Review Article

Analyzing Association of the XRCC3 Gene Polymorphism with Ovarian Cancer Risk

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This meta-analysis aims to examine whether the XRCC3 polymorphisms are associated with ovarian cancer risk. Eligible case-control studies were identified through search in PubMed. Pooled odds ratios (ORs) were appropriately derived from fixed effects models. We therefore performed a meta-analysis of 5,302 ovarian cancer cases and 8,075 controls from 4 published articles and 8 case-control studies for 3 SNPs of XRCC3. No statistically significant associations between XRCC3 rs861539 polymorphisms and ovarian cancer risk were observed in any genetic models. For XRCC3 rs1799794 polymorphisms, we observed a statistically significant correlation with ovarian cancer risk using the homozygote comparison (T2T2 versus T1T1: OR = 0.70, 95% CI = 0.54–0.90, \( P = 0.005 \)), heterozygote comparison (T1T2 versus T1T1: OR = 1.10, 95% CI = 1.00–1.21, \( P = 0.04 \)), and the recessive genetic model (T2T2 versus T1T1+T1T2: OR = 0.67, 95% CI = 0.52–0.87, \( P = 0.002 \)). For XRCC3 rs1799796 polymorphisms, we also observed a statistically significant correlation with ovarian cancer risk using the heterozygote comparison (T1T2 versus T1T1: OR = 0.91, 95% CI = 0.83–0.99, \( P = 0.04 \)). In conclusion, this meta-analysis shows that the XRCC3 were associated with ovarian cancer risk overall for Caucasians. Asian and African populations should be further studied.

1. Introduction

Ovarian cancer is the leading cause of the female reproductive system, with over 220,000 new cases and over 140,000 deaths worldwide in 2008 [1]. As most of the carcinomas, ovarian cancer is a multifactorial disease. Genetic factors are considered to influence the susceptibility of glioma genetic factors which all play significant roles in its susceptibility [2]. The genetic basis of ovarian carcinogenesis has been investigated in many studies. BRCA1, BRCA2, MLH1, MSH2, SMAD6, RAD51C, RAD51D, RBL1, LIN28B, CASP8, and MTDH have all been implicated [3–11]. Recently, several common susceptibility alleles in four loci to be strongly associated with ovarian cancer risk have been found in three genome-wide association studies (GWAS) [12–14]. Examination of gene polymorphisms may explain individual differences in cancer risk [15].

XRCC3 (X-ray repair cross-complementing group 3) belongs to a family of genes responsible for repairing DNA double strand breaks caused by normal metabolic processes or exposure to ionizing radiation [16]. XRCC3 interacts and stabilizes Rad51 and involves in HRR (homologous recombinational repair) for DBSs (double strand breaks of DNA) and cross-link repair in mammalian cells [17, 18]. The SNP rs861539 lead to Thr241Met amino acid substitution, that may affect the function and/or its interaction with other proteins involved in DNA damage and repair [17, 19]. The SNP rs1799794 (4541 A > G) is located in 5’ UTR and the SNP rs1799796 (17893 A > G) is located in intron 5 [20]. So the two SNPs do not change the proteins of XRCC3. XRCC3 polymorphism was associated with the risks of many cancers, such as lung cancer, breast cancer, and head and neck cancer [21–24]. The association between XRCC3 polymorphism and ovarian cancer has been studied [20, 25–29]; however, those experimental results remain confusing. To summarize the effect of the XRCC3 polymorphism on the risk for ovarian cancer, we performed a meta-analysis.
2. Methods

2.1. Search and Selection Process. The search of the PubMed database was performed using the following keywords: “X-ray repair cross-complementing group 3,” “XRCC3,” “rs861539,” “T241M,” “rs1799794,” “a4541g,” “rs1799796,” “a17893g,” “polymorphism,” “ovarian cancer,” and their combination. Two authors (Yuan and Wang) independently checked all the references retrieved to assess their appropriateness for the inclusion in this meta-analysis. In addition, we checked all the references cited in the articles and relevant reviews. For overlapping and republished studies, only the study with the largest samples was included. If an article reported results including different studies, each study was treated as a separate comparison in our meta-analysis.

Included studies met 3 criteria:
(1) evaluating the association between XRCC3 polymorphisms and ovarian cancer risk;
(2) using sufficient published data to enable estimation of an odds ratio (OR) with its 95% confidence interval (CI);
(3) using respective or prospective cohort case-control studies.

2.2. Data Extraction. Two authors (Yuan and Wang) independently extracted data from selected articles according to the inclusion criteria and reached a consensus on all items. The following information was extracted from each study if available: the first author, year of publication, countries, area of the cases, the ethnicity of the population, the cases source, the sample type of cases, the numbers of cases and controls, and the genotype distributions of XRCC3 in both cases and controls.

2.3. Quality Score Assessment. Two authors independently evaluated the quality of the 8 studies according to the scale for quality assessment (Table 1), which has been described previously [30, 31]. Quality score assessment was performed according to “source of cases,” “source of controls,” “specimens of cases for determining genotypes,” “Hardy-Weinberg equilibrium in controls,” and “total sample size.” Total scores ranged from 0 (worst) to 15 (best). Studies scoring ≥10 were defined as “high quality,” and those <10 were defined as “low quality.”

2.4. Statistical Analysis. Pooled ORs with 95% CIs were calculated to access the strength of association between XRCC3 polymorphism and ovarian cancer susceptibility, according to the genotype frequencies of cases and controls groups [32]. P < 0.05 was considered statistically significant; all tests and CIs were two sided. If the heterogeneity was significant, the pooled ORs were initially measured by the random effects model. Else, the fixed-effects model was chosen [33].

The XRCC3 polymorphism and ovarian cancer risk were performed for a homozygote comparison (T2T2 versus T1T1), heterozygote comparison (T1T2 versus T1T1), dominant genetic model (T1T2+T2T2 versus T1T1), and the recessive genetic model (T2T2 versus T1T1+T1T2). In addition, sensitivity analysis was performed by omitting each study. Publication bias was estimated using a funnel plot. The degree of asymmetry was examined by t Egger’s test (P < 0.05 was considered significant publication bias) [34]. The analysis was carried out using Review Manager statistical software (RevMan version 5.0.170; The Nordic Cochrane Center, Rigshospitalet, Copenhagen, Denmark) and STATA software (version 11.2, Stata Corporation, College Station, TX, USA). Hardy-Weinberg equilibrium (HWE) was calculated using a web-based statistical tool (http://ihg.gsf.de/cgi-bin/hw/hwa1.pl).

3. Results

3.1. Study Characteristics. Through the literature search, 13 articles were found. Eight articles [35–42] were excluded as irrelevant study. One study [26] was excluded because it was carried out on overlapping populations with another, more samples eligible study [27]. Total 4 articles including 8 studies were selected on 5,302 ovarian cancer cases and 8,075 controls for 3 SNPs [20, 25–27] (Figure 1). These studies were all published in English. The main characteristics of the 4 studies are shown in Table 2. All subjects in these studies were Caucasians. The sample sizes (cases and controls) ranged from 1,478 to 5,906. Quality scores for all studies were high quality (≥10). Distribution of rs861539 polymorphisms genotype frequencies among ovarian cancer cases and controls of the 2 studies is shown in Table 3. Distribution of
rs1799794 polymorphisms genotype frequencies is shown in Table 4 and distribution of rs1799796 polymorphisms genotype frequencies is shown in Table 5.

Hardy-Weinberg disequilibrium of genotype frequencies among the controls was calculated in three studies.

3.2. Association of Individual Polymorphisms with Ovarian Cancer. The heterogeneity analysis has been carried out. As it was shown in Tables 3, 4, and 5, the heterogeneities of 3 SNPs are all not significant. So the fixed-effects model was chosen for 3 SNPs.

The meta-analysis results of XRCC3 rs861539 polymorphisms are shown in Table 3. No statistically significant associations between XRCC3 rs861539 polymorphisms and ovarian cancer risk were observed in any genetic models (T2T2 versus T1T1: OR = 1.10, 95% CI = 1.00–1.21, P = 0.04), and the recessive genetic model (T2T2 versus T1T1+T1T2: OR = 0.97, 95% CI = 0.88–1.08, P = 0.63).

For XRCC3 rs1799794 polymorphisms, two studies [16, 18, 20, 21, 23, 24] (3,119 cases and 6,207 controls) were eligible. The meta-analysis results of rs1799794 polymorphisms are shown in Table 4. We observed a statistically significant correlation with ovarian cancer risk using the homozygote comparison (T2T2 versus T1T1: OR = 0.70, 95% CI = 0.54–0.90, P = 0.005), heterozygote comparison (T1T2 versus T1T1: OR = 1.10, 95% CI = 1.00–1.21, P = 0.04), and the recessive genetic model (T2T2 versus T1T1+T1T2: OR = 0.67, 95% CI = 0.52–0.87, P = 0.002). However, no statistically significant associations were observed in dominant genetic model (T1T1+T2T2 versus T1T1: OR = 1.06, 95% CI = 0.96–1.15, P = 0.24).

For XRCC3 rs1799796 polymorphisms, the meta-analysis results were shown in Table 4. We observed a statistically significant correlation with ovarian cancer risk using the heterozygote comparison (T1T2 versus T1T1: OR = 0.91, 95% CI = 0.83–0.99, P = 0.04). However no statistically significant associations were observed in homozygote comparison (T2T2 versus T1T1: OR = 1.07, 95% CI = 0.93–1.24, P = 0.33), dominant genetic model (T1T1+T2T2 versus T1T1: OR = 0.94, 95% CI = 0.86–1.03, P = 0.16), and the recessive genetic model (T2T2 versus T1T1+T1T2: OR = 1.13, 95% CI = 0.98–1.29, P = 0.08).

3.3. Publication Bias and Sensitivity Analysis. The publication bias was tested by Begg’s funnel plot and Egger’s test for three SNPs. Egger’s test results did not show any evidence of publication bias for any of the genetic models of the three SNPs (data not shown). The shape of the four Begg’s funnel plots showed no evidence of obvious asymmetry of the three SNPs (data not shown).

In the sensitivity analysis, the corresponding pooled ORs were not altered, when the fixed-effects model was changed to random-effects model. So it revealed that the results of this meta-analysis were stable.

4. Discussion

The XRCC3 gene is required for genomic stability [36]. It was reported that the XRCC3 polymorphism increased the risk of many cancers, including ovarian cancer [36]. However, the results have been inconsistent. We preformed the meta-analysis including 5,302 ovarian cancer cases and 8,075 controls for 3 SNPs of XRCC3.

For rs861539 polymorphisms, no correlation with ovarian cancer risk was observed in any genetic models. However, For XRCC3 rs1799794 and rs1799796 polymorphisms, we observed a statistically significant correlation with ovarian cancer risk. It was shown that the difference between different SNP sites was considerable for XRCC3.

All of the literature was of high quality. All study subjects were Caucasian. The global multcenter studies can provide more valuable conclusions. So further studies should be done to explore the possible relationships between XRCC3 polymorphisms and ovarian cancer risk in other ethnicities.

In conclusion, this meta-analysis shows that the XRCC3 were associated with ovarian cancer risk overall for Caucasians. Asian and African populations should be further studied.

Abbreviations

CIs: Confidence intervals
HWE: Hardy-Weinberg equilibrium
ORs: Odds ratios
XRCC3: X-ray repair cross-complementing group 3.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

Acknowledgments

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Table 2: Main characteristics of the studies included in the meta-analysis.

<table>
<thead>
<tr>
<th>First author</th>
<th>Year</th>
<th>Country</th>
<th>Area of the cases</th>
<th>Ethnicity</th>
<th>Cases source</th>
<th>Control source</th>
<th>Sample type of cases</th>
<th>Total cases/controls</th>
<th>Quality score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Quaye [25]</td>
<td>2009</td>
<td>Mixed (DK-UK-USA)</td>
<td>MALOVA from Denmark-SEARCH from the UK and GEOCS from the USA</td>
<td>Caucasian</td>
<td>Mixed (hospital and cancer registry)</td>
<td>Population</td>
<td>Blood</td>
<td>1461/2299</td>
<td>14</td>
</tr>
<tr>
<td>Webb [27]</td>
<td>2005</td>
<td>Australia</td>
<td>New South Wales-Victoria and Queensland</td>
<td>Caucasian</td>
<td>Mixed (hospital and cancer registry)</td>
<td>Volunteers</td>
<td>Mixed (blood and archival paraffin blocks)</td>
<td>1445/788</td>
<td>12</td>
</tr>
</tbody>
</table>
Table 3: Distribution of XRCC3 rs861539 genotype among ovarian cancer cases and controls included in the meta-analysis.

<table>
<thead>
<tr>
<th>First author</th>
<th>Year</th>
<th>Genotypes distribution (Case source)</th>
<th>Genotypes distribution (Controls source)</th>
<th>P-HWE</th>
<th>T2T2 versus T1T1 (OR (95% CI))</th>
<th>TIT2 versus T1T1 (OR (95% CI))</th>
<th>T1T2+T2T2 versus T1T1 (OR (95% CI))</th>
<th>T2T2 versus T1T1+T1T2 (OR (95% CI))</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Auranen [20]</td>
<td>2005</td>
<td>676 T1T1 762 T1T2 227 T2T2</td>
<td>1712 T1T1 1946 T1T2 583 T2T2</td>
<td>Yes</td>
<td>0.99 [0.83, 1.18] 0.88</td>
<td>0.99 [0.88, 1.12] 0.89</td>
<td>0.99 [0.88, 1.11] 0.87</td>
<td>0.99 [0.84, 1.17] 0.91</td>
<td></td>
</tr>
<tr>
<td>Beesley [26]</td>
<td>2007</td>
<td>291 T1T1 339 T1T2 101 T2T2</td>
<td>288 T1T1 351 T1T2 108 T2T2</td>
<td>Yes</td>
<td>0.93 [0.67, 1.27] 0.63</td>
<td>0.96 [0.77, 1.19] 0.69</td>
<td>0.95 [0.77, 1.17] 0.62</td>
<td>0.95 [0.71, 1.27] 0.72</td>
<td></td>
</tr>
<tr>
<td>Quaye [25]</td>
<td>2009</td>
<td>545 T1T1 612 T1T2 175 T2T2</td>
<td>784 T1T1 958 T1T2 282 T2T2</td>
<td>Yes</td>
<td>0.89 [0.72, 1.11] 0.31</td>
<td>0.92 [0.79, 1.07] 0.27</td>
<td>0.91 [0.79, 1.05] 0.21</td>
<td>0.93 [0.76, 1.14] 0.51</td>
<td></td>
</tr>
<tr>
<td>Webb [27]</td>
<td>2005</td>
<td>591 T1T1 656 T1T2 198 T2T2</td>
<td>307 T1T1 375 T1T2 106 T2T2</td>
<td>Yes</td>
<td>0.97 [0.74, 1.28] 0.83</td>
<td>0.91 [0.75, 1.10] 0.32</td>
<td>0.92 [0.77, 1.10] 0.37</td>
<td>1.02 [0.79, 1.32] 0.87</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>2103 T1T1 2369 T1T2 701 T2T2</td>
<td>3091 T1T1 3630 T1T2 1079 T2T2</td>
<td></td>
<td>0.95 [0.85, 1.06] 0.37</td>
<td>0.95 [0.88, 1.03] 0.22</td>
<td>0.95 [0.88, 1.02] 0.19</td>
<td>0.97 [0.88, 1.08] 0.63</td>
<td></td>
</tr>
</tbody>
</table>

Test for heterogeneity: P = 0.91
Test for heterogeneity: P = 0.88
Test for heterogeneity: P = 0.82
Test for heterogeneity: P = 0.77
Table 4: Distribution of XRCC3 rs1799794 genotype among ovarian cancer cases and controls included in the meta-analysis.

<table>
<thead>
<tr>
<th>First author</th>
<th>Year</th>
<th>Genotypes distribution (Case source)</th>
<th>Genotypes distribution (Controls source)</th>
<th>P-HWE (Controls)</th>
<th>T2T2 versus T1T1 OR (95% CI)</th>
<th>P</th>
<th>T1T2 versus T1T1 OR (95% CI)</th>
<th>P</th>
<th>T1T2+T2T2 versus T1T1 OR (95% CI)</th>
<th>P</th>
<th>T2T2 versus T1T1+T2T2 OR (95% CI)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Auranen [20] 2005</td>
<td>1060</td>
<td>T1T1 550 T1T2 48</td>
<td>2551 T1T1 1188 T1T2 161</td>
<td>Yes</td>
<td>0.72 [0.52, 1.00]</td>
<td>0.048</td>
<td>1.11 [0.98, 1.26]</td>
<td>0.087</td>
<td>1.07 [0.95, 1.20]</td>
<td>0.29</td>
<td>0.69 [0.50, 0.96]</td>
<td>0.027</td>
</tr>
<tr>
<td>Quaye [25] 2009</td>
<td>940</td>
<td>T1T1 484 T1T2 37</td>
<td>1505 T1T1 713 T1T2 89</td>
<td>Yes</td>
<td>0.67 [0.45, 0.99]</td>
<td><strong>0.04</strong></td>
<td>1.09 [0.94, 1.25]</td>
<td>0.25</td>
<td>1.04 [0.91, 1.19]</td>
<td>0.57</td>
<td>0.65 [0.44, 0.96]</td>
<td>0.027</td>
</tr>
<tr>
<td>Total 2000</td>
<td>1034</td>
<td>85</td>
<td>4056 T1T1 1901 T1T2 250</td>
<td>0.70 [0.54, 0.90]</td>
<td>0.005</td>
<td>1.10 [1.00, 1.21]</td>
<td>0.04</td>
<td>1.06 [0.96, 1.15]</td>
<td>0.24</td>
<td>0.67 [0.52, 0.87]</td>
<td>0.002</td>
<td></td>
</tr>
</tbody>
</table>

Test for heterogeneity $P = 0.77$ Test for heterogeneity $P = 0.83$ Test for heterogeneity $P = 0.78$ Test for heterogeneity $P = 0.80$
Table 5: Distribution of XRCC3 rs1799796 genotype among ovarian cancer cases and controls included in the meta-analysis.

<table>
<thead>
<tr>
<th>First author</th>
<th>Year</th>
<th>Genotypes distribution (Case source)</th>
<th>Genotypes distribution (Controls source)</th>
<th>P-HWE (Controls)</th>
<th>T2T2 versus TTT1</th>
<th>P</th>
<th>TIT2 versus TTT1</th>
<th>P</th>
<th>T1T2+T2T2 versus TTT1</th>
<th>P</th>
<th>T2T2 versus TTT1+T1T2</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Auranen [20]</td>
<td>2005</td>
<td>769 T1T1 692 T1T2 203 T2T2</td>
<td>1757 T1T1 1776 T1T2 433 T2T2</td>
<td>Yes</td>
<td>1.07 [0.89, 1.29]</td>
<td>0.47</td>
<td>0.89 [0.79, 1.01]</td>
<td>0.062</td>
<td>0.93 [0.83, 1.04]</td>
<td>0.188</td>
<td>1.13 [0.95, 1.35]</td>
<td>0.17</td>
</tr>
<tr>
<td>Quaye [25]</td>
<td>2009</td>
<td>676 T1T1 608 T1T2 177 T2T2</td>
<td>1040 T1T1 1006 T1T2 253 T2T2</td>
<td>Yes</td>
<td>1.08 [0.87, 1.33]</td>
<td>0.5</td>
<td>0.93 [0.81, 1.07]</td>
<td>0.31</td>
<td>0.96 [0.84, 1.09]</td>
<td>0.536</td>
<td>1.11 [0.91, 1.37]</td>
<td>0.30</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>1445 T1T1 1300 T1T2 380 T2T2</td>
<td>2797 T1T1 2782 T1T2 686 T2T2</td>
<td></td>
<td>1.07 [0.93, 1.24]</td>
<td>0.33</td>
<td>0.91 [0.83, 0.99]</td>
<td>0.04</td>
<td>0.94 [0.86, 1.03]</td>
<td>0.16</td>
<td>1.13 [0.98, 1.29]</td>
<td>0.08</td>
</tr>
</tbody>
</table>

Test for heterogeneity: P = 0.97, P = 0.65, P = 0.69, P = 0.90
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