Letter to Editor

GSTM1 and GSTT1 null genotype and diabetic retinopathy: a meta-analysis

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We read with great interest the paper written by Li Sun et al. entitled “GSTM1 and GSTT1 null genotype and diabetic retinopathy: a meta-analysis” and published in Int J Clin Exp Med 2015; 8 (2): 1677-1683 [1]. The Authors concluded that the null genotypes of GSTT1 and GSTM1 were associated with a significantly increased risk of diabetic retinopathy (DR). We would like to draw the attention to data presented in Figure 5. In the forest plot shown on Figure 5 all odds ratios (OR) of the individual studies are on the right of the line of no effect. In fact only one of 4 studies included in the meta-analysis reported that the deletion in the GSTM1 gene is associated with higher frequency of DR [2], whereas remained 3 studies demonstrated contrary findings: GSTM1 deficiency might confer protection against the development of DR [3-5]. Analysis of Figure 5 indicated that the interpretation of results of these studies presented by Li Sun et al. was wrong. Therefore, it is incorrect and misleading to state that “The null genotype of GSTM1 was associated with a significantly increased risk of DR when compared with present genotype (OR = 1.59; 95% CI, 1.22-2.06; Figure 5)".

In the interests of correcting the errors introduced into the literature by a paper published in such a prestigious journal, we performed meta-analysis based on the results of 4 above mentioned studies. The association between GSTM1 and risk of DR was expressed as OR and 95% confidence interval (CI). Statistical heterogeneity across studies included in the meta-analysis was assessed by Cochran’s Q statistic (a significant Q-statistic (P < 0.10) indicated heterogeneity across studies). An F statistic was conducted to evaluate whether inconsistencies among studies were attributed to heterogeneity rather than chance. The following suggested cut-off points were used: $I^2 = 0$-25%, no heterogeneity; $I^2 = 25$-50%, moderate heterogeneity; $I^2 = 50$-75%, large heterogeneity; $I^2 = 75$-100%, extreme heterogeneity [6]. If heterogeneity existed, the random effects models, was adopted to calculate the overall OR value [7]. Otherwise, the fixed effects model was used. To look for bias, we used: the funnel plot, and Egger’s linear regression test at the $P < 0.10$ level of significance [8]. Meta-analysis was carried out using StatsDirect version 2.8.0. All P values are two-sided at the P = 0.05 level, except where otherwise specified.

The meta-analysis resulted in a statistically non significant association between GSTM1 null genotype and DR. The overall OR was 0.57 (95% CI: 0.29-1.12, $P = 0.1$) with statistically significant between-study heterogeneity ($P_{\text{heterogeneity}} = 0.0002$; $I^2 = 85\%$) (Figure 1). The statistical results did not show publication bias (Egger test, $P = 0.636$). Due to small number of studies it was difficult to assess the symmetry of funnel plot (Figure 2).

Our study sought to synthesize evidence regarding the association between GSTM1 polymorphisms and DR risk but due to the small number and heterogeneity of studies the results should be interpreted with caution. Therefore further research is necessary to fully explore...
GSTM1 and GSTT1 null genotype and DR


Disclosure of conflict of interest

None.

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References


Figure 1. Meta-analysis of GSTM1 null genotype associated with DR.

Figure 2. Funnel plot of association between GSTM1 polymorphism and DR.

the possible interaction between GSTM1 and DR

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