X-ray repair cross-complementing group 3 common polymorphism is not associated with cervical cancer risk.

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Abstract

Recently, some reports investigated the association between X-ray Repair Cross-Complementing group 3 (XRCC3) and cervical cancer risk. However, the results were inconclusive. The meta-analysis, thus, assessed whether XRCC3 T241M polymorphism was associated with cervical cancer risk. Odds Ratios (ORs) with 95% Confidence Intervals (CIs) were calculated. Five case-control studies with a total of 806 cervical cancer cases and 850 controls were included. No association between XRCC3 T241M polymorphism and cervical cancer risk was found. In subgroup analysis, Asians with this polymorphism seemed to be associated with cervical cancer risk. Publication bias was not performed. In conclusion, this meta-analysis suggested that XRCC3 T241M polymorphism was not associated with cervical cancer risk.

Keywords: Cervical cancer, X-ray repair cross-complementing group 3, Meta-analysis, Polymorphism.
Data extraction

Two investigators independently extracted data: the first author’s name, year of publication, ethnicity of the study population, numbers of cases and controls.

Statistical analysis

The strength of association was assessed by calculating OR with 95% CI. The pooled ORs were performed for dominant model. Stratified analysis was performed by ethnicity. Departure from Hardy-Weinberg Equilibrium (HWE) in controls was tested by the chi-square test. The Q statistic and the $I^2$ statistic were used to assess the degree of heterogeneity among the studies included in the meta-analysis. If heterogeneity was observed among the studies, the random-effects model was used to estimate the pooled OR (the Dersimonian and Laird method). All statistical tests were performed with the software Revman 5.1 software (Nordic Cochrane Center, Copenhagen, Denmark). A P value<0.05 was considered statistically significant.

Results

Characteristics of studies

A total of 5 case-control studies with 806 cervical cancer cases and 850 controls were included for this meta-analysis. There were 3 studies of Asian population and 2 studies of Caucasian population. All studies suggested that the distribution of genotypes in the controls was consistent with HWE. The characteristics of each case-control study are presented in Table 1.

Table 1. Characteristics of the included studies.

<table>
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<th>First author</th>
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<th>Control number (n)</th>
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Results of meta-analyses

A random-effect model was used for synthesis of the data. The overall OR was 1.34 (95% CI, 0.89-2.01). Subgroup analysis by ethnicity was performed. There was no significant association with cervical cancer risk in Caucasian. However, Asians with this polymorphism seemed to be associated with cervical cancer risk.

Publication bias

Only 5 case-control studies were included in this meta-analysis. Thus, we did not perform to access the publication bias.

Discussion

This meta-analysis included 5 case-control studies with 806 cervical cancer cases and 850 controls. We did not find a significant association between XRCC3 T241M polymorphism and cervical cancer risk. There was also no significant association with cervical cancer risk in Caucasian. However, Asians with this polymorphism seemed to be associated with cervical cancer risk.

Zeng et al. indicated that the XRCC1 Arg399Gln polymorphism decreased the risk of cervical cancer [13]. Yang et al. suggested that AT haplotype in the ITPR3 gene may serve as a potential marker for genetic susceptibility to cervical squamous cell carcinoma [14]. Zhao et al. suggested that the GSTP1 Ile105Val polymorphism is not associated with the development of gynecological cancer [15]. Rotar et al. suggested that no link has been found between VEGF+936 C/T and cervical intraepithelial neoplasia [16].

Some limitations should be acknowledged. First, lacking of the original data of the eligible studies limited the evaluation of the effects of the gene-gene and gene-environment interactions in the development of cervical cancer. Second, potential publication bias might exist. Third, the included studies did not control all covariates.

In conclusion, no association between the XRCC3 T241M polymorphism and cervical cancer risk was found in this study.

Conflicts of Interest

None

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References


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