increased overall cancer risk in Asian populations and also significantly increases the risk of NPC. In the present study, the SNPs at -656 (A/C, rs1946519), -607(A/C, rs1946518), and -137 (G/C, rs187238) in the promoter region of the IL-18 gene were identified and analyzed in patients with NPC in Taiwan.

**Patients and methods**

**Study subjects**

During the period from 2003 to 2009, a total of 176 patients with NPC were included through the general surgery outpatient clinics in China Medical University Hospital. All the patients were asked to participate in the project freely and voluntarily and to complete a questionnaire, in addition to providing 5 mL of their peripheral blood samples. The well-designed questionnaire consisted of questions pertaining to basic characteristics and history of cancer. In addition, the frequency of alcohol consumption, areca chewing, and smoking behaviors were recorded, in which “ever” was defined as more than twice a week for at least 1 year and then reclassified during analysis. The histological status of NPC was identified and judged by expert surgeons according to the 1991 WHO classification system. The histologic types included keratinizing squamous cell carcinoma (WHO type I) in 5 (2.8%) and non-keratinizing carcinoma (WHO type II) in...
were observed.9

For each patient with NPC, twice the number of age- and gender-matched cancer-free healthy subjects were selected from the pool of individuals undergoing regular health examination (age-matching was done within <5 years of the patient's first diagnosis) and included in the final comparison and evaluation. Consequently, a total of 352 healthy individuals, exactly twice the number of patients with NPC, were subjected to genotyping and final analysis. All the patients and healthy volunteers provided written informed consent. The study was approved by the authority from the institutional review board of China Medical University Hospital (DMR101-IRB1-306).

DNA preparation
Genomic DNA isolated from the peripheral blood leukocytes of each study subject was prepared using the QIAamp Blood Mini Kit (Qiagen NV, Venlo, the Netherlands), stored for long term at −80°C, diluted, and aliquoted for genotyping as a working stock at −20°C, as we do frequently.28,29

IL-18 genotyping methodology
The genotyping discrimination of IL-18-607 (A/C, rs1946518) and -137 (G/C, rs187238) polymorphisms was assessed using the ABI StepOne™ Real-Time PCR System (Thermo Fisher Scientific, Waltham, MA, USA) and analyzed by the typical TaqMan assay. For genotyping the IL-18-656 (A/C, rs1946519) polymorphism, the PCR-restriction fragment length polymorphism technique was applied using the primers reported by Folwaczny et al.30 The forward primer 5'-AGGTCACTTTTCTATCATCTCCAGG-3' and the reverse primer 5'-GTGAACAGAAGTAAAGCTTGCCGAGAGG-3' were used to amplify a 120-bp fragment of the IL-18-656 (A/C) polymorphism. The PCR products were cut by the restriction enzyme MwoI, and the DNA fragments were resolved in 3.0% agarose gel, stained by ethidium bromide, and visualized under UV (260 nm) light. For the A allele, a 120 bp PCR fragment was observed, whereas for the C allele, two 96/24 bp fragments were observed.9

Statistical analysis
The genotypic and clinical data of all the 352 controls and the 176 patients with NPC were statistically analyzed. To ensure that the control subjects were representative of the Taiwan population and to prevent any possible genotyping errors, the deviation of the genotypic frequencies of the investigated SNPs in the control groups from those expected under the Hardy–Weinberg equilibrium was assessed using the goodness-of-fit test. In addition, Pearson’s chi-squared test was used for assessing the statistical significance in the distribution of the investigated genotypes and Cochran–Armitage test was applied for the trend analysis. Student’s t-test was used to examine the differences in age, which is a continuous index, between the two groups. The associations between NPC risk and IL-18 genotypes were determined statistically by calculating the ORs and the corresponding 95% CIs using the logistic regression analysis, adjusted or unadjusted for these confounders. Any P-value <0.05 was considered to be statistically significant.

Results
Comparisons of basic characteristics of NPC and control groups
The frequency distributions of age, gender, and personal behavioral habits of the 176 patients with NPC and 352 non-cancer control subjects are summarized in Table 1. Because we matched the patients with twice the number of controls, there was no significant difference in age and gender between the case and control groups (P>0.05). There was also no significant difference between the case and control groups in terms of the distributions of personal behavioral habits, including smoking, alcohol consumption, and areca chewing status (P>0.05) (Table 1).

Association analysis of IL-18 genotypes and NPC risk in the study subjects
The genotypes of -656 (A/C, rs1946519), -607(A/C, rs1946518), and -137 (G/C, rs187238) polymorphisms of IL-18 were determined in all the patients and the age- and gender-matched healthy controls, and the results are summarized in Table 2. The genotype frequencies of the -656, -607, and -137 polymorphisms of IL-18 in both the case and control groups fit the Hardy–Weinberg equilibrium.

The genotypes of the IL-18 promoter -607(A/C) SNP were found to be differently distributed between patients and controls (P_{trend}=0.0090) (Table 2, middle panel). In detail, the IL-18-607 (A/C) homozygous CC variant genotypes were associated with decreased risks of NPC (OR =0.46, 95% CI =0.25–0.78, P=0.0093) (Table 2, middle panel). In both the dominant and recessive models, there were significant associations with the risk of NPC (Table 2, middle panel). These
significant results persisted even after adjusting for potential confounders, including age, gender, smoking, alcohol consumption, and areca chewing habits (Table 2, middle panel). Neither the genotypes nor the alleles at positions -656 and -137 showed any correlation with the risk of NPC in any of the groups (Table 2).

We also performed allelic analysis, and the results are shown in Table 3. Supporting the findings shown in Table 2, the results showed that the frequency of the variant allele C was 41.8% in the group of patients with NPC, which was significantly much lower than that (50.3%) in the control group (adjusted OR = 0.77, 95% CI = 0.63–1.04, P = 0.0089). Again, the other two SNPs demonstrated no significant association with the risk of NPC (Table 3).

**Stratified analysis of IL-18 genotypes according to environmental factors**

We further performed stratified analyses of the genotypic association between the IL-18-6607 polymorphism and the risk of NPC according to potential environmental risk factors in Taiwan, including cigarette smoking, alcohol consumption, and areca chewing habits. The adjusted ORs for carriers with the genotypes AC and CC at IL-18-607 were 0.69 and 0.37 among nonsmokers (95% CI = 0.42–1.02 and 0.22–0.73, P-values = 0.0947 and 0.0091, respectively) and 0.81 and 0.62 among smokers (95% CI = 0.41–1.42 and 0.33–1.37, P-values = 0.6137 and 0.3385, respectively). The protective effects of the IL-18-607 genotype against the risk of NPC appeared to be more obvious among nonsmokers (Table 4).

**Discussion**

Unlike other head and neck cancers, NPC is characterized by its specific multifactorial etiology, worldwide geographical distribution, and extremely high sensitivity to radiotherapy and chemotherapy induction during therapeutic processes. For several years, the members of Terry Fox Cancer Research Laboratory have been working on genomic biomarkers for early detection and prediction in Taiwan, where NPC is prevalent and causes several cancer-related deaths. Cytokines play a complex role in the initiation and progression of inflammation and tumorigenesis. Studies have confirmed that the proinflammatory cytokine IL-18 possesses antitumor capacity against lung cancer in several murine models. In addition, preclinical trials used the recombinant human IL-18 as an antidote and found it to be beneficial for the examined patients. However, despite the conventional view that IL-18 is an anticancer agent, some reports have also suggested that this multifunctional cytokine exhibits a procancerous activity under some conditions. Recently, an increasing number of studies have shown that various genotypes of cytokine genes may influence the production and serum levels of cytokines, which may be closely associated with susceptibility to certain human diseases.
Table 2 Distribution of IL-18 genotypes among the NPC patients and noncancer healthy controls

<table>
<thead>
<tr>
<th></th>
<th>Controls</th>
<th>Patients</th>
<th>OR (95% CI)</th>
<th>OR (95% CI)</th>
<th>P-valueb</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>%</td>
<td>OR (95% CI)</td>
<td>OR (95% CI)</td>
<td></td>
</tr>
<tr>
<td><strong>IL-18-656</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>134</td>
<td>38.0</td>
<td>64</td>
<td>36.4</td>
<td>1.00</td>
</tr>
<tr>
<td>AC</td>
<td>150</td>
<td>42.6</td>
<td>80</td>
<td>45.4</td>
<td>1.12</td>
</tr>
<tr>
<td>CC</td>
<td>68</td>
<td>19.3</td>
<td>32</td>
<td>18.2</td>
<td>0.99</td>
</tr>
<tr>
<td><strong>P</strong>_trendc</td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Carrier comparison</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA+AC</td>
<td>284</td>
<td>80.7</td>
<td>144</td>
<td>81.8</td>
<td>1.00</td>
</tr>
<tr>
<td>CC</td>
<td>68</td>
<td>19.3</td>
<td>32</td>
<td>18.2</td>
<td>0.93</td>
</tr>
<tr>
<td>AA</td>
<td>134</td>
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<td>64</td>
<td>36.4</td>
<td>1.00</td>
</tr>
<tr>
<td>AC+CC</td>
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<td>62.0</td>
<td>112</td>
<td>63.6</td>
<td>1.07</td>
</tr>
<tr>
<td><strong>IL-18-607</strong></td>
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<td></td>
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<tr>
<td>AA</td>
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<td>24.4</td>
<td>59</td>
<td>33.5</td>
<td>1.00</td>
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<tr>
<td>AC</td>
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<td>50.6</td>
<td>87</td>
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<tr>
<td>CC</td>
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<td>25.0</td>
<td>30</td>
<td>17.1</td>
<td>0.50</td>
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<tr>
<td><strong>P</strong>_trendc</td>
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<tr>
<td><strong>Carrier comparison</strong></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>AA+AC</td>
<td>264</td>
<td>75.0</td>
<td>146</td>
<td>82.9</td>
<td>1.00</td>
</tr>
<tr>
<td>CC</td>
<td>88</td>
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<td>30</td>
<td>17.1</td>
<td>0.62</td>
</tr>
<tr>
<td>AA</td>
<td>86</td>
<td>24.4</td>
<td>59</td>
<td>33.5</td>
<td>1.00</td>
</tr>
<tr>
<td>AC+CC</td>
<td>266</td>
<td>75.6</td>
<td>117</td>
<td>66.7</td>
<td>0.64</td>
</tr>
<tr>
<td><strong>IL-18-137</strong></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>281</td>
<td>79.8</td>
<td>133</td>
<td>75.6</td>
<td>1.00</td>
</tr>
<tr>
<td>GC</td>
<td>65</td>
<td>18.5</td>
<td>38</td>
<td>21.6</td>
<td>1.24</td>
</tr>
<tr>
<td>CC</td>
<td>6</td>
<td>1.7</td>
<td>5</td>
<td>2.8</td>
<td>1.76</td>
</tr>
<tr>
<td><strong>P</strong>_trendc</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Carrier comparison</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG+GC</td>
<td>346</td>
<td>98.3</td>
<td>171</td>
<td>97.2</td>
<td>1.00</td>
</tr>
<tr>
<td>CC</td>
<td>6</td>
<td>1.7</td>
<td>5</td>
<td>2.8</td>
<td>1.69</td>
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<tr>
<td>GG</td>
<td>281</td>
<td>79.8</td>
<td>133</td>
<td>75.6</td>
<td>1.00</td>
</tr>
<tr>
<td>GC+CC</td>
<td>71</td>
<td>20.2</td>
<td>43</td>
<td>24.4</td>
<td>1.28</td>
</tr>
</tbody>
</table>

Notes: *Adjusted with age, gender, smoking, alcohol drinking, and areca chewing habits. |Based on chi-squared test without Yates’ correction. |Cochran–Armitage test was applied for the trend analysis. Bold values are statistically significant.
Abbreviations: IL-18, interleukin-18; NPC, nasopharyngeal carcinoma.

Table 3 Allelic frequency analysis for IL-18 polymorphisms and NPC

<table>
<thead>
<tr>
<th>Allele</th>
<th>Controls, n (%)</th>
<th>Patients, n (%)</th>
<th>OR (95% CI)b</th>
<th>P-valueb</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n (%)</td>
<td>n (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>IL-18-656</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>418 (59.4)</td>
<td>208 (59.1)</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>286 (40.6)</td>
<td>144 (40.9)</td>
<td>1.05 (0.84–1.23)</td>
<td>0.9294</td>
</tr>
<tr>
<td><strong>IL-18-607</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>350 (49.7)</td>
<td>205 (58.2)</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>354 (50.3)</td>
<td>147 (41.8)</td>
<td>0.77 (0.63–1.04)</td>
<td>0.0089*</td>
</tr>
<tr>
<td><strong>IL-18-137</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>627 (89.1)</td>
<td>304 (86.4)</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>77 (10.9)</td>
<td>48 (13.6)</td>
<td>1.15 (0.71–1.95)</td>
<td>0.2006</td>
</tr>
</tbody>
</table>

Notes: *OR was adjusted with age, gender, smoking, alcohol drinking, and areca chewing. |Based on chi-squared test without Yates’ correction. Bold values are statistically significant.
Abbreviations: IL-18, interleukin-18; NPC, nasopharyngeal carcinoma.

their binding capacity with transcription factors. The two IL-18 promoter polymorphisms -607 and -137 were previously shown to be positively associated with several types of cancers, including esophageal squamous cell carcinoma and prostate cancer in Chinese subjects, colorectal cancer in Greek subjects, ovarian cancer in US subjects (Hawaiians), and breast cancer in Iranian subjects. In contrast, studies have also reported negative findings regarding the
association between \(\text{IL-18}\) polymorphisms and squamous cell carcinoma of the head and neck cancers in Iranian subjects or oral cancer in Greek subjects. These discrepant results may be explained by the following three possibilities: the dual effects of \(\text{IL-18}\) on the tumor immune response, the different types of tumors, and the various populations that were investigated.

To our knowledge, this is the first study to investigate the SNPs at the positions -656 (G/T), -607 (C/A), and -137 (G/C) of the \(\text{IL-18}\) promoter region in patients with NPC and noncancer healthy control individuals in a Taiwanese population and evaluate their contribution to the prediction of NPC risk. The results showed significant protective effects of the CC homo-variant genotypes and the C allele at position -607 of the \(\text{IL-18}\) gene against NPC susceptibility (Tables 2 and 3). Regarding -656 and -137 genotypes of \(\text{IL-18}\), there was no significant association between any genotype or allelic type and the risk of NPC (Tables 2 and 3). The positive finding indicating that the genotype of the \(\text{IL-18}-607\) polymorphism was the determinant of NPC susceptibility and was found to be inconsistent with all the previous findings investigating the contribution of \(\text{IL-18}\) genotypes to the risk of NPC, which were reported by Pratesi et al,\(^{24}\) Farhat et al,\(^{25}\) and Nong et al.\(^{26}\) In 2013, the meta-analysis reported by Guo and Xia\(^{27}\) combined all the available limited and updated literature and demonstrated that the C allele of \(\text{IL-18}-607\) had a protective effect against the risk of NPC, especially for Asians, but not for Africans or Europeans. This is consistent with another meta-analysis reported in 2013.\(^{27}\) The first positive finding of this study, while uniquely consistent with the abovementioned overall meta-analysis, may be due to the fact that Taiwan is located in East Asia and is an island with conserved genetic, cultural, and environmental background. Although the sample size of this study is relatively larger than that of other studies, the contribution of \(\text{IL-18}\) genotypes, especially those at \(\text{IL-18}-607\), must be validated using larger samples and other populations across the world. All the results pertaining to the contribution of \(\text{IL-18}\) genotypes to the risk of NPC are concisely summarized in Table 5. Among the NPC susceptibility genes investigated in this study, the roles of human leukocyte antigen (HLA) genes have been most intensively examined and claimed to be associated with the outcome of NPC by different research groups across the world.\(^{41−47}\) However, the findings are still inconclusive, and the detailed mechanisms underlying the effect have not been completely elucidated. Similar to the case of HLA genes, further clinical studies investigating the contribution of \(\text{IL-18}\) genotypes to NPC using larger sample sizes from various ethnic groups are still needed to fulfill the possibility of enhancing the early diagnosis and personalized treatment of NPC.

Substratification of the patients with NPC and noncancer subjects according to their personal behavioral habits revealed that the \(\text{IL-18}-607\) genotype may play a significantly important role in the determination of the susceptibility to NPC among nonsmokers, but not smokers (Table 4). In 2017, Long et al reported that cigarette smoking was associated with an increased risk for NPC, especially for subjects who are young, male, and had early-onset, long-term, and undifferentiated type of NPC.\(^{4}\) However, the authors did not examine the effect of interaction between genotypes (such as \(\text{IL-18}-607\)) and smoking on the risk of NPC. Therefore, further investigations are needed to elucidate the detailed mechanisms underlying the interaction between \(\text{IL-18}\) and other molecules and environmental factors related to the etiology of NPC.

**Conclusion**

To our knowledge, this is the first study indicating a significant association between \(\text{IL-18}-607\) polymorphism and the risk of NPC in Taiwan. This is also the first study to investigate the interaction between \(\text{IL-18}\) genotypes and environmental factors in terms of the risk of NPC. The significant association between \(\text{IL-18}-607\) polymorphism and the risk of NPC was particularly observed in patients without...
smoking behavior. Additional data from a larger number of subjects and other populations are required to validate the positive findings of IL-18 genotypes as a biomarker for early detection and prediction of NPC. These results suggest that IL-18 plays an important role in the carcinogenesis of NPC in Taiwan and that the interaction between IL-18-607 polymorphism and smoking in NPC etiology is worth further research.

Acknowledgments

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Disclosure

The authors report no conflicts of interest in this work.

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