COMMENTARY

Commentary: “Meta-Analysis on The Association of Genetic Polymorphisms of The Angiotensin-Converting Enzyme and Coronary Artery Disease in the Chinese population”

Baohong Xue[1]
Lianping He[1]

1. College of experience industry, Anhui polytechnic university, Wuhu, Anhui, China
Correspondence: Baohong Xue, road No.8 Beijing– 241000 - Wuhu - China. Email: baohongxue@yeah.net

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We read with great interest the study by Zhang and colleagues[1] in which they demonstrated that the DD genotype of the angiotensin-converting enzyme gene might be a weaker risk factor for coronary heart disease in the Chinese Han population. We appreciate the contribution that this meta-analysis makes to the field. However, some questions should be addressed.

First, there are many risk factors for coronary artery disease, such as serum triglycerides [2]. Thus, the author should exclude some articles which included patients with some of these complications. Additionally, age also has an influence on the relationship between the DD genotype of the angiotensin-converting enzyme gene and coronary heart disease.

However, the authors failed to include more information in table one.

The authors further stated that “the database was statistically processed by Stata 12.0” in the statistic treatment section. However, no figure produced by Stata 12.0 was found in the results section. A funnel plot was also needed to present the publication bias. It is evident that the author should add more figures in this article.

When the heterogeneity is existing, the author should explore the sources of heterogeneity. In our opinions, a subgroup analysis should be performed when heterogeneity occurs[3].

REFERENCES

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