Letter to the Editor

The association between polymorphisms in the interleukin 4 (IL-4) promoter -589C/T gene and the risk of asthma

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Comment on: Zhu L, Liu T, Wang L, *et al.* Polymorphisms in the interleukin 4 promoter -589C/T gene and the risk of asthma: a systematic review and meta-analysis. Transl Pediatr 2021;10:2355-65.

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We read with interest the literature by Zhu *et al.* entitled "*Polymorphisms in the interleukin 4 promoter -589C/T gene and the risk of asthma: a systematic review and meta-analysis*" (1). They demonstrated that CT, TT, and T gene polymorphisms were risk factors for asthma by the research of interleukin 4 (C-590T) gene polymorphism. Whereas, after a careful learning of this study, we would like to raise several critical points that may need to be elucidated in order to enhance the validity of the conclusions.

First, according to the results of meta-analysis, the odds ratio (OR) values of CT, TT and T gene polymorphisms were 1.05 [95% confidence interval (CI): 0.89–1.24; P=0.59], 0.71 (95% CI: 0.33–1.52; P=0.38), and 1.98 (95% CI: 1.54–2.53; P<0.00001). Therefore, CT and TT gene polymorphisms were not statistically significant between patients with and without asthma because of P>0.05. Therefore, the conclusion that CT and TT gene polymorphisms were risk factors for asthma could not be confirmed.

Second, regarding the CT subgroups showed in figure 7, Zhu *et al.* found that CT gene polymorphism was a risk factor for asthma. However, we believe that the interpretation of the subgroup analysis was improper, as the differences between all 3 subgroups were not statistically significant (P=0.06). Hence, the conclusion that CT gene polymorphism was a risk factor for asthma could not be confirmed according to figure 7.

Third, with regard to the CC subgroups showed in figure 8, Zhu *et al.* demonstrated that CC gene polymorphism was a risk factor for asthma. However, we consider that the interpretation of the subgroup analysis was incorrect, because the differences between the 2 subgroups were not statistically significant (P=0.9). Therefore, the conclusion that CC gene polymorphism was a risk factor for asthma could not be demonstrated according to figure 8.

Finally, in the data synthesis and statistical analysis section of this article, the authors depicted that the relative ratio (RR) was used as an effect size. Whereas, in this meta-analysis, the effect size was OR showed in all forest plots and the RR was not reported in the results section. So we believe that the irrelevant effect size depicted would undoubtedly result in misunderstanding.

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Footnote

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have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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1. Zhu L, Liu T, Wang L, et al. Polymorphisms in the interleukin 4 promoter -589C/T gene and the risk of asthma: a systematic review and meta-analysis. Transl Pediatr 2021;10:2355-65.