Comments on: "A Meta-Analysis of the Association between Microrna-196A2 and Risk of Ischemic Stroke and Coronary Artery Disease in Asian Population"

Dear Editor,

Wang et al[1] recently published a meta-analysis on the role of miR-146a polymorphism (rs11614913 T > C) and susceptibility to ischemic stroke and coronary artery disease (CAD) in Asian population and concluded that the recalled variant "may contribute to CAD susceptibility." They showed the result related to the protective effect of CAD in homozygote model (CC versus TT, OR = .43, 95%CI = .39-.47, $P < .00001$), as their most significant result, and indicated that "carrying CC homozygote genotype may play a protective role in development of disease." While other results of their meta-analysis increased the risk of disease or had no significant effect (Fig 3 in Wang[1] meta-analysis). The result described in this article is actually due to a mistake in the meta-analysis which should be noticed.

Here, we aim to comment on the issue. For homozygote model, instead of comparing CC versus TT genotype frequencies, the comparison between TC versus CC genotype frequencies has been presented as significant differences between groups. The correct analysis is presented based on studies included in their meta-analysis.[2-9] Based on the analysis of homozygote model, we found that not only CC genotype has no protective effect in CAD, but there is a also trend toward the increasing risk of CAD 1.06 (0.97-1.17). We also found a significantly increasing risk for overdominant model in cases compared to the controls (TC versus TT+CC) 1.09 (1.02-1.16). Forest and funnel plots related to these results are shown in Figures 1 and 2.

Also we have 2 more comments, as has been described by authors all included studies belonged to Chinese and South Korean populations, due to ethnic diversity in Asian population, and also regarding 1000 Genomes and gnomAD-Genomes studies which identified T allele as more abundant allele in East Asian population versus other world populations which the C allele is rather the more frequent allele (https://www.ncbi.nlm.nih.gov/snp/rs11614913), thus it is more accurate for them to consider their population attributed to East Asia instead of Asian population as a whole.

Also in subgroup analysis, the authors show statistical result related to meta-analysis for Korean subgroup with only 1 included study which has no statistical interpretation outcome, these trivial data are misleading and were better to be excluded.

Finally, when we combine results from our analysis with the correct analysis in Wang etal[1] meta-analysis, it can be concluded that rs11614913 T > C may be related to increased risk of CAD in Chinese population.

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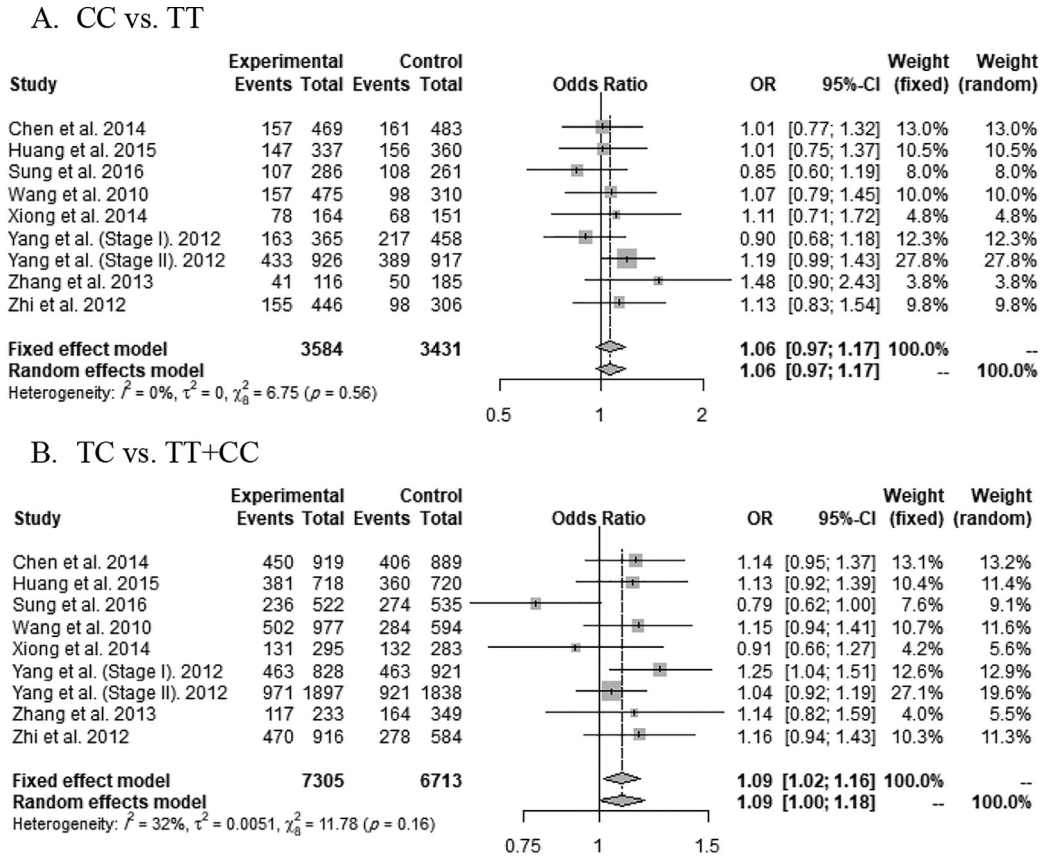

Figure 1. *Forest plots for the association between rs11614913 T > C and the risk of CAD (homozygote and overdominant models).*

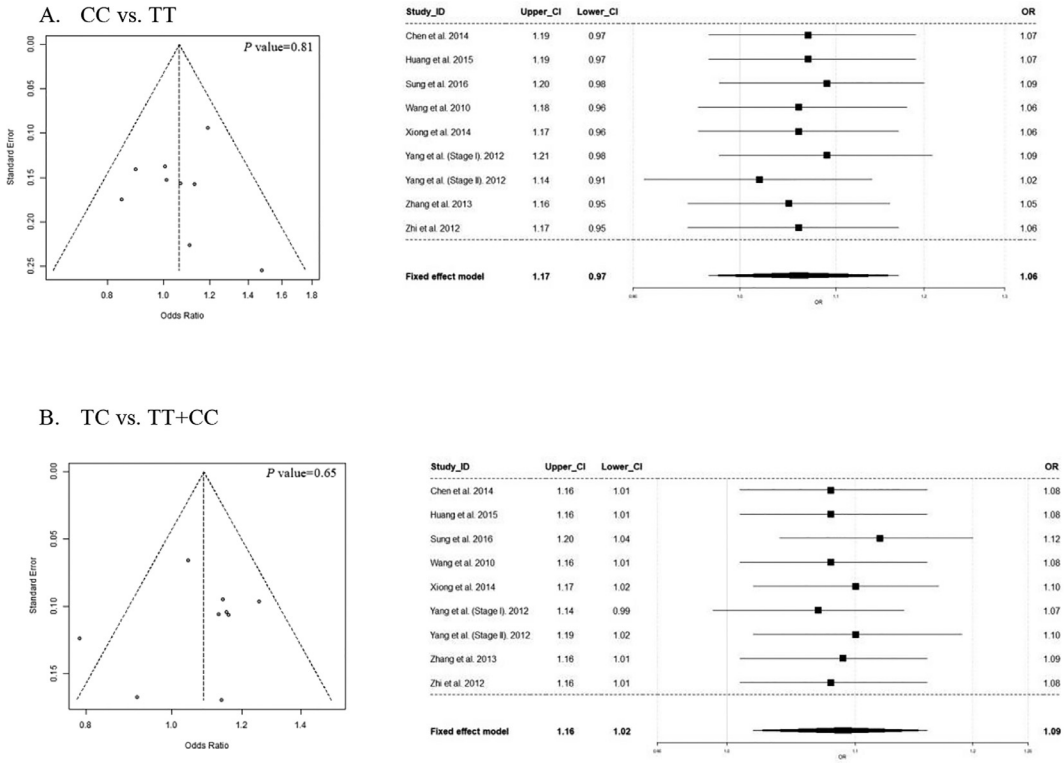

Figure 2. *Forest plots of sensitivity and funnel plots of publication bias for the association between rs11614913 T > C and the risk of CAD (homozygote and overdominant models).*

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