Evaluation of Associations of \textit{GSTM1/GSTT1} Null Genotypes with the Susceptibility to Age-Related Macular Degeneration, a Meta-Analysis

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Abstract

\textbf{Background:} The relationship between glutathione S-transferase M1 (\textit{GSTM1}) and T1 (\textit{GSTT1}) null genotypes (homozygotes for the null alleles) and the susceptibility to age-related macular degeneration (ARMD) have been reported and revealed inconsistent results. Therefore, the current meta-analysis was carried out.

\textbf{Methods:} Eligible published articles (before December 2020) were found by searching 8 databases. The data was extracted from articles. The heterogeneity across studies was estimated using $Q$ and $I^2$ statistics and the odds ratios (ORs) and its 95% confidence intervals (95% CI) were estimated.

\textbf{Results:} In total, 6 independent studies including 1089 participants (634 controls and 455 patients) were used in the current study. There was no heterogeneity between studies for both polymorphisms. Statistical analysis showed that the null genotypes of the \textit{GSTM1} (OR = 1.18, 95% CI: 0.91 - 1.53, $p = 0.191$) and \textit{GSTT1} (OR = 0.84, 95% CI: 0.60 - 1.18, $p = 0.328$) loci were not correlated with the susceptibility to ARMD.

\textbf{Conclusion:} The \textit{GSTT1} and \textit{GSTM1} genetic polymorphisms did not associated with the risk of ARMD in Caucasian populations.

\textbf{Keywords:} \textit{GSTM1}; \textit{GSTT1}; Age-related macular degeneration; Meta-analysis.

Introduction

Age-related macular degeneration (ARMD) is an extensively studied disease as a leading cause of visual disability in the aging population. It has been reported that both genetic and environmental elements have roles in the development of the disease.\textsuperscript{1, 2} The heritability of ARMD seems to be about 15-65 \%.\textsuperscript{3} Retina has the highest oxygen-consuming among human tissues.\textsuperscript{3} Based on the epidemiologic, genetic, and molecular pathologic studies it has been hypothesised that oxidative stress may play a key role in the aetiology of ARMD.\textsuperscript{2, 4} The members of glutathione S-transferases (GSTs, EC 2.5.1.18) superfamily belongs functionally to cellular detoxification system and they are classified to some classes, including theta (GSTT) and mu (GSTM) classes. The \textit{GSTT1} (MIM: 600436) and \textit{GSTM1} (MIM: 138350) genes are polymorphic. The null alleles of these loci have been reported in human populations. Several meta-analyses revealed that these polymorphisms were associated with numerous human complex diseases, such as cancer.\textsuperscript{5-9} It should be noted that the risks of cataract and glaucoma are associated with \textit{GSTM1/GSTT1} polymorphisms.\textsuperscript{10-12}
The relationship between the \textit{GSTM1/GSTT1} null genotypes (homozygotes for the null alleles) and the risk of ARMD have been reported and revealed inconsistent results.\textsuperscript{13-17} To evaluate the relationship between these genetic variations and the susceptibility to ARMD, the current meta-analysis was carried out.

Methods

Relevant published articles (before December 2020) were found by searching several databases, including PubMed, Scopus, Index Copernicus, DOAJ, Academic Journals Databases, SID, KoreaMed, and Google scholar. The following search terms were used: \textit{GSTT1, GSTM1, null genotype, age-related macular degeneration}. Only articles published in English were included in the study. In addition, the bibliographies of the retrieved studies were screened to identify relevant articles.

The eligible studies had raw data on genotype distributions in both patient and control groups. The exclusion criteria were related to reviews, editorials, abstracts, comments and studies with same or overlapping data. The application of the above-mentioned criteria yielded five reports.\textsuperscript{13-17} Study of Hunter et al\textsuperscript{17} had been reported two case-control groups, therefore, considered as two studies. The following data were extracted: author’s name, publication year, country, ethnicity of the participants and the frequencies of the genotypes for each polymorphism in ARMD patients and control subjects.

The heterogeneity across studies was estimated using Cochran’s $Q$ and $I^2$ statistics. If there was no heterogeneity between the studies ($I^2 < 50\%$ and $p > 0.10$ for $Q$ statistics), the fixed effects model\textsuperscript{18} was used for estimation of the odds ratios (ORs) and its 95 \% confidence intervals (95 \% CI).

Results

Tables 1 and 2 summarised the extracted data from 6 studies which were including in the current study. The studies were published between 2006 and 2016. In total, 6 eligible independent studies with 1,089 participants (634 controls and 455 patients) were used. All of the studies were conducted in Caucasian populations.

<table>
<thead>
<tr>
<th>Frst author</th>
<th>Country</th>
<th>Ethnicity</th>
<th>Total</th>
<th>Mean ± SD of age (Years)</th>
<th>Patient group</th>
<th>Control group</th>
<th>n</th>
<th>Male proportion</th>
<th>n</th>
<th>Age</th>
<th>Male proportion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oz</td>
<td>Turkey</td>
<td>Caucasian</td>
<td>2006</td>
<td>62.0 ± 8.6</td>
<td>159</td>
<td>63.0 ± 8.1</td>
<td>35</td>
<td>0.566</td>
<td>36</td>
<td>0.457</td>
<td>0.548</td>
</tr>
<tr>
<td>Guven</td>
<td>Turkey</td>
<td>Caucasian</td>
<td>2011</td>
<td>73.0 ± 10.0</td>
<td>198</td>
<td>75.0 ± 8.0</td>
<td>120</td>
<td>0.457</td>
<td>120</td>
<td>0.408</td>
<td>0.460</td>
</tr>
<tr>
<td>Liu</td>
<td>USA</td>
<td>Caucasian</td>
<td>2011</td>
<td>69.6 ± 9.8</td>
<td>103</td>
<td>79.4 ± 8.3</td>
<td>131</td>
<td>0.519</td>
<td>131</td>
<td>0.519</td>
<td>0.519</td>
</tr>
<tr>
<td>Othman</td>
<td>Iran</td>
<td>Caucasian</td>
<td>2012</td>
<td>63.2 ± 9.4</td>
<td>112</td>
<td>69.5 ± 8.9</td>
<td>112</td>
<td>0.607</td>
<td>112</td>
<td>0.607</td>
<td>0.607</td>
</tr>
<tr>
<td>Hunter, 1</td>
<td>USA</td>
<td>Caucasian</td>
<td>2016</td>
<td>77.8 ± 8.4</td>
<td>50</td>
<td>80.9 ± 6.5</td>
<td>37</td>
<td>0.420</td>
<td>37</td>
<td>0.420</td>
<td>0.420</td>
</tr>
<tr>
<td>Hunter, 2</td>
<td>USA</td>
<td>Caucasian</td>
<td>2016</td>
<td>77.3 ± 10.5</td>
<td>50</td>
<td>79.4 ± 8.0</td>
<td>48</td>
<td>0.520</td>
<td>48</td>
<td>0.520</td>
<td>0.520</td>
</tr>
</tbody>
</table>

*Mean ± SD of age (Years); **Male proportion; ***Sex-matched controls

Table 2: Genotypes of the studied polymorphisms in age-related macular degeneration patients and controls

<table>
<thead>
<tr>
<th>Frst author/ Polymorphisms</th>
<th>Control group</th>
<th>Patient group</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{GSTM1} Genotypes</td>
<td>Positive genotype</td>
<td>Null genotype</td>
</tr>
<tr>
<td>Oz</td>
<td>18</td>
<td>17</td>
</tr>
<tr>
<td>Guven</td>
<td>102</td>
<td>96</td>
</tr>
<tr>
<td>Liu</td>
<td>33</td>
<td>47</td>
</tr>
<tr>
<td>Othman</td>
<td>71</td>
<td>41</td>
</tr>
<tr>
<td>Hunter, 1</td>
<td>28</td>
<td>22</td>
</tr>
<tr>
<td>Hunter, 2</td>
<td>36</td>
<td>14</td>
</tr>
</tbody>
</table>

| \textit{GSTT1} Genotypes   | Positive genotype | Null genotype | Positive genotype | Null genotype |
| Oz                         | 25            | 10            | 118            | 41            |
| Guven                      | 157           | 41            | 100            | 20            |
| Liu                        | 63            | 17            | 71             | 15            |
| Othman                     | 81            | 31            | 85             | 27            |
The associations of the null genotypes of the GSTM1 (Figure 1A) and GSTT1 (Figure 1B) with the risk of ARMD were investigated. There was no heterogeneity across studies for any of the polymorphisms (For GSTM1: Q statistics = 5.84, df = 5, p = 0.322, F = 14.3 %; For GSTT1: Q statistics = 0.70, df = 3, p = 0.873, F = 0.00). Statistical analysis showed that GSTM1 (OR = 1.18, 95 % CI: 0.91 - 1.53, p = 0.191) and GSTT1 (OR = 0.84, 95 % CI: 0.60 - 1.18, p = 0.328) polymorphisms were not associated with the susceptibility to ARMD.

Figure 1: Forest plots of the relationship between the null genotypes versus active genotypes of the GSTM1 (A) and GSTT1 (B) and the susceptibility to age-related macular degeneration

For evaluation of the publication bias, the funnel plot and Egger’s test were used. There was no evidence for publication bias (p > 0.320, data not shown). The stability of the findings was evaluated by removing of individual studies sequentially. Sensitivity tests indicated that the present findings were stable.

Discussion

Numerous studies indicated that ARMD has many risk factors. High oxidative stress level is one of the most important risk factors for development of ARMD.23 Many reactive oxygen species (ROS) such as superoxide, hydrogen peroxide etc, are generated in the retina during transformation of light into vision.23 The GST superfamily plays a key roles in defence against ROS and oxidative stress.

Considering that the null genotypes of GSTT1 and GSTM1 were associated with several multifactorial human complex diseases.5-12 There were studies investigated the relationship between these polymorphisms and the risk of ARMD.13-17 the results were inconsistent. Considering that association studies usually were done on a relatively small samples size, in order to increase the sample size and aid the generalisation of the results to larger populations, the present meta-analysis was carried out. To the best of author’s knowledge, the current study is the first meta-analysis undertaken to investigate the relationship between the susceptibility to ARMD and null-genotypes of GSTT1/GSTM1 loci. Overall, the present findings indicated that there was no association between the study null genotypes and the risk of ARMD. Due to some limitations of this study, which are described below, the present results should be interpreted with caution.

Study Limitations

A number of limitations of the current study should be acknowledged. All of the studies used for the present meta-analysis were conducted in Caucasian participants. Therefore, there was no data from Asian and African populations. Considering that the risk of other multifactorial complex traits (such as diabetes mellitus and gastric cancer) with polymorphisms (such as the GSTT1 and GSTM1) were not similar between the ethnic groups10, 11, 19-22 further association studies from African and Asian populations are required. Considering that environmental factors in the pathogenesis of the ARMD is involved1, 2 and reports which were included in the analysis did not report the environmental factors, further studies are necessary to examine the interaction between genes and environments, as well as the combinations of polymorphisms.

Conclusion

The current study suggests that the GSTM1/GSTT1 null genotypes are not significantly associated with the susceptibility to age-related macular degeneration.
None.

None.

References