

Genetic polymorphism in cytochrome P450 2E1 and alcoholic pancreatitis susceptibility: a meta-analysis

Wu C¹, Wu D¹, Liu Y², Zhong Y^{1,2,3}

¹ICU Center of the Second Xiangya Hospital

²Hematological department of the Third Xiangya Hospital
Central South University, Changsha, China

³Department of Surgery of University of Pittsburgh, Pittsburgh, Pennsylvania, USA

Abstract

Background: The association between *cytochrome P450 2E1 (CYP2E1)* polymorphism and the risk of alcoholic pancreatitis is contentious. This meta-analysis aimed to demonstrate the association between *CYP2E1* RsaI/PstI, or DraI polymorphisms and the susceptibility of alcoholic pancreatitis.

Materials and Methods: We searched for sources and background in Pubmed, Medline, Web of science and CNKI (Chinese national knowledge infrastructure), using the following keywords: “cytochrome P450 2E1” or “CYP2E1”, “polymorphism” or “genotype”, in combination with “alcoholic pancreatitis”. All meta-analyses were performed with Stata 12.0. Subgroup analyses on ethnicity and type of alcoholic pancreatitis were conducted as well.

Results: Eleven articles, which met the inclusion criteria, included 595 patients with alcoholic pancreatitis, and 1767 controls. For the general population, our analysis suggested no obvious association between *CYP2E1* RsaI/PstI or DraI polymorphisms and the risk of alcoholic pancreatitis. However, in the non-Asian subgroup, significant associations were found between the risk for alcoholic pancreatitis and *CYP2E1* RsaI/PstI polymorphism [dominant model: odds ratio (OR)=1.92, 95 % confidence interval (CI): 1.25-2.95, $p=0.003$; allelic contrast model: OR=1.99, 95 % CI: 1.35-2.92, $p<0.001$. There was not a significant association found within the Asian group. Meanwhile, the susceptibilities of chronic alcoholic pancreatitis were significantly increased for dominant and allelic contrast models of *CYP2E1* RsaI/PstI polymorphism [OR=1.62, 95 % CI: 1.12-2.34; $p=0.011$; OR=1.62, 95 % CI: 1.17-2.24, $p=0.004$, respectively] but not for acute alcoholic pancreatitis for all population.

Conclusions: *CYP2E1* RsaI/PstI polymorphism may increase the risk of alcoholic pancreatitis in the non-Asian population. Additionally, the *CYP2E1* RsaI/PstI polymorphism may increase the susceptibility for chronic alcoholic pancreatitis for all population. HIPPOKRATIA 2018, 22(2): 60-67.

Keywords: Cytochrome P450 2E1, CYP2E1, polymorphism, alcoholic pancreatitis, meta-analysis

Corresponding author: Zhong Yanjun, MD, PhD, No. 139 Renmin Middle Road, Furong, Changsha 410011, China, tel: +86073185295270, fax: +86073185295270, e-mail address: zhongyanjun@csu.edu.cn

Introduction

Alcohol abuse is a severe medical and socioeconomic problem¹, which is known to cause pancreatitis, a type of inflammation of the pancreas. There are two forms of alcoholic pancreatitis, acute and chronic. They are essentially the same disease but at different stages. Alcohol is the leading cause of chronic pancreatitis in approximately 70 % to 80 % of the patients living in developed societies^{2,3}. It was reported that characterization of intestinal microbiota contributed to the occurrence of pancreatitis in alcoholics⁴. In addition, genetic factors also play a significant role in the risk of pancreatic injury, and the inflammatory processes^{5,6}.

Cytochrome P450 2E1 (CYP2E1), a member of CYP family, metabolizes low-molecular-weight com-

pounds, such as endogenous substrates, centrally acting drugs, and bio-activating toxins^{7,8}. CYP2E1 is primarily expressed in the liver, but also exists in the pancreas⁹. The human *CYP2E1* gene exhibits two point mutations in the 5' flanking region (RsaI/PstI), which are in complete linkage disequilibrium, and one mutation in 6' flanking region (DraI, alleles D and C). *CYP2E1* polymorphisms also play a role in transcriptional activation of the *CYP2E1* gene¹⁰. Previous meta-analyses suggested that *CYP2E1* polymorphisms were significantly associated with the susceptibilities of many diseases, such as lung cancer, gastric cancer, cervical neoplasia, and breast cancer¹¹⁻¹⁴.

Plenty of studies investigated the association of *CYP2E1* RsaI/PstI and DraI polymorphisms with the

risk of alcoholic pancreatitis. Despite this effort, whether CYP2E1 genetic polymorphism can influence the risk of alcoholic pancreatitis remains unclear. Therefore, this meta-analysis was performed to explicate this relationship.

Materials and methods

Data sources and search strategy

In the literature review process, we searched for articles in Pubmed, Medline, Web of science, and CNKI (Chinese national knowledge infrastructure) (ended on May 2018), using the following keywords: “cytochrome P450 2E1” or “CYP2E1”, “polymorphism” or “genotype”, in combination with “alcoholic pancreatitis”. All studies that met the inclusion criteria were then manually screened by two authors, according to the titles and abstracts. Then, the full texts of these articles were retrieved and independently reviewed by two authors and then referred to another author in the instance of disagreements.

Inclusion and exclusion criteria

Studies were searched to fulfill all of the following criteria: First, the study’s primary focus had to pertain to the association of alcoholic pancreatitis and polymorphism of *CYP2E1*. Secondly, it had to be an observational study. Lastly, the study must have provided information about the sample size, ethnicity, and genetic distribution of the sample group. Exclusion criteria included: unrelated theme, absence of control subjects, and undetectable mutant type.

Data extraction

Two investigators independently extracted data. If necessary, a discussion and re-examination were conducted to achieve an agreement. When same authors published an additional article using the same case series, the most complete and recent publication was selected. When studies involved several separate control groups

(healthy alcoholics, healthy non-alcoholic volunteers or blood donors, respectively), pooled data of these three control groups were considered as one control group for analysis. Data were extracted from the included studies as follows: the first author, year of publication, number of cases, country, race, control type, age, and type of alcoholic pancreatitis.

Statistical analysis

Our meta-analysis followed the recommendations of the PRISMA statement. Newcastle-Ottawa Scale (NOS) criteria were used to assess the study quality. Those studies that met five or more NOS criteria were considered of high quality. The odds ratio (OR) was plotted to measure any possible sample size bias. Heterogeneity analysis was performed using I^2 value. Results were summarized using forest plots. Egger’s test and the funnel plot were performed to evaluate the publication bias. Subgroup analyses were also performed on race and type of alcoholic pancreatitis. STATA 12.0 software was used to perform all the statistical analyses (Stata Corp., Texas, USA).

Results

Study characteristics

As shown in Figure 1, we identified for this meta-analysis 38 publications, 18 irrelevant papers, four review articles¹⁵⁻¹⁸, and two papers on animal studies^{19,20} that were discarded. One conference paper²¹ was discarded because it did not show any genotype results. After the entire exclusion process, 13 observational studies met the inclusion criteria. Four of these 13 studies²²⁻²⁵ used the same two case series, so the most recent publications were included^{22,25}. Ultimately, 11 publications were included^{6,22,25-33}, including 595 patients with alcoholic pancreatitis, and 1767 controls.

Nine out of 11 studies were published in English^{6,22,25,26,28-31,33}, one in Russian³², and one in Korean language²⁷. The detailed information is shown in Table 1.

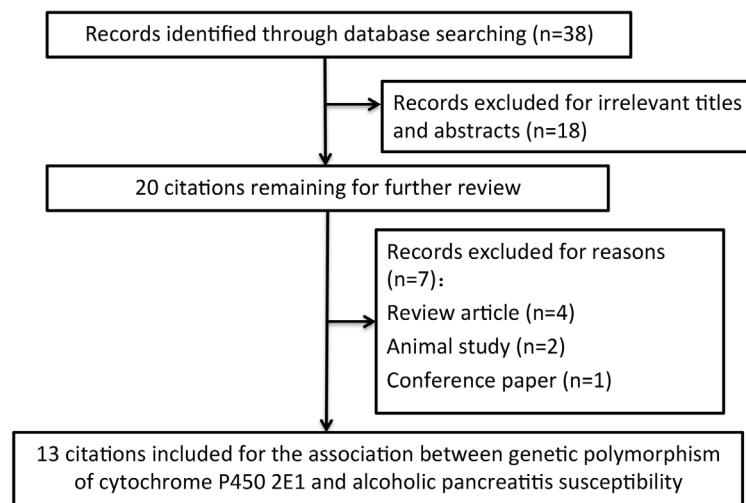


Figure 1: Flow diagram of the search strategy and study selection of the present Meta-Analysis.

Table 1: Characteristics of the studies included in the present meta-analysis.

| First author | Publication year | Country | Racial decent | Number of cases (M/F) | Number of controls (M/F) | Type of controls | Median (or mean) age, (range or SD)year (Cases/Controls) | Studied genes |
|---------------------------|------------------|-----------|---------------|-----------------------|--------------------------|---|--|----------------|
| Matsumoto ²⁸ | 1996 | Japan | Japanese | 52 (48/4) | 244 (214/30) | Healthy alcoholics | 48±11/51±11 | RsaI/PstI |
| Chao ²⁵ | 1997 | China | Chinese | 48 (42/6) | 119 (119/0) | Healthy alcoholics and non-drinker healthy volunteers | 41.6±10.8/26.8±? * | RsaI/PstI |
| Maruyama ³³ | 1999 | Japan | Japanese | 54 (NM) | 46 (NM) | Healthy alcoholics | NM | RsaI/PstI |
| Yang ³¹ | 2001 | England | Caucasian | 57 (NM) | 201 (NM) | Alcoholic controls and normal controls | NM | RsaI/PstI/DraI |
| Frenzer ²⁶ | 2002 | Australia | Caucasian | 71 (61/10) | 257(166/91) | Healthy alcoholics and blood donors | 53±NM/48±NM | RsaI/PstI/DraI |
| Verlaan ²⁹ | 2004 | Dutch | Caucasian | 82 (56/26) | 221 (139/82) | Alcoholics controls and healthy subjects | 50±9/45±? * | RsaI/PstI/DraI |
| Kim ²⁷ | 2004 | Korea | Korean | 29 (27/2) | 100 (44/56) | Healthy blood donors | 50.4±26.6/49.2±20.3 | RsaI/PstI |
| Burim ³⁰ | 2004 | Brazil | Brazilian | 14 (NM) | 262 (NM) | Healthy alcoholics and non-alcoholics controls | NM | RsaI/PstI |
| Cichoz-Lach ²² | 2008 | Poland | Polish | 44 (8/36) | 97 (22/75) | Healthy alcoholics and non-drinker healthy volunteers | 45.00±9.44/47.05±?* | RsaI/PstI |
| Gubergits ³² | 2014 | Russia | Russian | 72 | 80 | Healthy individuals | NM | RsaI/PstI |
| Singh ⁶ | 2015 | India | Indian | 72 (72/0) | 140 (100/40) | alcoholic control and healthy control | 38.5±8.3/33.15±?* | DraI |

M: male, F: female, *: The standard deviation (SD) cannot be decided for controls included 2 separated groups, NM: not mentioned.

Table 2: Distribution of *cytochrome P450 2E1 (CYP2E1)* RsaI/PstI genotype among alcoholic pancreatitis cases and controls included in the meta-analysis.

| First author | Year | Type of AP | Controls | | | | Cases | | | Controls | | Cases | |
|---------------------------|------|------------|----------|-------|-------|---------------|-------|-------|-------|----------|----|-------|----|
| | | | c1/c1 | c1/c2 | c2/c2 | HWE (p value) | c1/c1 | c1/c2 | c2/c2 | c1 | c2 | c1 | c2 |
| Matsumoto ²⁸ | 1996 | CAP | 39 | 21 | 2 | >0.05 | 9 | 2 | 0 | 99 | 25 | 20 | 2 |
| Chao ²⁵ | 1997 | AAP | 68 | 43 | 8 | >0.05 | 30 | 15 | 3 | 179 | 59 | 75 | 21 |
| Maruyama ³³ | 1999 | CAP | 30 | 15 | 1 | >0.05 | 30 | 21 | 2 | 75 | 17 | 81 | 25 |
| Yang ³¹ | 2001 | CAP | 192 | 9 | 0 | >0.05 | 37 | 1 | 0 | 393 | 9 | 75 | 1 |
| Frenzer ²⁶ | 2002 | AAP | 192 | 9 | 0 | >0.05 | 18 | 1 | 0 | 393 | 9 | 37 | 1 |
| | | CAP | 242 | 15 | 0 | >0.05 | 65 | 6 | 0 | 499 | 15 | 136 | 6 |
| Burim ³⁰ | 2004 | CAP | 234 | 27 | 1 | >0.05 | 11 | 3 | 0 | 495 | 29 | 25 | 3 |
| Kim ²⁷ | 2004 | NM | 51 | 34 | 15 | >0.05 | 17 | 11 | 1 | 136 | 64 | 45 | 13 |
| Verlaan ²⁹ | 2004 | CAP | 122 | 6 | 0 | >0.05 | 75 | 7 | 0 | 250 | 6 | 157 | 7 |
| Cichoz-Lach ²² | 2008 | CAP | 97 | 0 | 0 | >0.05 | 42 | 2 | 0 | 194 | 0 | 86 | 2 |
| Gubergits ³² | 2014 | CAP | 55 | 22 | 3 | >0.05 | 36 | 26 | 10 | 132 | 28 | 98 | 46 |

HWE: Hardy-Weinberg Equilibrium, AP: alcoholic pancreatitis, CAP: chronic alcoholic pancreatitis, AAP: acute alcoholic pancreatitis, NM: not mentioned.

Five studies were performed in Asia^{22,24,25,30,31}, and the other six outside of Asia^{22,26,29-32}. Ten of the 11 studies focused on RsaI/PstI polymorphism of *CYP2E1* (523 patients and 1627 controls)^{22,25-33}, and four on DraI polymorphism (282 patients and 819 controls)^{6,26,29,32}. All studies were considered of high quality according to NOS criteria. Distributions of

the *CYP2E1* RsaI/PstI and DraI genotypes are presented in Table 2 and Table 3, respectively.

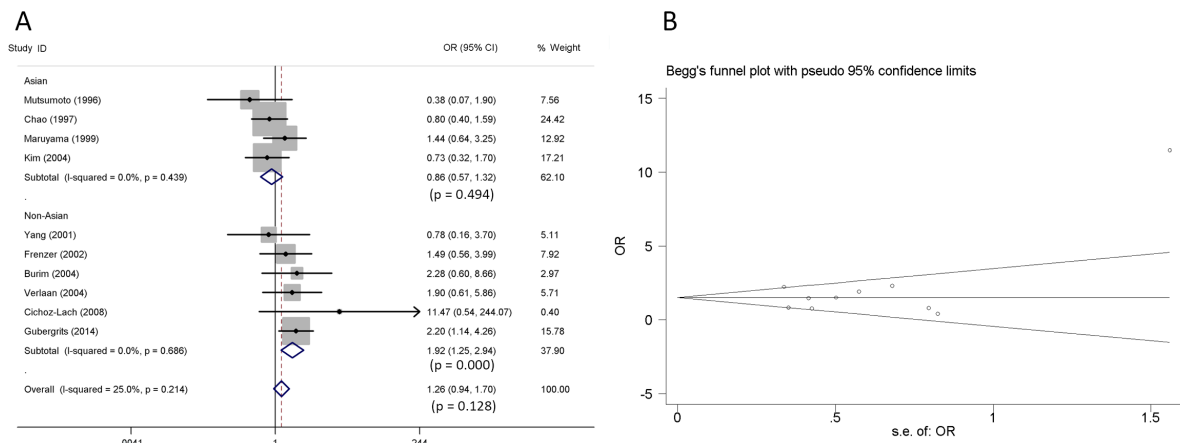
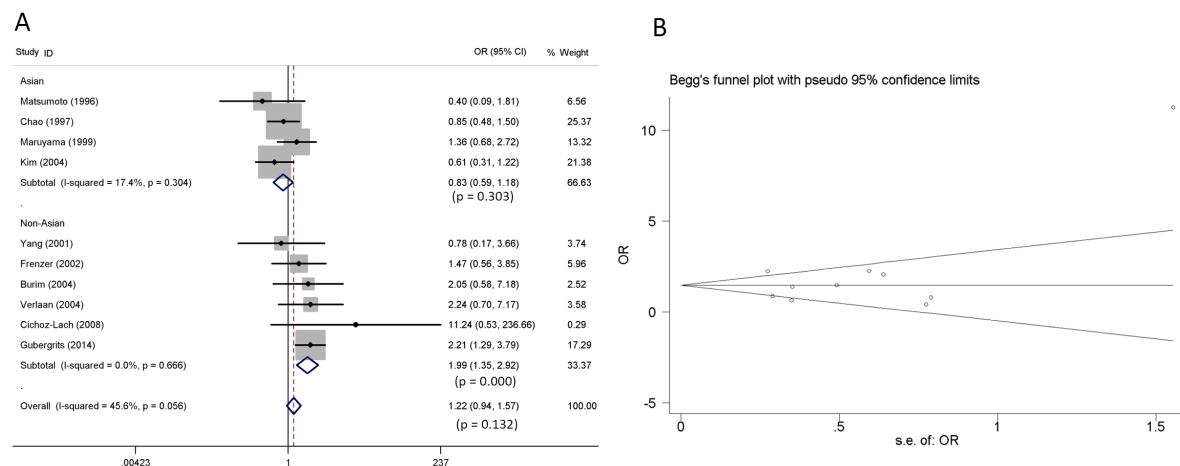
Test of heterogeneity

As shown in Figures 2-6, we analyzed the heterogeneity of the dominant (c2c2+c1c2 vs c1c1, or CD+CC

Table 3: Distribution of *cytochrome P450 2E1 (CYP2E1)* DraI genotype among alcoholic pancreatitis cases and controls included in the meta-analysis.

| First author | Year | Country | Race | Control | | | HWE (p value) | AP | | | Control | | AP | |
|-----------------------|------|-----------|-----------|---------|----|----|------------------|----|----|----|---------|----|-----|----|
| | | | | DD | CD | CC | | DD | CD | CC | D | C | D | C |
| Yang ³¹ | 2001 | England | Caucasian | 152 | 38 | 1 | >0.05 | 45 | 10 | 2 | 342 | 40 | 100 | 14 |
| Frenzer ²⁶ | 2002 | Australia | Caucasian | 216 | 38 | 3 | >0.05 | 54 | 17 | 0 | 470 | 44 | 125 | 17 |
| Verlaan ²⁹ | 2004 | Dutch | Caucasian | 122 | 6 | 0 | >0.05 | 75 | 7 | 0 | 250 | 6 | 157 | 7 |
| Singh ⁶ | 2015 | India | Indian | 101 | 29 | 0 | >0.05 | 61 | 10 | 1 | 231 | 29 | 132 | 12 |

HWE: Hardy-Weinberg Equilibrium, AP: alcoholic pancreatitis.

**Figure 2:** A) *Cytochrome P450 2E1 (CYP2E1)* RsaI/PstI polymorphism was not associated with the risk of alcoholic pancreatitis for a dominant model (c2c2+c1c2 vs c1c1). B) There was no obvious publication bias test for this model by funnel plot.**Figure 3:** A) *Cytochrome P450 2E1 (CYP2E1)* RsaI/PstI polymorphism was not associated with the risk of alcoholic pancreatitis for an allelic contrast model (c2 vs c1). B) There was no obvious publication bias test for this model by funnel plot. =1.92, 95 %

vs DD), and allelic contrast (c2 vs c1 allele, or C vs D allele) models for both *CYP2E1* RsaI/PstI and DraI polymorphisms. No significant heterogeneities were found in the dominant contrast *CYP2E1* RsaI/PstI polymorphism (c2c2+c1c2 vs c1c1: $I^2=25\%$, $p=0.214$, Figure 2A) and in the allelic comparison model (c2 vs c1: $I^2=45.6\%$, $p=0.056$, Figure 3A); this was also the case for the both DraI polymorphism models (CD+CC vs DD: $I^2=33.5\%$, $p=0.211$, Figure 4A; C vs D: $I^2=0.0\%$, $p=0.398$, Figure

6A). Subgroup analyses on the ethnicity and type of alcoholic pancreatitis showed that there was no significant heterogeneity ($I^2=0.0\%$, $p=0.568$ for the Asian group, $I^2=0.0\%$, $p=0.666$ for the non-Asian group, Figure 3A) in the subgroup analysis according to ethnicity, as well as in subgroup analysis according to the type of alcoholic pancreatitis [$I^2=16.1\%$, $p=0.307$ for CAP group, $I^2=0.0\%$, $p=0.766$ for the alcoholic acute pancreatitis (AAP) group, Figure 4B].

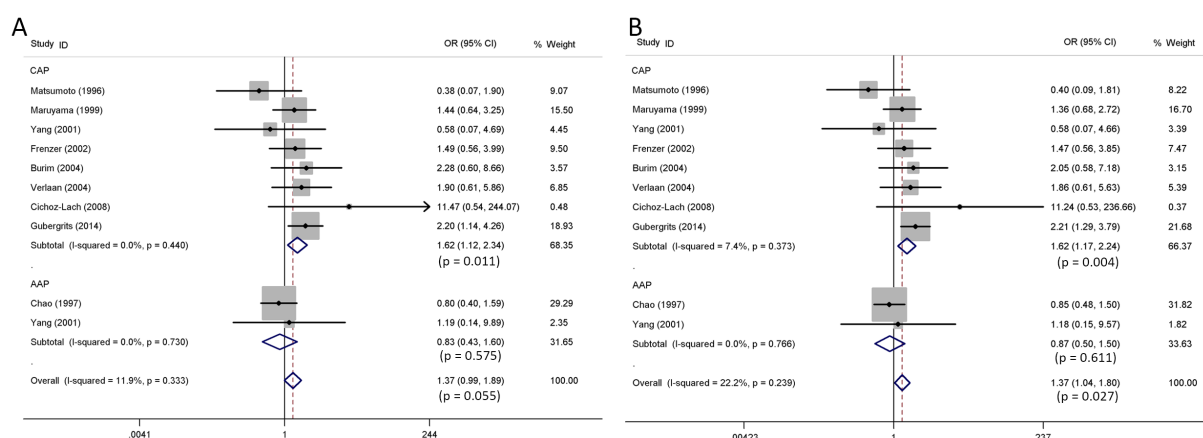


Figure 4: A) *Cytochrome P450 2E1 (CYP2E1)* RsaI/PstI polymorphism was significant associated with the risk of chronic alcoholic pancreatitis (CAP) [odds ratio (OR) =1.62, 95 % confidence interval (CI): 1.12-2.34; p=0.011] but not among the acute alcoholic pancreatitis (AAP) group for a dominant model (c2c2+c1c2 vs c1c1); B) *CYP2E1* RsaI/PstI polymorphism was significant associated with the risk of CAP (OR=1.62, 95 % CI: 1.17-2.24, p=0.004), but not among the AAP group for an allelic contrast model (c2 vs c1).

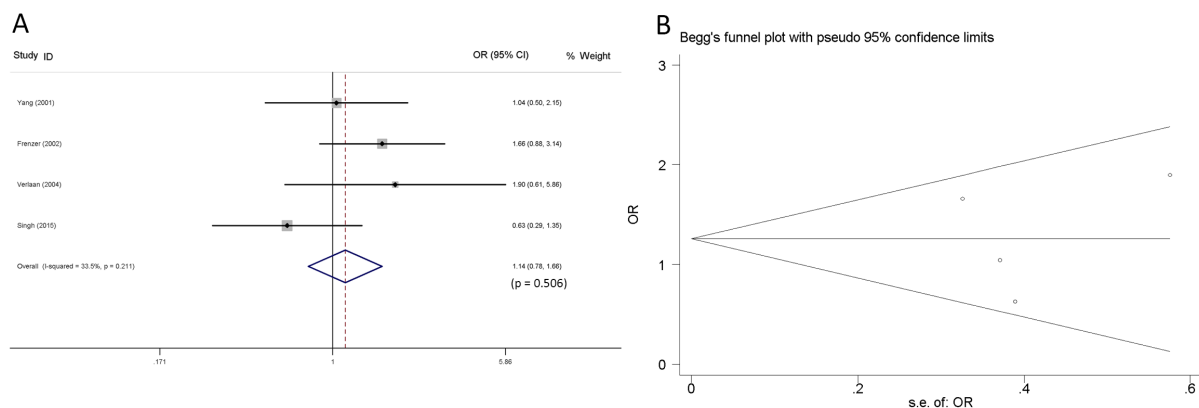


Figure 5: A) *Cytochrome P450 2E1 (CYP2E1)* DraI polymorphism was not associated with the susceptibility of alcoholic pancreatitis risk for a dominant model (CC+CD vs DD). B) There was no obvious publication bias test for this model by funnel plot.

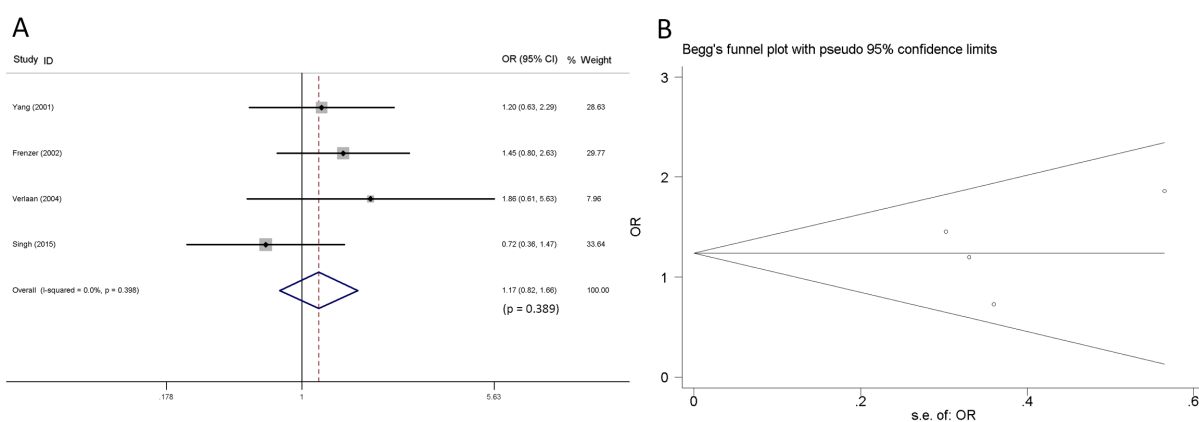


Figure 6: A) *Cytochrome P450 2E1* DraI polymorphism was not associated with the susceptibility of alcoholic pancreatitis risk for an allelic contrast model (C vs D). B) There was no obvious publication bias test for this model by funnel plot.

Results of Meta-Analysis

The meta-analysis showed that there was no significant association between *CYP2E1* RsaI/PstI polymorphism and alcoholic pancreatitis risk [OR =1.26, 95 % confidence interval (CI): 0.94-1.70, p=0.128, Figure 1A,

and OR=1.22, 95 % CI: 0.94-1.57, p=0.132, Figure 3A], for the dominant, and allelic contrast models respectively. *CYP2E1* RsaI/PstI polymorphism was not associated with the risk of alcoholic pancreatitis (Figure 2A, and Figure 3A). Subgroup analysis based on ethnicity suggested that there was a significant increase in alcoholic

pancreatitis risk in the non-Asian subgroup. The dominant model demonstrated a significant relationship (OR =1.92, 95 % CI: 1.25-2.94, $p=0.003$), as well as the allelic contrast model (OR =1.99, 95 % CI: 1.35-2.92, $p<0.001$). The Asian group, however, was not significantly associated for either the dominant (OR =0.86, 95 % CI: 0.57-1.32, $p=0.494$), or the allelic contrast model (OR =0.83, 95 % CI: 0.59-1.18, $p=0.303$) (Figure 2A, and Figure 3A). The interaction of ethnicity with *CYP2E1* polymorphism may increase the risk of alcoholic pancreatitis. Subgroup analysis on the type of alcoholic pancreatitis suggests that there were significant increases in the chronic alcoholic pancreatitis (CAP) group for the dominant (OR =1.62, 95 % CI: 1.12-2.34, $p=0.011$) and the allelic (OR =1.62, 95 % CI: 1.17-2.24, $p=0.004$) contrast models, but not among the AAP group for the dominant (OR =0.83, 95 % CI: 0.43-1.60, $p=0.575$), or the allelic contrast model (OR =0.87, 95 % CI: 0.50-1.50, $p=0.611$) (Figure 4A and B). *CYP2E1* RsaI/PstI polymorphism may increase the risk of CAP, but not AAP.

Results of the meta-analysis of the association between *CYP2E1* DraI polymorphism and alcoholic pancreatitis risk showed that the ORs were 1.14 (95 % CI: 0.78-1.66, $p=0.506$), and 1.17 (95 % CI: 0.82-1.66, $p=0.389$), for the dominant, and allelic contrast models, respectively. *CYP2E1* DraI variations may not be associated with the risk of alcoholic pancreatitis (Figure 5A, and Figure 6A).

Sensitivity analysis and publication bias

The sensitivity analysis showed that, when altered according to the effect models, these two models did not show significant changes. When we omitted any given single study, the significances of the overall results did not change (data not shown), which indicated the stability of the results.

The results of the funnel plots indicated no obvious publication biases for the dominant (Figure 2B for RsaI/PstI polymorphism, and Figure 5B for DraI polymorphism), nor for the allelic contrast (Figure 3B for RsaI/PstI polymorphism, and Figure 6B for DraI polymorphism) models. The Egger's tests also suggested that there were no significant publication biases for RsaI/PstI polymorphism (dominant model: $t=1.53$, $p=0.164$; allelic contrast model: $t=1.29$, $p=0.232$), and for DraI polymorphism (dominant model: $t=0.50$, $p=0.667$; allelic contrast model: $t=0.61$, $p=0.603$).

Discussion

Alcohol abuse is a severe medical and socio-economic problem, which leads to the damage of many organs: some of which are the liver^{34,35}, pancreas^{36,37}, heart^{38,39} and brain^{40,41}. When damage occurs in the pancreas, it is common for acute or chronic pancreatitis to develop. The occurrence of alcohol-induced pancreatitis has no differences in gender and alcohol consumption patterns⁴². It is reported that the genetic differences in alcohol-metabolizing enzymes may result in different metabolizing rates

and affect the susceptibility of alcoholic pancreatitis^{43,44}. *CYP2E1* plays an important role in the initial stage of alcohol metabolism, especially in the microsomal ethanol oxidizing system³⁴. Therefore, we performed this meta-analysis to demonstrate the association between genetic polymorphism of *CYP2E1* and the risk of alcoholic pancreatitis. Our results for the overall data suggested that *CYP2E1* RsaI/PstI and DraI polymorphisms were not associated with risk of alcoholic pancreatitis.

CYP2E1 genetic polymorphism varies marked in frequency among different ethnic and racial groups⁴⁵. *CYP2E1* RsaI/PstI polymorphism may modify the susceptibility to head and neck carcinoma and nasopharyngeal carcinoma in Asians, but not among Caucasians and African-Americans^{13,46}. Thus, in order to determine the ethnic difference of the association between *CYP2E1* RsaI/PstI polymorphism and alcoholic pancreatitis risk, a subgroup analysis on ethnicity (divided into two groups: Asian and non-Asian populations) was performed. The results showed significantly increased alcoholic pancreatitis risk among the Non-Asians with c2 allele or c2c2+c1c2 genotypes. *CYP2E1* polymorphism in different ethnicities may influence the risk of alcoholic pancreatitis⁴⁷. *CYP2E1* variations were different among ethnicities. Therefore, *CYP2E1* RsaI/PstI polymorphism may influence the risk of alcoholic pancreatitis differently in different races.

Moreover, this study suggested that the interaction of race and *CYP2E1* polymorphism may have a significant influence on the risk of alcoholic pancreatitis. In non-Asians, c2 allele and c2c2+c1c2 genotypes of *CYP2E1* RsaI/PstI may significantly increase the susceptibility of alcoholic pancreatitis. In Asians, c2 allele and c2c2+c1c2 genotypes of *CYP2E1* RsaI/PstI may increase the susceptibility of alcoholic pancreatitis, without significant statistical difference.

There are two forms of pancreatitis: acute and chronic pancreatitis, both of which can progress to pancreatic cancer⁴⁸. About 20 % of acute pancreatitis will progress into chronic pancreatitis^{49,50}. Therefore, in order to demonstrate the effect of the type of alcoholic pancreatitis on the association between *CYP2E1* RsaI/PstI polymorphism and alcoholic pancreatitis, we performed subgroup analysis regarding the type of alcoholic pancreatitis. The results showed that *CYP2E1* RsaI/PstI polymorphism significantly increased the risk of CAP, but not AAP, although this may also be due to the small number of studies concerning AAP.

There was no significant degree of linkage disequilibrium between *CYP2E1* RsaI/PstI and DraI in normal controls and alcoholic subjects⁵¹. In the present meta-analysis, two models, the dominant and allelic contrast models, were analyzed to measure the impact of *CYP2E1* RsaI/PstI and DraI polymorphisms on alcoholic pancreatitis susceptibility. Interaction of race with *CYP2E1* RsaI/PstI polymorphism may significantly influence alcoholic pancreatitis risk in dominant and allelic contrast models, but not in the homozygote comparison model

(c2c2 vs c1c1, data not shown). The results may be due to the rare frequency of c2c2 homozygote in individuals with alcoholic pancreatitis, healthy alcoholics, or healthy controls. Thus, further investigation with large sample sizes is needed to investigate the role of *CYP2E1* polymorphism on the susceptibility of alcoholic pancreatitis.

Some possible limitations of this meta-analysis include race, age, sex, occupation, smoking history, and so on. However, we only performed subgroup analysis on ethnicity and the type of alcoholic pancreatitis; subgroup analyses on other risk factors could not be performed due to the limited information of the included studies. Secondly, this meta-analysis only included in published articles; thus, publication bias may exist. Thirdly, only 11 studies were included in our meta-analysis, ten for RsaI/PstI polymorphism and four for DraI polymorphism. Although subgroup analysis for RsaI/PstI polymorphism was performed, there were only four articles for the Asian group, and six for the non-Asian group. Therefore, large sample, preferable studies were needed to demonstrate the results.

In conclusion, though the overall data failed to suggest the relationship of *CYP2E1* RsaI/PstI and DraI polymorphisms with the risk of alcoholic pancreatitis, the variant c2 allele and c2c2+c1c2 genotypes of *CYP2E1* RsaI/PstI polymorphism may play a role in the susceptibility of alcoholic pancreatitis within the non-Asian population, as shown by the subgroup analysis. The variant c2 allele and c2c2+c1c2 genotypes of *CYP2E1* RsaI/PstI polymorphism may also increase the risk of CAP. Studies with large samples and more specified designs were needed to demonstrate the results of this study more clearly and definitively.

Conflict of Interest

All authors declared that there were no potential conflicts of interest.

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