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Original Article

Association between the *C-reactive protein* rs1205 C>T polymorphism and cancer susceptibility: a meta-analysis involving 74,567 subjects

Feng Yao[1*], Tianxiang Chen[1*], Weifeng Tang[2,3*], Yang Zhao[1], Haitang Yang[1], Chao Liu[2], Boyang Chen[3], Haiyong Gu[1], Heng Zhao[1]

[1]Department of Thoracic Surgery, Shanghai Chest Hospital, Shanghai Jiaotong University, Shanghai, China; [2]Department of Cardiothoracic Surgery, Affiliated People's Hospital of Jiangsu University, Zhenjiang, Jiangsu Province, China; [3]Department of Thoracic Surgery, Affiliated Union Hospital, Fujian Medical University, Fuzhou, Fujian Province, China. [*]Equal contributors.

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Abstract: The *C-reactive protein* (*CRP*) rs1205 C>T polymorphism was considered a risk modifier for cancer development in many studies. Yet, it remained controversial as there was evidence suggesting otherwise. To consolidate this association, we conducted a meta-analysis involving a total of 11,074 cancer cases and 63,493 controls. Literatures were searched in PubMed and EMBASE databases up to March 27, 2014. The cancer risk associated with the *CRP* rs1205 C>T polymorphism was assessed by odds ratios (ORs) with the 95% confidence intervals (95% CIs). Sensitivity analysis, publication bias and heterogeneity were also evaluated. Our results indicated that the *CRP* rs1205 C>T polymorphism was not associated with cancer susceptibility in overall cancer or in subgroup analyses stratified by ethnicity. While in the stratified analysis by cancer type, *CRP* rs1205 C>T polymorphism was associated with a significant increased risk in colorectal cancer subgroup. In summary, this meta-analysis demonstrates that *CRP* rs1205 C>T polymorphism may be a risk factor for colorectal cancer.

Keywords: Cancer, gene polymorphism, CRP, susceptibility, meta-analysis

Introduction

Recently, the association between chronic inflammation and cancer has gained accumulating research interest. Mounting evidence has suggested that the inflammatory cells and cytokines contribute to the malignant tumor metastasis and immunosuppression [1] and the inflammatory component of chronic infections play an important role in the development and progression of cancer [2, 3]. Conceivable mechanisms may involve DNA damage caused by reactive oxygen [4] as well as alterations in tumor microenvironment and cell-cell communication induced by the pro-inflammatory cytokines [5].

C-reactive protein (CRP) is one of the most common acute-phase proteins induced by hepatocytes. In the previous studies, elevated level of CRP was associated with the increased risk of multiple cancers, such as colorectal, esophageal, hepatic, breast and pancreatic cancer [6-10]. Recently, the *CRP* rs1205 C>T single nucleotide polymorphism (SNP) was widely investigated for its association with cancer risk; however, the results were conflicting. Zhang and colleagues first reported a meta-analysis involving 17,705 subjects on the association between *CRP* rs1205 C>T polymorphism and cancer risk [11], yet the result was limited by sample size. Thus, we conducted this analysis and recruited more subjects. Numerous polymorphisms in *CRP* gene have been identified, including rs1205 C>T, rs1417938 T>A, rs1800947 C>G, rs2808630 C>T, rs3093075 G>T and rs1130864 G>A polymorphisms, etc. Among them, rs1205 C>T polymorphism was the most extensively studied for susceptibility to cancer. Therefore, to further investigate the

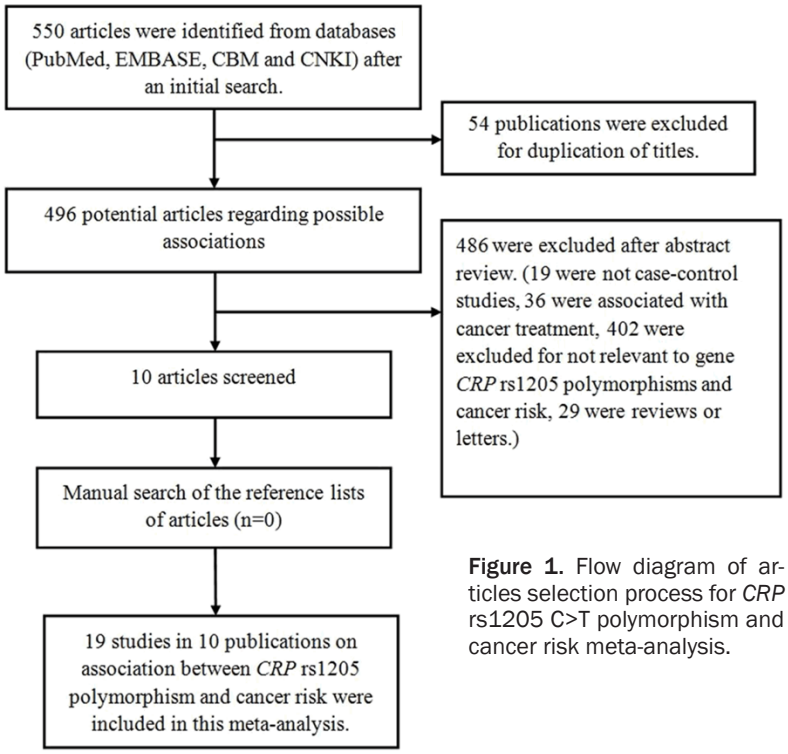

Figure 1. Flow diagram of articles selection process for *CRP* rs1205 C>T polymorphism and cancer risk meta-analysis.

correlation between the *CRP* rs1205 C>T polymorphism and tumorigenesis, we performed the comprehensive meta-analysis.

Materials and methods

Search strategy

PubMed and EMBASE (the last search was updated on March 27, 2014) were used simultaneously with combination of the following terms: 'c-reactive protein' or 'CRP', 'polymorphism' or 'mutation' or 'variant' or 'SNP', and 'cancer' or 'carcinoma' or 'malignancy'. All citations in the retrieved articles and reviews were checked to identify additional publications.

Inclusion and exclusion criteria

Recruited publications had to meet the major inclusion criteria: (1) evaluated the association between *CRP* rs1205 C>T polymorphism and cancer risk, (2) designed as a case-control study or cohort study, (3) data on genotype or allele frequency in cases and controls were available. Accordingly, not case-control studies or non-cohort studies, reviews and overlapping data were excluded. For studies that did not offer raw data of allele frequencies in publications, we attempted to get this information by the correspondence with the authors. In case that the information could not be obtained, the publications were excluded.

Data extraction

For each included study, the following data were independently extracted by three reviewers (F. Yao, T. Chen and W. Tang): (1) first author, (2) cancer type, (3) year of publication, (4) country, (5) ethnicity of study subjects, (6) number of cases and controls, (7) genotype method, (8) allele and genotype frequency and (9) Hardy-Weinberg equilibrium (HWE) in controls. Disagreements were settled by discussions among all reviewers.

Methodological quality assessment

The quality of investigations was carefully assessed according to the "methodological quality assessment scale" by three reviewers (F. Yao, T. Chen and W. Tang) independently [12, 13]. Scores ranges from 0 to 10, studies with score ≥6 were categorized in the "high quality" group, and others were defined as "low quality".

Statistical analysis

An internet-based HWE calculator (http://ihg.gsf.de/cgi-bin/hw/hwa1.pl) was used to test whether genotype frequencies of controls were in HWE. The strength of the association between *CRP* rs1205 C>T polymorphism and cancer risk was measured by the crude odds ratios (ORs) with the corresponding 95% confidence intervals (95% CIs). The significance of the pooled OR was measured by Z-test and *P*-value, and $P<0.05$ (two-tailed) was defined statistically significant. A Chi-square based I^2-statistic test was utilized to evaluate potential heterogeneity among studies (I^2 value of less than 25% indicates low heterogeneity, $25\% \leq I^2 \leq 50\%$ indicates moderate heterogeneity, and $I^2>50\%$ indicates large heterogeneity) [14]. If the result of the heterogeneity test was

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

Study	Year	Ethnicity	Country	Cancer type	Sample size	Study type	Source of control	Genotype method	Quality scores
Gong et al. (Pre-EA)	2013	Caucasians	USA	breast cancer	186/167	case-control study	PB	MALDI-TOF	9.0
Gong et al. (Post-EA)	2013	Caucasians	USA	breast cancer	149/148	case-control study	PB	MALDI-TOF	9.0
Gong et al. (Pre-AA)	2013	Africans	USA	breast cancer	242/196	case-control study	PB	MALDI-TOF	8.0
Gong et al. (Post-AA)	2013	Africans	USA	breast cancer	216/210	case-control study	PB	MALDI-TOF	9.0
Xu et al.	2013	Asians	China	lung cancer	96/124	case-control study	HP	Golden Gate assay	6.5
Yang et al.	2011	Asians	China	colorectal cancer	421/218	case-control study	PB	Taqman	7.0
Slattery et al. (CC)	2011	mixed	USA	colorectal cancer	1574/1970	case-control study	PB	Golden Gate assay	7.0
Slattery et al. (RC)	2011	mixed	USA	colorectal cancer	791/999	case-control study	PB	Golden Gate assay	8.0
Minamiya et al.	2010	Asians	Japan	lung cancer	146/139	case-control study	HP	PCR-RFLP	6.5
Allin et al. (A)	2010	Caucasians	Denmark	combined cancer type	1616/7782	cohort study	PB	Taqman	9.0
Allin et al. (B)	2010	Caucasians	Denmark	combined cancer type	4305/31738	cohort study	PB	Taqman	9.0
Chaturvedi et al.	2010	mixed	USA	lung cancer	378/447	case-control study	PB	Golden Gate assay	7.0
Tsilidis et al.	2009	mixed	USA	colorectal cancer	208/381	case-control study	PB	Taqman	6.5
Pierce et al. (EA)	2009	Caucasians	USA	prostate cancer	175/1758	cohort study	PB	Taqman	8.0
Pierce et al. (AA)	2009	Africans	USA	prostate cancer	40/300	cohort study	PB	Taqman	8.0
Siemes et al. (CRC)	2006	Caucasians	Holland	colorectal cancer	189/5767	cohort study	PB	Taqman	8.0
Siemes et al. (LC)	2006	Caucasians	Holland	lung cancer	113/5843	cohort study	PB	Taqman	7.0
Siemes et al. (BC)	2006	Caucasians	Holland	breast cancer	172/3380	cohort study	PB	Taqman	7.0
Siemes et al. (PCa)	2006	Caucasians	Holland	prostate cancer	230/2174	cohort study	PB	Taqman	8.0

MALDI-TOF MS: Matrix-Assisted Laser Desorption/Ionization Time of Flight Mass Spectrometry. PCR-RFLP: polymerase chain reaction-restriction fragment length polymorphism. PB: population based study. HB: hospital based study. Pre-EA: Premenopausal European American. Post-EA: Postmenopausal European American. Pre-AA: Premenopausal African American. Post-AA: Postmenopausal African American. CC: Colon cancer. RC: Rectal cancer. A: the Copenhagen City Heart Study. B: the Copenhagen General Population Study. EA: European American. AA: African American. CRC: Colorectal cancer. LC: Lung cancer. BC: Breast cancer. PCa: Prostate cancer.

I^2>50% or P<0.10, the random-effects model (the DerSimonian-Laird method) [15] was used to pool the data or the fixed-effects model was utilized (the Mantel-Haenszel method) [16]. Furthermore, subgroup analyses were performed according to ethnicity, cancer type, source of controls and so on. One-way sensitivity analysis and nonparametric "trim-and-fill" method were performed to determine the stability of our findings. Galbraith radial plot was used to identify the major source of heterogeneity. The Begg's funnel plot and Egger's test were utilized to assess potential publication bias of the literatures. In addition, for interpretation of the publication bias, statistical significance was defined as P<0.1. In current meta-analysis, all statistical analyses were performed using STATA software package version 12.0 (Stata Corporation, College Station, TX).

Results

Characteristics

A total of 503 potentially relevant publications were identified through an online literature search. According to the inclusion and exclusion criteria, 19 case-control studies in 10 publications were eligible. The process of selecting is listed in **Figure 1**.

There were two or more subgroups in some publications [3, 17-20], we treated them separately. In total, 19 individual investigations involving 11,074 cancer cases and 63,493 controls were included. Among them, five investigated colorectal cancer [3, 18, 21, 22], five investigated breast cancer [3, 17], four investigated lung cancer [3, 23-25], three investigated prostate cancer [3, 20] and two investigated combined cancer [19]. As for subjects in these studies, nine were Caucasians [3, 17, 19, 20], three were Asians [21, 23, 24], three were Africans [17, 20] and four were mixed populations [18, 22, 25]. For study type, 11 were case-control study [17, 18, 21-25] and eight were cohort study [3, 19, 20]. The study characteristics and distribution of the *CRP* rs1205 C>T polymorphism are summarized in **Tables 1** and **2**, respectively.

Quantitative synthesis

After combining all eligible studies, null association of *CRP* rs1205 C>T polymorphism with overall cancer risk was observed (**Table 3**;

Table 2. Distribution of *CRP* rs1205 C>T polymorphisms genotype and allele among multiple cancer patients and controls

Study	Case			Control			Case		Control		HWE
	CC	CT	TT	CC	CT	TT	T	C	T	C	
Gong et al. (Pre-EA)	88	75	16	53	79	26	107	251	131	185	0.705352
Gong et al. (Post-EA)	57	62	17	65	70	9	96	176	88	200	0.080906
Gong et al. (Pre-AA)	150	81	8	126	54	14	97	381	82	306	0.021557
Gong et al. (Post-AA)	131	74	10	131	67	11	94	336	89	329	0.529020
Xu et al.	43	44	9	56	57	11	62	130	79	169	0.512637
Yang et al.	72	197	152	40	111	67	501	341	245	191	0.613454
Slattery et al. (CC)	700	659	163	882	845	157	985	2059	1159	2609	0.021531
Slattery et al. (RC)	295	325	79	406	403	92	483	915	587	1215	0.584260
Minamiya et al.	26	54	66	21	57	61	186	106	179	99	0.212235
Allin et al. (A)	708	710	198	3354	3538	890	1106	2126	5318	10246	0.350054
Allin et al. (B)	1938	1885	482	14023	14056	3659	2849	5761	21374	42102	0.128930
Chaturvedi et al.	167	168	40	204	188	54	248	502	296	596	0.296546
Tsilidis et al.	99	83	24	167	156	51	131	281	258	490	0.136553
Pierce et al. (EA)	85	72	18	786	773	199	108	242	1171	2345	0.667581
Pierce et al. (AA)	27	11	2	171	83	6	15	65	95	425	0.266034
Siemes et al. (CRC)	78	92	19	2584	2595	588	130	248	3771	7763	0.088582
Siemes et al. (LC)	39	51	23	2623	2636	584	97	129	3804	7882	0.036305
Siemes et al. (BC)	72	89	11	1489	1552	339	111	233	2230	4530	0.024941
Siemes et al. (PCa)	102	99	29	999	947	228	157	303	1403	2945	0.871989

HWE: Hardy-Weinberg equilibrium. Pre-EA: Premenopausal European American. Post-EA: Postmenopausal European American. Pre-AA: Premenopausal African American. Post-AA: Postmenopausal African American. CC: Colon cancer. RC: Rectal cancer. A: the Copenhagen City Heart Study. B: the Copenhagen General Population Study. EA: European American. AA: African American. CRC: Colorectal cancer. LC: Lung cancer. BC: Breast cancer. PCa: Prostate cancer.

Figure 2). In a stratified analysis by ethnicity, the results were similar (**Table 3**). However, in a stratified analysis by cancer type, there was an increased risk of colorectal cancer in two genetic models: TT vs. CT+CC (OR=1.18; 95% CI, 1.02-1.37; *P*=0.026) and TT vs. CC (OR=1.19; 95% CI, 1.01-1.40; *P*=0.035) (**Table 3**). The results of methodological quality assessment indicated that all included studies were high quality (**Table 1**).

Tests for publication bias, sensitivity analyses, and heterogeneity

Begg's funnel plot and Egger's test created to estimate the publication bias (**Figure 3**). The shape of Begg's funnel plot showed no evidence of publication bias (T vs. C: Begg's test *P*=0.834, Egger's test *P*=0.528; TT vs. CC: Begg's test *P*=0.484, Egger's test *P*=0.799; TT+CT vs. CC: Begg's test *P*=0.484, Egger's test *P*=0.518; TT vs. CT+CC: Begg's test *P*=0.263, Egger's test *P*=0.836).

We used one-way sensitivity analysis to assess the influence of each study on the pooled one. The results showed that our findings were robust (**Figure 4**) (data not shown). Nonparametric "trim-and-fill" method was also implemented for sensitivity analysis. The adjusted ORs and CIs were essentially unchanged, suggesting that our results were reliable (TT+CT vs. CC: adjusted pooled OR=0.98, 95% CI: 0.94-1.03, *P*=0.423; TT vs. CT+CC: adjusted pooled OR=1.06, 95% CI: 0.93-1.21, *P*=0.356; TT vs. CC: adjusted pooled OR=1.05, 95% CI: 0.91-1.21, *P*=0.517; T vs. C: adjusted pooled OR=1.00, 95% CI: 0.94-1.06, *P*=0.932) (**Figure 5**).

Given the significant heterogeneity in current meta-analysis, we conducted subgroup analyses to detect the sources of heterogeneity (**Table 3**). The results indicated that lung cancer, breast cancer, Caucasians subgroups might contribute to the major sources of heterogeneity. Significant heterogeneity was observed in homozygote comparison model (**Table 3**). Thus, Galbraith radial plot was also conducted (**Figure 6**) and the result demonstrated that two outliers might contribute to the major source of heterogeneity [3, 17].

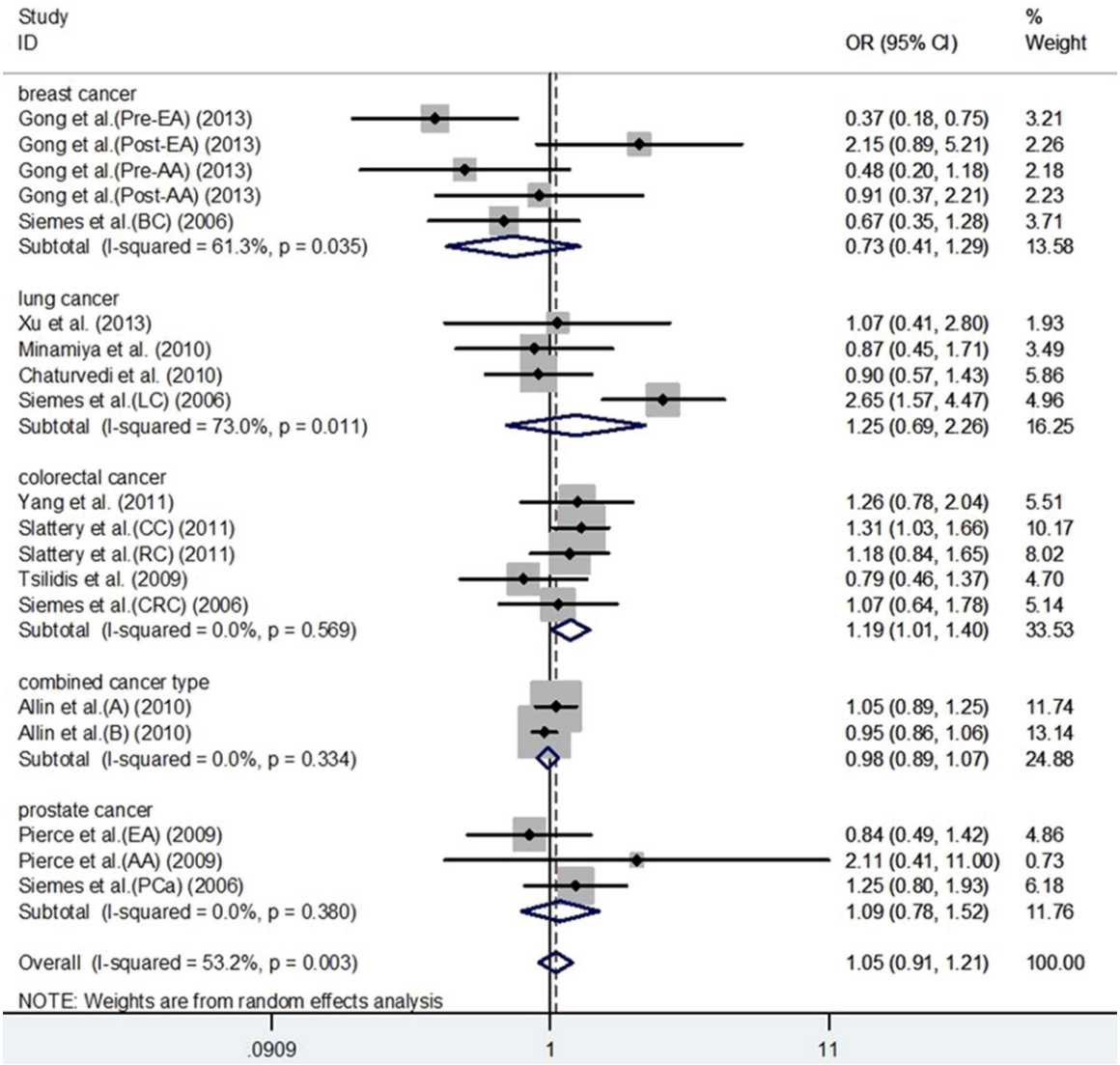

Figure 2. Meta-analysis with a random-effects model for the association between the risk of cancer and the *CRP* rs1205 C>T polymorphism (TT vs. CC compare genetic model).

Discussion

The association of *CRP* rs1205 C>T polymorphism with cancer risk was widely investigated; however, the findings were inconclusive. To verify the association, we carried out a meta-analysis including 19 studies involving 11,074 cancer cases and 63,493 controls. The result indicated that *CRP* rs1205 C>T polymorphism was not associated with the susceptibility of overall cancer. To the best of our knowledge, our study is the most comprehensive meta-analysis which assessed the relationship between *CRP* rs1205 C>T polymorphism and cancer risk.

Chronic inflammation plays an important role in tumor initiation, promotion, progression, invasion, and metastasis of cancer [26]. Results of previous studies indicated that inflammatory responses might promote carcinogenesis by damaging DNA, stimulating angiogenesis and cell proliferation, as well as inhibiting apoptosis [27, 28].

CRP is the phenotype acute-phase protein induced by hepatocytes. Plasma CRP level may dramatically increase by up to 10,000-fold at the time of acute responses to severe tissue damage or serious infection [29]. Elevated circulating level of CRP is associated with

Table 3. Summary of results of the meta-analysis from different comparative genetic models in the subgroup analysis

	No. (cases/ controls)	T vs. C			TT vs. CC			TT+CT vs. CC			TT vs. CT+CC		
		OR (95% CI)	*P*	*P* (Q-test)	OR (95% CI)	*P*	*P* (Q-test)	OR (95% CI)	*P*	*P* (Q-test)	OR (95% CI)	*P*	*P* (Q-test)
Total	11074/63493	1.02 (0.97-1.08)	0.460	0.031	1.05 (0.91-1.21)	0.517	0.003	0.99 (0.95-1.04)	0.763	0.318	1.06 (0.93-1.21)	0.356	0.007
Ethnicity													
Asians	663/481	1.07 (0.90-1.28)	0.424	0.708	1.11 (0.77-1.59)	0.589	0.684	1.00 (0.75-1.35)	0.992	0.766	1.18 (0.90-1.54)	0.226	0.797
Caucasians	7115/58744	1.01 (0.92-1.12)	0.776	0.002	1.05 (0.84-1.32)	0.656	0.001	1.00 (0.90-1.11)	0.976	0.037	1.06 (0.87-1.30)	0.559	0.002
Africans	494/663	1.00 (0.80-1.24)	0.977	0.931	0.75 (0.41-1.35)	0.336	0.268	1.06 (0.82-1.38)	0.635	0.914	0.72 (0.40-1.28)	0.260	0.207
Mixed	2802/3605	1.05 (0.98-1.13)	0.184	0.481	1.15 (0.97-1.36)	0.106	0.266	1.04 (0.94-1.15)	0.414	0.657	1.14 (0.97-1.34)	0.120	0.215
Cancer type													
Breast cancer	941/4085	0.93 (0.75-1.16)	0.520	0.036	0.73 (0.41-1.29)	0.275	0.035	0.96 (0.73-1.26)	0.770	0.055	0.74 (0.44-1.25)	0.260	0.057
Lung cancer	730/6552	1.12 (0.88-1.43)	0.343	0.045	1.25 (0.69-2.26)	0.467	0.011	1.13 (0.93-1.37)	0.223	0.275	1.24 (0.76-2.02)	0.388	0.018
Colorectal cancer	3037/9144	1.07 (1.00-1.15)	0.062	0.641	1.19 (1.01-1.40)	0.035	0.569	1.06 (0.96-1.16)	0.276	0.726	1.18 (1.02-1.37)	0.026	0.487
Prostate cancer	445/4192	1.00 (0.86-1.16)	0.982	0.466	1.08 (0.77-1.50)	0.664	0.380	0.97 (0.79-1.18)	0.732	0.577	1.10 (0.81-1.51)	0.541	0.448
Combined	5921/39520	0.98 (0.94-1.02)	0.371	0.548	0.98 (0.89-1.07)	0.648	0.334	0.97 (0.92-1.02)	0.247	0.941	1.00 (0.91-1.09)	0.941	0.258
Source of control													
PB	10832/63230	1.02 (0.96-1.09)	0.455	0.015	1.05 (0.90-1.23)	0.497	0.001	0.99 (0.95-1.04)	0.792	0.225	1.06 (0.92-1.22)	0.402	0.003
HB	242/263	0.99 (0.76-1.29)	0.946	0.853	0.93 (0.54-1.62)	0.803	0.741	0.93 (0.62-1.39)	0.721	0.615	1.06 (0.70-1.60)	0.796	0.989
Sample sizes													
<1000	2053/2266	0.97 (0.88-1.07)	0.572	0.153	0.90 (0.67-1.20)	0.465	0.095	0.96 (0.84-1.09)	0.536	0.355	0.98 (0.82-1.17)	0.821	0.113
≥1000	9021/61227	1.04 (0.98-1.11)	0.223	0.030	1.13 (0.95-1.33)	0.162	0.005	1.00 (0.95-1.05)	0.921	0.262	1.12 (0.96-1.31)	0.166	0.006
Study type													
Case-control	4234/4791	1.03 (0.97-1.10)	0.325	0.102	0.98 (0.78-1.24)	0.883	0.033	1.02 (0.93-1.11)	0.677	0.312	1.03 (0.85-1.25)	0.784	0.065
Cohort	6840/58702	1.03 (0.95-1.11)	0.491	0.054	1.10 (0.90-1.34)	0.367	0.011	0.98 (0.94-1.04)	0.550	0.317	1.09 (0.90-1.32)	0.371	0.013
HWE													
P≥0.05	9028/52192	0.99 (0.96-1.03)	0.578	0.222	0.99 (0.91-1.07)	0.779	0.274	0.98 (0.93-1.03)	0.358	0.450	1.01 (0.94-1.09)	0.800	0.451
P<0.05	2046/11301	1.11 (0.92-1.34)	0.258	0.034	1.11 (0.61-2.03)	0.733	0.001	1.08 (0.97-1.21)	0.161	0.303	1.04 (0.58-1.88)	0.887	0.001

HWE: Hardy-Weinberg equilibrium.

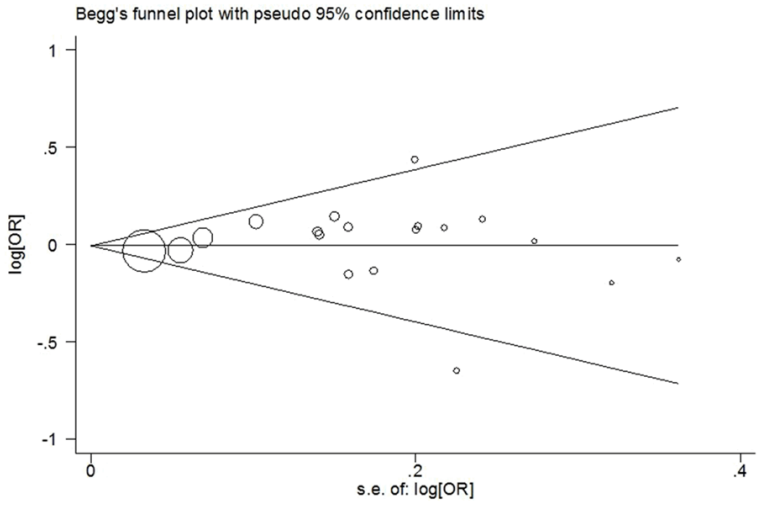

Figure 3. Begg's funnel plot of meta-analysis of between the *CRP* rs1205 C>T polymorphism and the risk of cancer in the dominant model.

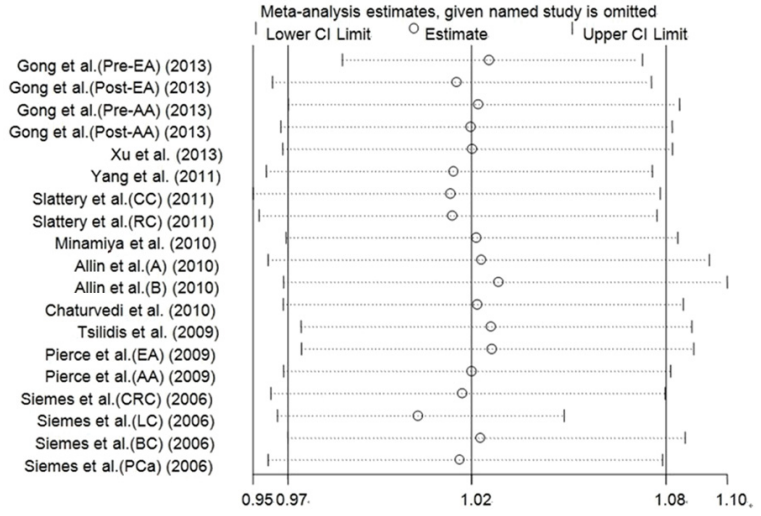

Figure 4. Sensitivity analysis of the influence of T vs. C compare genetic model in overall cancer meta-analysis (random-effects estimates).

increased risk of cardiovascular disease, colorectal, hepatic, pancreatic, breast and esophageal cancer [6-10, 30-32].

Lately, the hypothesis that whether *CRP* rs1205 C>T polymorphism was relevant to cancer risk has been explored; however, the results remained conflicting. One individual study reported negative signal of *CRP* rs1205 C>T polymorphism with breast cancer [17]; however, the other two studies reported positive correlation with lung cancer and colorectal cancer [3, 18]. As a single study could be underpowered, we performed this comprehensive meta-analysis to evaluate the association of *CRP* rs1205 C>T polymorphism with cancer risk in several cancer types and different ethnicities. As demonstrated in overall genetic model, the association was not significant, even in different populations. As for cancer type, our results suggested *CRP* rs1205 C>T polymorphism was associated with increased risk of colorectal cancer in recessive model and homozygote model. We also found the borderline evidence of an association between *CRP* rs1205 C>T polymorphism and an increased risk of colorectal cancer in allele genetic model. Previous studies indicated that *CRP* gene polymorphisms were associated with altered plasma concentration of CRP [32, 33]. Our analysis suggested that the C⟶T variant in *CRP* gene increased the risk of colorectal cancer might be attribute to the altered plasma concentration of CRP. Although there were four studies deviated from HWE [3, 17, 18], the outcomes were not materially changed when these studies were excluded, suggesting our results were robust (**Table 3**). However, the results should be interpreted with very caution. Considering only 19 separate studies were included in our study and some small sample size investigations were recruited, further extensive studies with large sample size and more types of cancer should be performed to confirm or refute our findings.

In general, sources of heterogeneity comprise ethnicity, cancer type, sample size, source of control, study type, HWE in controls and so on. We therefore performed stratified analyses accordingly. The pooled subgroup analysis of a subset of breast cancer, lung cancer, Caucasian population, populations based study, large

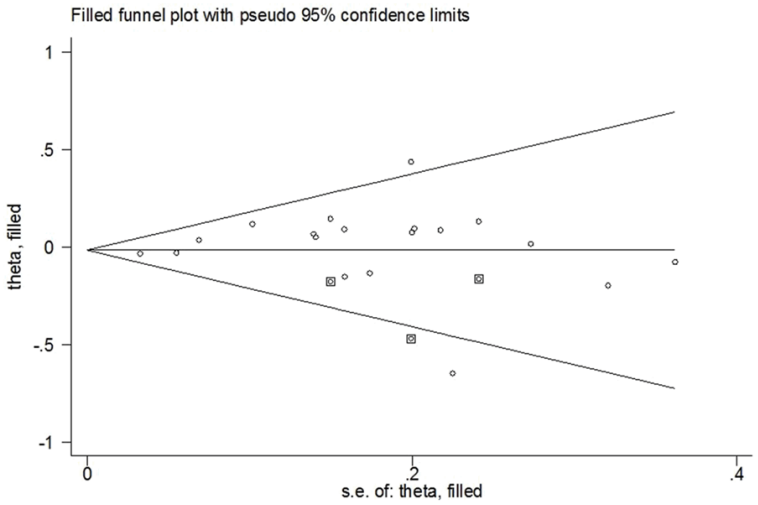

Figure 5. Filled funnel plot of meta-analysis of between the *CRP* rs1205 C>T polymorphism and the risk of cancer in the dominant model.

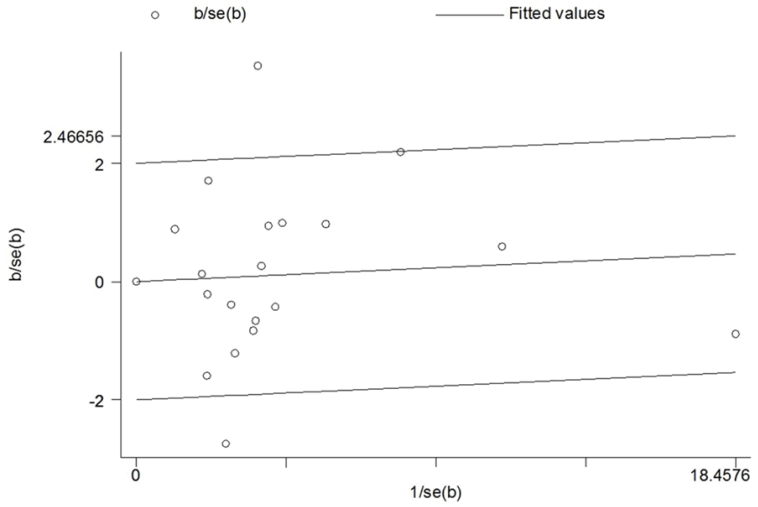

Figure 6. Galbraith radial plot of meta-analysis (TT vs. CC compare genetic model).

sample size, studies deviated from HWE and cohort study, suggested an association with more noteworthy heterogeneity. Combining a forest plot (**Figure 2**) and Galbraith radial plot (**Figure 6**), we could identify two major outliers [3, 17]. In these publications, the study design involved some limitations, for example, one investigation deviated from HWE in controls and the other study was conducted in Caucasian population. In all recruited studies, a methodological quality assessment was performed. Results of quality assessment indicated that the included studies were high quality (score ≥6), suggesting that our results were reliable.

However, some limitations need to be addressed. Large heterogeneity was observed in the present meta-analysis, which meaned our findings should be interpreted with caution. Additionally, all the recruited studies in our meta-analysis were published; therefore, certain publication bias might inevitably exist. Furthermore, for lack of original and uniform information in the included studies, the further stratified analyses were limited. As well, all included investigations focused on the association between *CRP* rs1205 C>T polymorphism and epithelial tumor risk, and did not consider non-epithelial tumor. Finally, our results were derived from crude estimates. A more precise assessment should be carried out, if individual data such as smoking, alcohol consumption, other lifestyle factors and levels of CRP were available.

In conclusion, despite the limitations, our results suggest that rs1205 C>T polymorphism in *CRP* is not associated with overall cancer risk; however, it may contribute to an increased risk for colorectal cancer. Nevertheless, in the future, further studies are needed to confirm or refute the influence of *CRP* rs1205 C>T polymorphism on cancer risk.

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Disclosure of conflict of interest

None.

Address correspondence to: Haiyong Gu and Heng Zhao, Department of Thoracic Surgery, Shanghai Chest Hospital, Shanghai Jiaotong University, No. 241 West Huaihai Street, 200030, Shanghai, China. Tel: 86-13381808896; Fax: 86-021-22200000-2908; E-mail: haiyong_gu@hotmail.com (HYG); Tel: 86-13701865603; Fax: 86-021-22200000-2908; E-mail: h_zhao28@163.com (HZ)

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