A meta-analysis of caspase-8 -652 6N del polymorphism and digestive tract cancer risk

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Abstract

Caspase-8 (CASP8) is one key regulator of apoptosis of T lymphocytes and is encoded by the CASP8 gene. It has been reported that the six-nucleotide deletion polymorphism (-652 6N del) of the CASP8 gene had effect on some cancer risk. Few studies explored the association between CASP8 gene polymorphism and digestive tract cancer risk. To evaluate the association between the CASP8 -652 6N del polymorphism and the risk of digestive tract cancer, we conducted this meta-analysis. We found that CASP8-652 6N del polymorphism was associated with a significantly reduced risk of digestive tract cancer in the co-dominant model (del/del vs. ins/ins: OR = 0.82, 95% CI = 0.72–0.95; del/ins vs. ins/ins: OR = 0.92, 95% CI = 0.87–0.97; dominant model (del/del + del/ins vs. ins/ins: OR = 0.91, 95% CI = 0.87–0.96, recessive model: del/del vs. del/ins + ins/ins: OR = 0.85, 95% CI = 0.75–0.97). In the stratified analysis by cancer types, we found that all genetic models had protective effect on gastric cancer. Similar results were observed for colorectal cancer under heterozygote comparison and dominant model, but not under homozygote comparison or recessive model. In addition, a significantly decreased risk was found on esophageal cancer for most genetic models, except heterozygote comparison. When stratified by ethnicity and source of control, an evidently decreased risk was identified in the Asian populations and population-based studies. In conclusion, there exists an association between the CASP8 -652 6N del polymorphism and reduced digestive cancer risk, especially among Asians and population-based studies.

Keywords: caspases-8, polymorphism, digestive tract cancer risk

Introduction

The activity of many genes influences a cell’s likelihood of activating its apoptotic program[1], which is mainly regulated by caspases, a family of cysteine proteases, that play a crucial role in the development and progression of cancer[2]. Several meta-analyses have confirmed that the gene variants of caspases-2, 5, 7, 8, 9 and 10 disturbed the apoptotic mechanism and thus affected the risk of some cancers[3–10].

Caspase-8 (CASP8) is a key regulator of apoptosis of T lymphocytes and is encoded by the CASP8 gene[8].

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The CASP8 (MACH, FLICE, Mch5) gene contains at least 11 exons spanning ~30 kb on human chromosome band 2q33–34 and encodes 479 amino acids, including prodomain and caspase domain. There are 353 single-nucleotide polymorphisms (SNP) of the CASP8 reported in the dbSNP database. It has been reported that polymorphic variation in CASP8 influences cancer risk, such as the variant D302H (rs1045485), the 652 6N insertion/deletion (ins/del) promoter variant (rs3834129), and the IVS12-19G/A (rs3769818). Previous meta-analysis suggested CASP8 -652 6N promoter polymorphism is associated with reduced renal cell carcinoma risk and breast cancer risk. However, there was no evidence on the association between the -652N ins/del and digestive tract cancer due to limited publications. Digestive tract cancers represent a homogeneous group of malignancies. Given the amount of data now available on the association between CASP8 -652 6N promoter polymorphism and digestive system cancer risk, we performed the meta-analysis based on published case-control studies.

Materials and methods

Search strategy and inclusion criteria

We carried out a search in PubMed and Embase databases with the following keywords: 'CASP8' or 'caspase-8', or 'rs3834129', 'cancer' or 'neoplasm' or 'carcinoma' or 'tumor' and 'polymorphism' or 'single nucleotide polymorphisms' or 'SNPs' (last search was updated on Dec 31, 2015). The titles and abstracts of all eligible studies were examined carefully, and the bibliographies of the selected papers were also checked manually. If the same patient population was included in multiple publications, only the most recent or complete study was used in this meta-analysis.

Selected studies in our meta-analysis had to meet all the following criteria: (a) only case-control or cohort studies; (b) evaluation of the CASP8 -652 6N promoter polymorphism and digestive tract cancer susceptibility; (c) data available on genotype frequency or the value of the OR.

Data extraction

For each study, the following information was extracted by two evaluators: first author's name, year of publication, country, ethnicity, source of control, sample size and genotyping results of cases and controls (Table 1). Data were independently extracted by two investigators. If consensus was not reached by discussion, the third investigator was rereading.

Statistical analysis

Our meta-analysis assessed the overall association

| Study   | Year | Country | Ethnicity | Cancer  | Design | Number (case/control) | Genotypes (case/control) | P for HWE |
|---------|------|---------|-----------|---------|--------|-----------------------|--------------------------|----------|
| Sun     | 2007 | China   | Asian     | Esophageal | PB     | 1,018/937 | 652/543, 328/338, 38/56 | 0.724 |
| Umar    | 2011 | Indian  | Asian     | Esophageal | PB     | 259/259  | 139/138, 103/93, 17/28  | 0.046 |
| Mailk   | 2011 | Indian  | Asian     | Esophageal | PB     | 135/195  | 68/96, 59/75, 8/24     | 0.126 |
| Sun     | 2007 | China   | Asian     | Gastric  | PB     | 420/410  | 262/233, 142/152, 16/25 | 0.974 |
| Liamarkopoulos | 2011 | Greece | Caucasian | Gastric | HB     | 88/480   | 35/120, 42/254, 11/106  | 0.194 |
| Mailk   | 2011 | Indian  | Asian     | Gastric  | PB     | 108/195  | 59/96, 44/75, 5/24     | 0.126 |
| Sun     | 2007 | China   | Asian     | Colorectal | PB     | 918/890  | 605/528, 280/304, 33/58 | 0.116 |
| Pittman | 2008 | UK      | Caucasian | Colorectal | PB     | 3,879/2,777 | 995/8, 1,897/1,872, 987/897 | 0.170 |
| Liu     | 2010 | China   | Asian     | Colorectal | PB     | 370/1202 | 233/892, 116/278, 21/32 | 0.538 |
| Theodoropoulos | 2011 | Greece | Caucasian | Colorectal | HB     | 402/480  | 103/120, 201/254, 98/106 | 0.194 |
| Xiao    | 2013 | China   | Asian     | Colorectal | HB     | 305/342  | 187/212, 107/115, 11/15 | 0.904 |
| Wu      | 2013 | China   | Asian     | Colorectal | HB     | 451/631  | 284/358, 152/244, 15/29 | 0.118 |
| Pardini | 2014 | Spanish | Caucasian | Colorectal | PB     | 1,978/1,647 | 500/425, 996/802, 482/420 | 0.289 |

PB: population-based; HB: hospital-based.
between CASP8 -652 6N promoter polymorphism and digestive system cancer risk. The pooled ORs were performed for homozygote comparison (del/del vs. ins/ins), heterozygote comparison (del/ins vs. ins/ins), dominant model (del/ins + del/del vs. ins/ins), and recessive model (del/del vs. del/ins + ins/ins), respectively. \( P < 0.05 \) was considered as statistically significant. Subgroup analyses were carried out by the cancer types and ethnicity, respectively. We used either the fixed (Mantel-Haenszel) or random (DerSimonian-Laird) effects models to get pooled ORs. If the \( P \) was more than 0.05 for the Q-test, the heterogeneity was considered significant. When there was no heterogeneity among studies, the pooled OR estimate of each study was calculated by the fixed-effects model \([13]\). Otherwise, the random-effects model was used \([14]\). The Begg’s test and the Egger’s test were used to test possible publication bias in this meta-analysis. Hardy-Weinberg equilibrium (HWE) in the controls was evaluated using the chi-square test. Meta-analyses were performed using Stata 11.0 software.

**Results**

**Study characteristics**

As shown in Table 1, 18 separate studies including a total of 15,086 patients and 16,374 controls were finally retrieved. Among them, there were 3 esophageal cancer studies \([12,15–16]\), 3 gastric cancers \([12,15,17]\) and 12 colorectal cancers (including studies) \([15,18–23]\) (Fig. 1). In addition, there were 9 studies in Asians populations, 9 in Caucasians populations and 13 were population-based studies, and 5 hospital-based studies. The distribution of genotypes in the controls was consistent with HWE, except for only one study \([16]\).

**Meta-analysis results**

Overall, a significant reduced risk of digestive tract cancer was associated with the CASP8-652 6N del polymorphism for the co-dominant model (del/del vs. ins/ins: OR = 0.82, 95%CI = 0.72–0.95, Fig. 2A; del/ins vs. ins/ins: OR = 0.92, 95%CI = 0.87–0.97, Fig. 2B); dominant model (del/ins + del/del vs. ins/ins: OR = 0.91, 95%CI = 0.87–0.96, Fig. 2C), recessive model (del/del vs. del/ins + ins/ins: OR = 0.85, 95%CI = 0.75–0.97, Fig. 2D).

In the stratified analysis by cancer types, we found all genetic models had protective effect on gastric cancer: del/del vs. ins/ins: OR = 0.43, 95%CI = 0.28–0.67; del/ins vs. ins/ins: 0.79 (0.63–0.99); del/ins + del/del vs. ins/ins: 0.73 (0.59–0.95); del/del vs. del/ins + ins/ins: 0.50 (0.33–0.77). Similar results were observed for colorectal cancer under heterozygote comparison (OR = 0.94, 95%CI = 0.88–0.99, Supplementary Fig. 1A, available online) and dominant model (OR = 0.93, 95% CI = 0.88–0.99, Supplementary Fig. 1B, available online), but not under homozygote comparison or recessive model. In addition, a significant decreased risk was found on esophageal cancer for the mostly genetic models: del/del vs. ins/ins: 0.56 (0.40–0.78); del/ins + del/del vs. ins/ins: 0.83 (0.71–0.97); del/del vs. del/ins + ins/ins: 0.57 (0.41–0.79), except the heterozygote comparison.

When stratified by ethnicity, two distinct results

![Flow diagram of study identification.](image-url)
appeared in Asian populations and European populations. An evidently decreased risk for Asian populations in any genetic models (del/del vs. ins/ins: OR = 0.62, 95% CI = 0.51–0.76, Supplementary Fig. 2A, available online; del/ins vs. ins/ins: OR = 0.87, 95% CI = 0.79–0.95, Supplementary Fig. 2B, available online; del/ins + del/del vs. ins/ins: OR = 0.83, 95% CI = 0.76–0.91, Supplementary Fig. 2C, available online; del/del vs. del/ins + ins/ins: OR = 0.61, 95% CI = 0.46–0.83, Supplementary Fig. 2D, available online). In stratified analysis by source of control, we found significant reduced CRC risk in population-based studies (del/del vs. ins/ins: OR = 0.82, 95% CI = 0.70–0.96; del/ins vs. ins/ins: OR = 0.92, 95% CI = 0.87–0.98; del/ins + del/del vs. ins/ins: OR = 0.91, 95% CI = 0.86–0.96; del/del vs. del/ins + ins/ins: OR = 0.83, 95% CI = 0.71–0.97), but not in hospital-based studies (figure not shown).

Publication bias

Begg's funnel plot and Egger's test were used to assess the publication bias. As shown in Fig. 3, the shape of the funnel plot for the heterozygous model did not show any obvious asymmetry, which suggested no publication bias existing in all comparison models. And the P values were 0.914, 95% CI were −1.461–1.317 in Egger's test, insinuating no publication bias (there were no publication bias in other genetic models, data not shown).

Sensitivity analysis

Sensitivity analysis was conducted repeatedly when the special studies had been left out at a time. For example, after excluding the study deviated from HWE[16], the overall result did not been influenced significantly (heterozygous model: OR = 0.84, 95% CI: 0.73–0.96). The sensitivity analysis results revealed that
no individual studies significantly affected the pooled ORs under heterozygous model of CASP8 -652 6N polymorphism (Fig. 4), suggesting that our results are stable.

**Heterogeneity analysis**

There was potential heterogeneity among studies in overall analysis and some subgroup analysis under homozygous and recessive model (Table 2). To explore the source of heterogeneity, we conducted a subgroup analysis by cancer types, ethnicity and the source of control. As a result, there presented little or no heterogeneity across studies. Furthermore, we found that colorectal cancer, Caucasian and population-based studies contributed to substantial heterogeneity.

**Discussion**

Apoptosis plays critical roles in a wide variety of physiologic processes during fetal development and in adult tissues[24]. Defects in apoptotic cell death regulation contribute to many diseases, such as some cancers[24]. Caspase 8 is a central regulator of apoptosis or programmed cell death. Caspase-8 gene mutation
can influence the rate of apoptosis, and thus affect cancer risk. The most widely reported mutation in CASP8 gene is the six-nucleotide deletion polymorphism (-652 6N del). The -652 6N del variant involves a six-nucleotide deletion in the promoter region of the CASP8 gene. The deletion abolishes an Sp1 binding site and is associated with decreased RNA expression in lymphocytes and lower CASP8 activity and activation-induced cell death of T lymphocytes. It is known that apoptosis plays an important role in cancer growth, progression, and drug resistance. Previous studies found that genetic mutations of caspases 8 in tumor cells reduce the cell sensitivity to apoptosis, which may be related to the occurrence and development of tumors. Our meta-analysis based on 18 case-control studies suggested that the CASP8 -652 6N del polymorphism is associated with decreased risk of digestive tract cancer, which was similar with the results of Yin et al. and Zhang et al. However, there was potential heterogeneity under the four genetic models in digestive system cancer. Therefore, we also carried out the stratification analysis by ethnicity, cancer type and source of control. In stratification by cancer type, we also found the reduced cancer risk remained for subgroups of colorectal cancer, gastric cancer and esophageal cancer. What is more, similar results were found in Asians and population-based studies. Peng et al. reached a similar conclusion that CASP8 -652 6N ins/del polymorphism may play a protective role in colorectal cancer development. But their sample size was relatively small, not having enough statistical power to explore the real association. Our study with a large sample size provides additional evidence of the association between CASP8 -652 6N ins/del polymorphism and colorectal cancer risk.

There was a significant reduced association between the -652 6N del polymorphism and digestive tract cancer risk among Asian populations, but not in Caucasians. One explanation may be genetic differences and diverse living environments between Asian and Caucasian populations. On the other hand, the Asian population are relatively homogeneous, who mainly come from Han Chinese. However, Caucasian population consisted of people from various countries with diverse living environments. Difference between Asians and Caucasians may explain the distinct findings. In addition, gene-gene and gene-environmental interactions may lead to the result bias. Among the included studies, 13 were population-based samples and 5 were hospital-based samples, respectively. Borderline significantly decreased risks were found for population-based studies. One explanation may be the hospital-based studies have some biases because such controls may be a sample of ill-defined reference population, particularly when the genotypes under investigation were associated with the disease conditions. On the other hand, the insufficient hospital-based samples tended to have underestimated cancer risks.

### Table 2 Associations between CASP8-652 6N ins/del genotype and digestive tract cancer risk

| Stratification | Total | Colorectal cancer | Gastric cancer |
|----------------|-------|-------------------|----------------|
| del/del vs. ins/ins | OR (95%CI) | 0.82(0.72–0.95) | 0.93(0.82–1.05) | 0.43(0.28–0.67) |
| | P | 0.01 | 0.247 | <0.001 |
| | Ps | <0.001 | 0.018 | 0.554 |
| del/ins vs. ins/ins | OR (95%CI) | 0.92(0.87–0.97) | 0.94(0.88–0.99) | 0.79(0.63–0.99) |
| | P | 0.004 | 0.025 | 0.043 |
| | Ps | 0.401 | 0.529 | 0.304 |
| del/del vs. del/ins + ins/ins | OR (95%CI) | 0.85(0.75–0.97) | 0.96(0.87–1.07) | 0.73(0.59–0.95) |
| | P | 0.013 | 0.444 | 0.004 |
| | Ps | <0.001 | 0.019 | 0.241 |
| del/del + del/ins vs. ins/ins | OR (95%CI) | 0.91(0.87–0.96) | 0.93(0.88–0.99) | 0.50(0.33–0.77) |
| | P | <0.001 | 0.016 | 0.001 |
| | Ps | 0.071 | 0.190 | 0.641 |

P: P value of the comparison of ORs; Ps: P value of the Q-test for heterogeneity test.
Some limitations of this meta-analysis should be addressed. First, in the subgroup analyses of cancer type, the number of esophageal cancer and gastric cancer were relatively small, not having sufficient statistical power to explore the real association. Second, our results were based on unadjusted estimates, because not all published studies presented adjusted ORs. More precise analysis should be carried out, which would allow for the adjustment by other variance, such as sex, age, smoking status, drinking status, obesity and other lifestyles. Thirdly, the experiment method for each study was without restrictions, which affected the accuracy of the results to a certain extent.

In conclusion, our meta-analysis supports the association between the CASP8-652 6N del polymorphisms and reduced digestive tract cancer risks, especially in Asians. Future studies with large sample sizes are required to confirm current findings.

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