RESEARCH ARTICLE

N-Acetyltransferase 2 Gene Polymorphisms are Associated with Susceptibility to Cancer: a Meta-analysis

Fang-Shuo Tian1,2, Li Shen1,2, Yang-Wu Ren1,2, Yue Zhang1,2, Zhi-Hua Yin1,2, Bao-Sen Zhou1,2*

Abstract

N-acetyltransferase 2 (NAT2) is a polymorphic enzyme that plays an important role in the metabolism of various potential carcinogens. In recent years, a number of studies have been carried out to investigate the relationship between the rs1799930 and rs1799931 polymorphism in NAT2 and cancer risk in multiple populations for different types of cancer. However, the results were not consistent. Therefore, we performed a meta-analysis to further explore the relationship between NAT2 polymorphism and the risk of cancer. A total of 21 studies involving 15,450 subjects for rs1799930 and 13,011 subjects for rs1799931 were included in this meta-analysis. Crude odds ratios (ORs) with 95% confidence intervals (CIs) were used to assess strength of associations. We also evaluated the publication bias and performed a sensitivity analysis. Overall, our results showed an apparent significant association between the NAT2 rs1799930 polymorphism and cancer susceptibility in Asians (GA vs. GG: OR=1.22, 95% CI=1.03-1.45; dominant model: OR=1.22, 95% CI=1.03-1.43) and population-based controls (GA vs. GG: OR=1.10, 95% CI=1.01-1.19; dominant model: OR=1.09, 95% CI=1.01-1.18). In contrast, a significant association was observed between the NAT2 rs1799931 G>A polymorphism and decreased cancer susceptibility in overall meta-analysis (AA vs. GG: OR=0.55, 95% CI=0.33-0.93; GA vs. GG: OR=1.00, 95% CI=0.86-1.14; dominant model: OR=0.97, 95% CI=0.86-1.10; recessive model: OR=0.56, 95% CI=0.34-0.94) and the Asian group (AA vs. GG: OR=0.50, 95% CI=0.26-0.94; recessive model, OR=0.50, 95% CI=0.27-0.94). We found that the NAT2 rs1799930 may be a risk factor, while the NAT2 rs1799931 polymorphism is associated with a decreased risk of cancer and is likely a protective factor against cancer development.

Keywords: NAT2 - polymorphism - association - cancer susceptibility - meta-analysis

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Introduction

N-acetyltransferase 2 (NAT2) gene, located in chromosomal region 8p21.3-23.1, encodes a phase II xenobiotic metabolizing enzyme (Blum et al., 1990; Hickman et al., 1998). As one of the phase II metabolizing enzymes, it played a essential part in the metabolism of aromatic, heterocyclic amines and hydrazines via N-acetylation and O-acetylation which was significant ultimate carcinogens involved in the initiation process of cancer (Hein et al., 1993; De Stefani et al., 1998).

In recent years, some studies have reported the association NAT2 variants such as the polymorphism rs1799930 (G590A) and rs1799931 (G857A) with risk of several types of cancer, including colorectal cancer, lung cancer, breast cancer and acute lymphoblastic leukemia. However, the results of these studies have still been discordant Kown et al (Kown et al., 2013) have conducted a study which showed that Asian Americans experienced disproportionate incidence and mortality rates of certain cancers, for example, liver cancer and stomach cancer were perceived as higher cancer risks among Asian Americans than among the general population. Our study was a meta-analysis of all relevant studies published up to May 2013. It presented the more precise estimation on the relationship between NAT2 G590A and G857A and susceptibility to the development of cancer.

Materials and Methods

Literature search

Databases of Medline, PubMed, Embase, Web of Science and China National Knowledge Infrastructure (CNKI) were performed (between January 2005 and May 2013). The following search words and their combinations were used: (“genetic polymorphism” or “polymorphism” or “SNP” or “gene mutation” or “genetic variants”) and (“cancer” or “lymphocytic leukemia” or “carcinoma” or “malignancy”) and (“NAT2” or “G590A” or “rs1799930” or “G857A” or “rs1799931”). All searched studies were retrieved, and their bibliographies were checked for the other relevant publications. For overlapping and
In our meta-analysis, we investigated the association between NAT2 rs1799930 and rs1799931 polymorphism and cancer risk according to pooled OR with corresponding 95% CI. For rs1799930, we estimated cancer risk associated with the co-dominant (AA versus GG; GA versus GG), dominant model (AA+GA versus GG) and recessive model (AA versus GA+GG) ; for rs1799931, we also applied co-dominant (AA versus GG; GA versus GG), dominant model (AA+GA versus GG) and recessive model (AA versus GA+GG) to evaluate cancer risks. Stratification analysis was performed by ethnicity, type of cancer and source of controls. The significance of the pooled ORs was determined by the Z test and \( p \leq 0.05 \) was considered as statistically significant.

In our study, HWE was tested using the chi-squared goodness-of-fit test. The heterogeneity of studies was examined through the Q-test and the I² test (Colditz et al., 1995; Higgins et al., 2002). If between-study heterogeneity was significant (\( p \leq 0.05 \) for the Q-test and I² \( \geq 50\% \)), we used a random-effects model (DerSimonian-Laird method) (DerSimonian et al., 1986). Otherwise, the fixed-effects model (AA versus GA+GG) was used. Sensitivity was performed by omitting individual studies, in order to determine the stability of results in this meta-analysis. To assess the potential publication bias, Begg’s funnel plot was generated as the visual inspection to detect bias (Begg et al., 1994), besides Egger’s test was also conducted to analyze the publication bias statistically (Egger et al., 1997). All the \( p \)-values were two-sided. All analyses were calculated using STATA Version 11.0 software (Stata Corporation, College Station, TX, USA).

**Results**

**Characteristics of included studies**

By searching the databases, 474 abstracts were collected according to the search criteria. Of these 474 articles, 303 were excluded after reviewing the title...
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Table 2. Results of Meta-Analysis for NAT2 rs1799930 Polymorphism and Cancer Risk

<table>
<thead>
<tr>
<th>NAT2 rs1799930</th>
<th>AA vs. GG OR (95% CI)</th>
<th>GA VS. GG OR (95% CI)</th>
<th>Dominant model OR (95% CI)</th>
<th>Recessive model OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Ethnicity</td>
<td>1.01 (0.89, 1.14)</td>
<td>1.06 (0.99, 1.14)</td>
<td>1.05 (0.99, 1.12)</td>
<td>0.97 (0.87, 1.10)</td>
</tr>
<tr>
<td>Caucasian</td>
<td>0.96 (0.84, 1.11)</td>
<td>1.04 (0.96, 1.12)</td>
<td>1.03 (0.95, 1.10)</td>
<td>0.95 (0.83, 1.08)</td>
</tr>
<tr>
<td>Asian</td>
<td>1.23 (0.91, 1.65)</td>
<td>1.22 (1.03, 1.45)</td>
<td>1.22 (1.03, 1.43)</td>
<td>1.10 (0.83, 1.46)</td>
</tr>
<tr>
<td>Type of cancer</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Colorectal cancer</td>
<td>1.00 (0.82, 1.20)</td>
<td>1.08 (0.97, 1.19)</td>
<td>1.06 (0.96, 1.17)</td>
<td>0.96 (0.80, 1.16)</td>
</tr>
<tr>
<td>Lung cancer</td>
<td>0.83 (0.54, 1.28)</td>
<td>0.98 (0.79, 1.22)</td>
<td>0.96 (0.78, 1.18)</td>
<td>0.84 (0.55, 1.29)</td>
</tr>
<tr>
<td>Breast cancer</td>
<td>0.94 (0.70, 1.28)</td>
<td>1.05 (0.88, 1.25)</td>
<td>1.03 (0.87, 1.22)</td>
<td>0.92 (0.69, 1.23)</td>
</tr>
<tr>
<td>Gastric cancer</td>
<td>0.64 (0.39, 0.96)</td>
<td>0.89 (0.68, 1.15)</td>
<td>0.84 (0.65, 1.09)</td>
<td>0.68 (0.42, 1.10)</td>
</tr>
<tr>
<td>Other cancer</td>
<td>1.12 (0.84, 1.50)</td>
<td>1.11 (0.94, 1.31)</td>
<td>1.11 (0.95, 1.30)</td>
<td>1.07 (0.81, 1.42)</td>
</tr>
<tr>
<td>Source of controls</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Population-based</td>
<td>1.07 (0.92, 1.24)</td>
<td>1.10 (1.01, 1.19)</td>
<td>1.09 (1.01, 1.18)</td>
<td>1.03 (0.89, 1.18)</td>
</tr>
<tr>
<td>Hospital-based</td>
<td>0.89 (0.72, 1.09)</td>
<td>1.00 (0.89, 1.13)</td>
<td>0.98 (0.88, 1.10)</td>
<td>0.88 (0.72, 1.08)</td>
</tr>
</tbody>
</table>

Table 3. Results of Meta-Analysis for NAT2 rs1799931 Polymorphism and Cancer Risk

<table>
<thead>
<tr>
<th>NAT2 rs1799931</th>
<th>AA VS. GG OR (95% CI)</th>
<th>GA VS. GG OR (95% CI)</th>
<th>Dominant model OR (95% CI)</th>
<th>Recessive model OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Ethnicity</td>
<td>0.55 (0.33, 0.93)</td>
<td>1.00 (0.88, 1.14)</td>
<td>0.97 (0.86, 1.10)</td>
<td>0.56 (0.34, 0.94)</td>
</tr>
<tr>
<td>Caucasian</td>
<td>1.07 (0.29, 4.00)</td>
<td>1.13 (0.94, 1.35)</td>
<td>1.13 (0.94, 1.35)</td>
<td>1.10 (0.29, 4.15)</td>
</tr>
<tr>
<td>Asian</td>
<td>0.50 (0.26, 0.94)</td>
<td>0.95 (0.77, 1.17)</td>
<td>0.90 (0.73, 1.10)</td>
<td>0.50 (0.27, 0.94)</td>
</tr>
<tr>
<td>Type of cancer</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Colorectal cancer</td>
<td>1.40 (0.23, 5.83)</td>
<td>1.10 (0.87, 1.39)</td>
<td>1.10 (0.88, 1.39)</td>
<td>1.40 (0.23, 5.80)</td>
</tr>
<tr>
<td>Lung cancer</td>
<td>0.48 (0.16, 1.38)</td>
<td>1.08 (0.78, 1.50)</td>
<td>1.01 (0.74, 1.39)</td>
<td>0.47 (0.16, 1.35)</td>
</tr>
<tr>
<td>Gastric cancer</td>
<td>2.86 (0.12, 7.21)</td>
<td>1.05 (0.64, 1.71)</td>
<td>1.08 (0.66, 1.75)</td>
<td>3.09 (0.12, 76.83)</td>
</tr>
<tr>
<td>Other cancer</td>
<td>0.49 (0.22, 1.12)</td>
<td>1.01 (0.81, 1.28)</td>
<td>0.97 (0.78, 1.22)</td>
<td>0.50 (0.22, 1.13)</td>
</tr>
<tr>
<td>Source of controls</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Population-based</td>
<td>0.61 (0.31, 1.22)</td>
<td>1.01 (0.86, 1.19)</td>
<td>0.99 (0.84, 1.17)</td>
<td>0.62 (0.31, 1.24)</td>
</tr>
<tr>
<td>Hospital-based</td>
<td>0.48 (0.22, 1.06)</td>
<td>0.99 (0.80, 1.21)</td>
<td>0.94 (0.77, 1.16)</td>
<td>0.49 (0.23, 1.08)</td>
</tr>
</tbody>
</table>

Meta-analysis results

NAT2 rs1799930 By pooling genotype datum from all 20 studies, the meta-analysis results of NAT2 rs1799930 were listed in Table 2. Overall, The combined results based on all studies showed that no significant association was found between the NAT2 rs1799930 polymorphism and cancer risk (AA vs. GG: OR=1.01, 95% CI=0.89-1.14; GA vs. GG: OR=1.06, 95% CI=0.99-1.14; dominant model: OR=1.05, 95% CI=0.99-1.12; recessive model: OR=0.97, 95% CI=0.87-1.10).

Several stratified analyses were performed according to the ethnicity, type of cancer and source of controls (Table 2). Subgroup analyses for the different ethnic groups were therefore conducted. There was significant association with the risk of cancer in Asian (GA vs. GG: OR=1.22, 95% CI=1.03-1.45; Figure 1; dominant model: OR=1.22, 95% CI=1.03-1.43) but not in Caucasian. The result of subgroup analyses in different source of controls showed that rs1799930 G>A polymorphism increased the cancer risk in population-based control (GA vs. GG: OR=1.10, 95% CI=1.01-1.19; Figure 2; dominant model: OR=1.10, 95% CI=1.01-1.19).
Sensitivity analysis and publication bias

An independent study involved in this meta-analysis was performed to evaluate the influence of the individual data set on the pooled ORs each time. The results were not substantially altered, indicating that our results were stable and robust. Begg’s funnel plots were conducted to assess publication bias, and the shapes revealed no evidence of obvious asymmetry. Egger’s test was based on linear regression of the standard normal deviate against its precision, which was performed to test the existence of publication bias. The results did not show any evidence of publication bias for NAT2 rs1799930 (t=-0.24, \( p = 0.815 \) for AA vs. GG; t=0.80, \( p = 0.433 \) for GA vs. GG). Meanwhile, the results indicated publication bias for NAT2 rs1799931 (t=0.89, \( p = 0.394 \) for AA vs. GG; t=-0.31, \( p = 0.763 \) for GA vs. GG).

Discussion

NAT2 mainly encoded drug phase-II metabolic enzyme, namely N-acetyltransferase 2, which was most frequently present in the liver and the intestinal mucosa. Allelic polymorphism of the NAT2 enzyme has been investigated for a long time, first detected phenotypically, based on enzyme activity distribution in healthy subjects, and later these activity differences were bound to an allelic polymorphism (Le Marchand et al., 1996). Probst Hensch et al. reported an inverse association between NAT2 rapid genotypes and colorectal adenomas among African Americans, but an increased risk among whites (Probst-Hensch et al., 1995). Other studies found that NAT2 rapid genotypes played a great role in susceptibility of colorectal cancer (Osian et al., 2006), but not in susceptibility of lung cancer (Borlak et al., 2006). Currently available data were not concordant due to ethnic differences and differences in types of cancer.

NAT2 catalyzed the reaction in which environment carcinogens (such as aromatic, heterocyclic amines, hydrazines) combined with some strong polar groups (such as methyl and acetyl) can be metabolized out of the body (Windmill et al., 2000; Pande et al., 2003; Yamada et al., 2004).
et al., 2009). There were some sites of mutation in NAT2 gene polymorphism, G590A and G857A of which were high-profile (Hickman et al., 1992). At the 590 position a G>A substitution resulted in the arginine 197 to glutamine substitution. A G>A substitution at position 857 produced replacement of glycine by gluta in the 286th amino acid of the protein (Hein et al., 1988). The locus mutation directly caused to change activity of metabolic enzyme, which affected the metabolism of some drugs and carcinogens inactivation or activation and made incidence of cancer increase or decrease. Although, the markedly association between NAT2 rs1799930 and rs1799931 polymorphism and cancer risk was found in some publications (Majumdar et al., 2008; Zanrosso et al., 2012), while some other studies indicated that rs1799930 and rs1799931 had no any correlation with the risk of cancer (Gemignani et al., 2007; Al-Moundhri et al., 2007). In order to resolve this contradiction, we performed a meta-analysis involving in 21 eligible studies to understand if the rs1799930 and rs1799931 polymorphism were significantly associated with risk of cancer in ethnicity, types of cancer and source of controls.

For rs1799930 G>A, the result of this meta-analysis indicated that there was a weak association with risk of cancer in Asian and population-based control, but not in Caucasian and hospital-based control, which indicated that the differences in genetic backgrounds might be a critical factor on the effects of the association between NAT2 rs1799930 G>A polymorphism and the risk of cancer.

For rs1799931 G>A, a negative association with cancer susceptibility was found, which showed a protective effect of the rs1799931 against cancer development. In the subgroup analysis by ethnicity, rs1799931 might decrease the risk of cancer in the Asian population, but not in the Caucasian population, while it was not associated with cancer risk in other subgroups. Those results indicated that the different ethnicity may influence cancer susceptibility by different genetic back-grounds and environmental exposures through gene-gene and gene-environmental interactions.

Our meta-analysis also had many advantages compared with others’ work. Firstly, sufficient data was extracted form well-selected studies, providing stable and robust power for this meta-analysis. Secondly, all of studies we included didn’t show obvious publication bias, according to Begg and Egger’s formal statistical test. Besides, the results were consistent with Hardy-Weinberg equilibrium in control population of all the studies.

Some limitations of this study should be acknowledged and taken into consideration. First, detailed information, such as the mean age and sex of the case and control populations, was not available in all of the selected studies. Secondly, the controls were not uniformly defined. Some of the controls may potentially have benign disease. In addition, our results were based on unadjusted estimates without adjustment for other risk factors such as age, smoking status, drinking status, obesity, environmental factors and so on.

In conclusion, our meta-analysis indicated that the NAT2 rs1799930 had an association with risk of cancer in Asian and population-based control while NAT2 rs1799931 polymorphism was associated with a decreased risk of cancer and was likely a protective factor against cancer development. Whereas it is necessary to conduct large sample studies so that improving statistical power and overcoming the limitations of individual studies. Furthermore, gene-gene and gene-environment interactions should also be considered in the analysis. Further studies will take these factors into account to evaluate the association between NAT2 rs1799931 and rs1799930 polymorphism and cancer susceptibility more precisely.

Acknowledgements

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References


