

A meta-analysis on the association of genetic polymorphism of the angiotensin-converting enzyme and coronary artery disease in the chinese population

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SUMMARY

OBJECTIVE: To investigate the association between genotype insertion or deletion polymorphism of the angiotensin-converting enzyme gene (ACE) and susceptibility to coronary artery disease (CAD) in Chinese Han population.

METHODS: We conducted a comprehensive search for the OR value of contrast between the group of genotype insertion or deletion polymorphism of the ACE and the group of CAD as an effective index. A meta-analysis (Stata 12.0) was used to test the heterogeneity of the results, combine the values for effect, conduct sensitivity analysis, and basic evaluation.

RESULTS: A total of 638 studies were found on the association between polymorphisms of the angiotensin-converting enzyme gene and CAD, of which 44 studies met the inclusion criteria. In total, our study included 5619 cases and 4865 controls. The heterogeneity test of each study ($P < 0.001$) was carried out using a random effect model. The OR value of DD/ID+II was 1.95, 95% confidence interval (95%CI) (1.66-2.29). The OR value of II/DI+DD was 0.63, 95%CI (0.55-0.72). The funnel figure is basically symmetrical and the results of the sensitivity analysis were stable.

CONCLUSION: The DD genotype of the angiotensin converting enzyme gene may be a weaker risk factor for CAD in the Chinese Han population.

KEYWORDS: Angiotensin-converting enzyme gene, Gene polymorphism. Coronary artery disease. Meta-Analysis.

INTRODUCTION

The pathogenesis of coronary artery disease (CAD) is unknown. The angiotensin-converting enzyme (ACE) is a key enzyme in the renin angiotensin system, which catalyzes the conversion of angiotensin I to angiotensin II and inactivates bradykinin. The hu-

man angiotensin I converting enzyme gene is located on autosomal 17q23, according to whether there is a 287bp sequence in its intron 16. It is divided into two types of alleles, insertion(I) and deletion(D), (ACE Gene I/D polymorphism). There are three genotypes

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(DD, II, ID) in human populations. Although the pathogenesis is still unidentified, recent studies showed that I/D polymorphism in intron 16 of the ACE gene is associated with CAD.

At present, a lot of research is being carried out on the relationship between ACE polymorphism and CAD, but no consensus has been achieved.

According to the results of a randomly chosen study by Camblen et al.¹² the frequency of DD homozygous was significantly increased in patients with CAD compared to that in normal controls. The DD genotype was considered an independent risk factor for CAD, and ACE I/D polymorphism is closely related to Myocardial Infarction in Caucasians. However, a recent 2010 study that included 224 randomly chosen CAD patients of an Iranian population showed that there was no association between the DD genotype homozygote of the ACE gene and the risk of CAD³. Alazhary's et al.⁴ study on the Saudi Arabian population showed that the ACE gene DD homozygotes were not associated with the risk of CAD.

The distribution of genetic polymorphism varies in different races and populations. Over 3000 studies in our references pointed out that there is an obvious racial and regional difference in the distribution frequencies of ACE genotypes. For example, in Caucasians, DD was 36.25%⁵. In the first generation of white immigrants living in London, DD was 23%, 30.9% in the African population, 18.3% in South Asian population⁶, and 8% in the Japanese population⁷. Studies in Chinese Han populations⁸

In the study of Jing et al.⁹, the results showed that the DD genotype was not associated with CAD in the Han population. They found that the DD genotype was associated with CAD in the Hui population, whereas it had no relation to the Han people. Therefore, it is of great significance and value to study the genetic polymorphism of ACE in the Chinese Han population. This study collected the relevant literature of the Chinese population for comprehensive quantitative analysis; a meta-analysis can control the heterogeneity of the study and the individual level of related factors to investigate the relationship between ACE and CAD.

METHODS

1.1 Literature search on Medline, Pubmed, CBM, Chinese Biomedical Literature Database and For-

eign Biomedical Literature Journal Service system, etc. and keywords: Angiotensin-converting enzyme; Genetic polymorphism; Coronary artery disease; Evidence based medicine. Meta-Analysis to search for insertion/deletion of intron 16 of the ACE gene reported in China published before January 2018 on the relationship between I / D polymorphism and CAD disease risk.

1.2 Research Inclusion Criteria For the case-control study published independently in China, the literature needed to provide comprehensive statistical indicators: the case group was CAD, and the control group was the healthy population. The observation index was the odds ratio (OR) of the two groups of patients with genotype frequency, including ACE DD (ID +II) OR and II (ID+ DD) OR. Those who reported incomplete information or studies with only special samples, such as patients with myocardial infarction or CAD complicated with diabetes, or minority populations, as well as those in the control group that did not comply with the law of genetic balance were removed. If studies included the same sample of multiple literature reports, we selected the most recently published.

1.3 Quality assessment Two investigators independently screened the literature according to the predetermined inclusion and exclusion criteria. If there were disagreements that could be discussed or resolved by third parties in order to determine the methodological quality of the NOS, to Newcastle-Ottawa scale was used. The scale uses a "star rating" to determine the quality of the observational study, with NOS scores between zero and nine stars. A score higher than or equal to 7 points is considered to be high-quality literature, and the evaluation includes three items: the selection of the case group and the control group (4 points), comparability (2 points), and exposure (3 points).

1.4 Statistic treatment The Excel database was established by double input. The genotypes of the control group were tested using the Hardy-Weinberg (H-W) genetic balance test, and the database was statistically processed by Stata 12.0 analysis software, including OR value, 95% confidence interval (95%CI) and the heterogeneity test of each study. According to the test results, a fixed effect model or random effect model was selected to combine the data and a funnel chart was drawn for linear regression analysis to assess result bias.

TABLE 1 CHARACTERISTICS OF STUDIES INCLUDED IN THE META-ANALYSIS

First author	Year	Region (province/city)	CAD patients		non-CAD control		NOS score
			Total	D frequency	Total	D frequency	
Xiang et al.10	1995	shanghai	80	0.64	48	0.38	7
Kario et al.11	1996	china	276	0.409	147	0.411	8
Gu et al.12	1998	beijing	95	0.54	100	0.35	8
Shi et al.13	1998	zhejiang	148	0.446	159	0.425	7
Qiu et al.14	1999	zhejiang	73	0.58	102	0.38	8
Jia et al.15	1999	jiangsu	187	0.497	160	0.537	8
Sui et al.16	1999	tianjing	40	0.46	50	0.4	7
Tan et al.17	1999	shandong	137	0.639	63	0.436	8
Shi et al.18	2000	tianjing	169	0.583	94	0.441	8
Xie et al.19	2001	jiangsu	106	0.44	86	0.36	7
Chen et al.20	2001	hubei	51	0.422	30	0.3	8
Deng et al.21	2002	sichuan	55	0.34	102	0.36	7
Liu et al.22	2002	jiling	51	0.61	83	0.45	8
Su et al.23	2002	jiangsu	157	0.5637	112	0.3884	7
Zhu et al.24	2002	jiangsu	140	0.421	106	0.3585	8
Zhang et al.25	2003	guangdong	102	0.43	148	0.33	7
Huang et al.26	2003	jiangsu	89	0.567	75	0.413	8
Mao et al.27	2004	hunan	100	0.64	54	0.4537	7
Wang et al.28	2004	hubei	50	0.6	56	0.41	9
Zhu et al.29	2004	beijing	192	0.359	98	0.342	7
Lin et al.30	2005	guangdong	72	0.417	50	0.350	8
Wang et al.31	2006	guangdong	105	0.4381	50	0.32	8
Shi et al.32	2006	zhejiang	169	0.49	168	0.4167	9
Wang33	2006	jiangxi	161	0.56	109	0.46	7
Yang et al.34	2007	sichuan	80	0.581	80	0.413	7
Li et al.35	2008	hebei	80	0.63	100	0.62	8
Jia et al.36	2008	shanxi	110	0.605	80	0.444	8
Shi et al.37	2008	sichuan	80	0.56	80	0.41	8
Zhao et al.38	2008	shang hai	115	0.46	47	0.34	8
Yun et al.39	2009	hai nan	150	0.46	150	0.343	7
Yang et al.40	2009	xin jiang	42	0.4405	82	0.36	7
Chen41	2009	hu nan	86	0.57	38	0.25	8
Xie et al.42	2009	nei menggu	94	0.367	67	0.358	8
Liu and He43	2010	nei menggu	54	0.6665	88	0.4886	7
Wang et al.44	2010	jiang xi	158	0.55	109	0.47	7
Yang et al.45	2011	shan dong	146	0.55	113	0.46	7
Peng et al.46	2011	guang dong	196	0.643	200	0.435	8
Yi et al.47	2011	guang dong	180	0.609	180	0.467	8
Wang et al.48	2012	qing hai	89	0.567	75	0.413	8
Hu et al.49	2013	hu nan	86	0.57	38	0.25	7
Zhao et al.50	2015	he bei	233	0.51	99	0.42	7
Zhang et al.51	2016	liao ning	568	0.345	580	0.267	8
Jing et al.52	2016	qing hai	59	0.305	193	0.35	8
Dai53	2017	shan dong	208	0.45	216	0.34	8

RESULTS

Results of the Literature Search and Analysis of Research Quality

A total of 638 related research papers were retrieved. The genotype distribution of the control group in 11 papers did not conform to the Hardy-Weinberger (H-W) genetic balance test law and were removed; 44 papers were found to meet the requirements (Table 1). Among them, 8 were published in English (or in Chinese/English), 31 in Chinese only, and 5 were officially published master's theses. The published time of the literature was from 1995 to January of 2018, the study population was comprised of 5619 cases of 44 studies in more than twenty provinces/cities of China and 4865 normal control. The diagnosis of CAD cases in each study was in accordance with the WHO standard. The angiotensin-converting enzyme (ACE) genotyping was based on three internationally recognized genotypes of DD, II, and ID. The detection methods were polymerase chain reaction (PCR) and gel electrophoresis.

Analysis Of Angiotensin Converting Enzyme Genotypes

The Q values of DD/DI +II and II/DI +DD genotype heterogeneity test of ACE gene were 105.74 and 100.56 respectively ($P < 0.001$) and the combined DD/(DI+ II) OR was 1.95, 95%CI (1.66-2.29) , $Z = 8.09$ (P

< 0.001) (Fig. 1) . The combined II/ (DD+DI) OR was 0.63, 95%CI (0.55-0.72) , $Z=6.64$, ($P < 0.001$).

Sensitivity Analysis And Bias Assessment

Concerning the polymorphic susceptibility analysis of the gene, after removing the largest sample and applying a random effect model analysis, the OR value of the comprehensive effect of the DD genotype was 2.00, 95%CI (1.70 – 2.34) , $Z=8.55$ ($P < 0.001$). The comprehensive OR value of the genotype II was 0.62 , 95 %CI (0.54-0.71) $Z= 6.68$ ($P < 0.001$) .

According to the combined effect value of the three groups (sample size < 100 , $100 \sim 200$, ≥ 200) , the Q value for the DD/DI +II and II/DI +DD genotype heterogeneity test was 7.54 ($P=0.023$) and 11.98 ($P=0.003$) ; the OR value was combined with the random effect model. The OR value of combined DD/(DI+II) was 1.92, 95 %CI (1.51-2.44) , $Z = 5.33$, ($P < 0.001$), and the OR value of combined II/ (DI+DD) was 0.66 , 95%CI (0.51-0.86) ($P = 0.002$). The sensitivity analysis results were stable. A meta-analysis is an observational study, in which publication bias is very common. Among the 44 articles collected, 29 reported that ACE DD genotype was associated with the risk of CAD, and 15 were not associated with the risk of CAD. The funnel map (based on ACE (I / D) polymorphism and the OR value of CAD risk were drawn as the horizontal coordinate and the standard

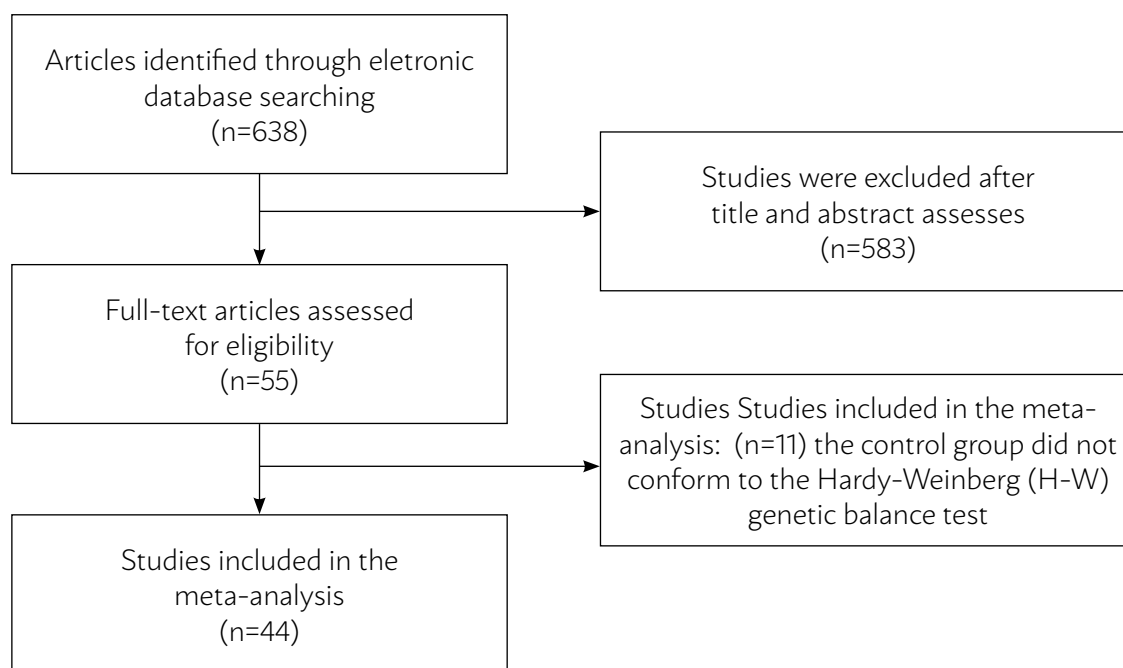


FIGURE 1 FLOWCHART OF THE SELECTION OF STUDIES INCLUDED IN THE META-ANALYSIS.

of OR value as the vertical coordinate). The Egger linear regression analysis was used to test the symmetry of the funnel graph. The Y-axis intercept of the DD genotype was 2.17 (95% CI 0.78-3.56) P=0.003, and the II genotype was -2.47 (95% CI -3.75 - 1.19) , P<0.001. According to the standard of P=0.1, the two funnel graphs were both asymmetrical.

DISCUSSION

A total of 44 works of literature published in the past more than twenty years was included, with 5619 cases and 4865 controls. A meta-analysis revealed that ACE gene insertion/deletion (I / D) polymorphism was correlated with the risk of CAD in the Chinese Han population. The risk of CAD in individuals with DD genotype increased by 95% compared with the DI/II genotype. There is evidence that the DD genotype may increase the risk of left ventricular hypertrophy after myocardial infarction ⁵⁴, and the incidence of chronic heart failure in patients with CAD who carried DD genotype and D allele increased significantly. Moreover, the genotype can be used as a marker for the deterioration of cardiac function⁵⁵. Studies have shown that the change of single nucleotide polymorphism of ACE gene increased the level of angiotensin II (Ang II) and bradykinin in peripheral or local circulation by influencing the level of ACE expression, which stimulates the release of aldosterone in blood vessels and enhances the re-

lease of norepinephrine from sympathetic nerves. Consequently, the process of local inflammatory response in patients with atherosclerotic CAD was affected, and the process of atherosclerosis was aggravated ⁵⁶. The DD genotype was clearly associated with acute coronary syndrome, especially in acute myocardial infarction patients. The ACE activity of individuals carrying D alleles is improved, causing the coronary plaque to become unstable, prone to rupture and form ulcers, which leads to the formation of thrombus^{57,58}. This study was consistent with the results of the meta-analysis conducted by Zhou et al.⁵⁹ in the Chinese population.

According to the results of Alazhary et al.⁶⁰, no association between ACE I / D gene polymorphism and CAD in Saudi children was found, possibly due to regional and ethnic differences in this association. Although a study conducted in Japan indicated that ACE I / D gene polymorphism was associated with CAD, it was not linked to the severity of coronary artery stenosis, and the DD genotype was probably unrelated to the development of coronary artery stenosis⁶¹.

This study was divided into three groups according to the sample size. ACE I/D gene polymorphism was found to be related to the risk of CAD in subgroups with sample size ranging from 100 to 200 and greater than 200, while no correlation was found in the subgroup with a sample size smaller than 100. As only two pieces of literature were included in the subgroup, the reliability of the consolidation effect values was low. Sensitivity analysis depicted there

TABLE 2 SUMMARY ODDS RATIO FOR THE ASSOCIATION OF ANGIOTENSIN-CONVERTING ENZYME INSERTION OR DELETION POLYMORPHISM AND CORONARY ARTERY DISEASE GROUPED BY SIZE

Study group (N° of studies)	N° of patients with DD genotype/DI and II N° of patients		Combined OR(95%-CI)	N° of patients with II genotype/ DI and DD N° of patients		Combined OR(95%-CI)
	CAD cases	No CAD controls		CAD cases	No CAD controls	
<100 cases (2)	23/68	11/69	2.303[0.772,6.870]	34/57	33/47	0.792[0.422,1.488]
100-200 cases (22)	581/1211	283/1298	2.311 [1.883, 2.836]	439/1353	593/988	0.499[0.406, 0.612]
≥200 case (20)	1002/2734	577/2627	1.680 [1.337, 2.111]	1222/2514	1276/1928	0.745[0.632, 0.879]
Test for heterogeneity	Q=7.54	P=0.023		Q=11.98	P=0.003	
Combined OR(95%CI)	1.919	[1.510, 2.438]		0.659	[0.505, 0.860]	
	Z=5.33	P<0.001		Z= 3.07	P=0.002	

was almost no change in the results after removing the largest sample, suggesting that the meta-analysis results were of good stability. The Egger regression analysis of funnel pattern represents the symmetry of graphs, and no publication bias exists.

In conclusion, ACE gene (I / D) polymorphism is related to the risk of CAD in Chinese Han population. In this study, recognized scientific methods were adopted, such as the joint use of multiple approaches

to literature retrieval, the formulation of rigorous inclusion criteria, and the inclusion of documents. When we sifted through the literature, we took into account factors that may affect the results, and every study was in accordance with the law of genetic balance. The study population, which covers the Han population in most parts of China, has certain representativeness and guarantees the reliability of the meta-analysis results.

RESUMO

OBJETIVO: Investigar a associação entre o polimorfismo de inserção ou deleção do genótipo do gene da enzima conversora da angiotensina (ACE) e a susceptibilidade da etnia Han chinesa para a doença arterial coronariana (DAC). **Métodos:** Foi realizada uma pesquisa abrangente para o valor de OR (Odds Ratio) de contraste entre o grupo de polimorfismo de inserção ou deleção do genótipo do gene da enzima conversora da angiotensina (ACE) e o grupo de doença arterial coronariana (DAC) como um índice de eficácia. Uma meta-análise (Stata 12,0) foi utilizada para testar a heterogeneidade dos resultados, combinar os valores de eficácia, realizar análises de sensibilidade e de avaliação básica.

RESULTADOS: Um total de 638 estudos foram encontrados sobre a associação entre polimorfismos do gene da enzima conversora da angiotensina e doença arterial coronariana, dos quais 44 satisfaziam os critérios de inclusão. Nosso estudo incluiu 6246 casos e 5713 controles. O teste de heterogeneidade de cada estudo ($p < 0,001$) foi realizado seguindo o modelo de efeito randômico. O valor de OR para DD/ID+II foi 1,95, com 95% de intervalo de confiança de (95%CI) (1,66-2,29). O valor de OR para II/DI+DD foi 0,63, com 95% IC (0,55-0,72). A figura do funil é basicamente simétrica e os resultados da análise de sensibilidade foram estáveis.

CONCLUSÃO: O genótipo DD do gene da enzima conversora da angiotensina podem ser um fator de risco mais fraco para doença coronariana na população chinesa Han.

PALAVRAS-CHAVE: Peptidil Dipeptidase A. Polimorfismo Genético. Doença da Artéria Coronariana. Metanálise.

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