Qualitative assessment of previous evidence and an updated meta-analysis confirms lack of association between the ESR1 rs2234693 (PvuII) variant and coronary heart disease in men and women

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\begin{abstract}
\textbf{Background:} Coronary heart disease (CHD) is the leading cause of mortality worldwide. CHD clusters in families but this familial aggregation remains largely unexplained. ESR1 is a candidate gene for CHD although recent meta-analyses of the rs2234693 variant reported inconsistent evidence for association with myocardial infarction (MI) in men. The objectives of this study were to perform a qualitative and a quantitative assessment of all evidence to date regarding this association.

\textbf{Methods:} We performed structured literature searches for studies addressing the association between the ESR1 rs2234693 and CHD. We assessed the quality of these studies collectively and individually according to recently published guidelines on the reporting and interpretation of genetic association studies. We also performed a meta-analysis of all studies to date, including a sample of MI cases and controls from our region.

\textbf{Results:} The qualitative assessment indicated that many studies met a low proportion of the criteria proposed by the current guidelines. No significant association between ESR1 rs2234693 and MI was observed in our sample or in the meta-analysis (16 studies; $N \sim 32,000; \text{OR} \sim 1$). Strong between-study heterogeneity was largely explained by a quality score based on the quality criteria. Studies that reported significant associations were generally of poorer quality.

\textbf{Conclusion:} We confirm the lack of association between the ESR1 rs2234693 and CHD, and show that inconsistencies between previous studies is explained by differences in their quality.

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\end{abstract}

1. Introduction

Coronary heart disease (CHD) is the leading cause of mortality worldwide [1]. CHD clusters in families with estimates of heritability ranging from 38 to 57% [2]. A positive family history of CHD remains a strong risk factor even after adjustment for traditional risk factors [3], suggesting that genetic variation could play an important role in CHD risk. Although recent studies have identified some variants associated with this disease, to date the genetic architecture of CHD remains largely unexplained by known gene variants [4,5].

Using the candidate gene association study approach, many single gene variants have been reported to be associated with common diseases including CHD, although replication of such studies is often inconsistent [6]. Recently, a framework for assessing cumulative epidemiological evidence in genetic association studies [7] and a set of best practices for the design, conduct, reporting and publication of replication studies [8] have been proposed.

Among the genes that have been studied as potential modulators of CHD risk [4], ESR1, which encodes Estrogen Receptor $\alpha$, is an interesting candidate because estrogen has beneficial effects on cardiovascular health. Premenopausal women have a lower incidence of CHD than postmenopausal women [9], in whom CHD risk approaches that observed in men. Genetic variants in ESR1 have been reported to be associated both with CHD risk factors [10], as well as clinical endpoints like stroke [10] and myocardial infarction (MI) [11]. However, the results of these studies have been inconsistent, and further investigation is required.
Recently two meta-analyses have been published in relation to the role of the *ESR1* rs2234693 (*PvuII*; IVS1-397 T > C) variant in risk of MI. Shearman et al. [11] reported a significant association between rs2234693 and MI, but this was not replicated by Kjaergaard et al. [12].

The objectives of this study were: (i) to perform a qualitative assessment of all evidence reported to date regarding the association between the *ESR1* rs2234693 variant and MI using recently published guidelines on the reporting and interpretation of genetic association studies; and, (ii) to update and expand the previously published meta-analyses, including new data from our study and other new published association studies, and extending the meta-analysis to coronary heart disease and to women.

2. Materials and methods

2.1. Candidate gene association study (REGICOR study)

The study sample was composed of 423 cases of MI, aged 29–74, and 1269 age- and sex-matched controls (case–control ratio, 1:3). Cases were survivors of a first MI who were recruited consecutively in the reference hospital (Hospital Universitari de Girona Dr. Josep Trueta) of the REGICOR (Registre Gironí del Cor) study catchment area (Girona, Spain [13]). MI was defined on the basis of MONICA criteria [14]. Controls were randomly selected from two cross-sectional studies carried out in the province of Girona, in 1994–1996 and 1999–2001 to establish the prevalence of cardiovascular risk factors in this region [13]. Controls were free from angina and MI, as determined by clinical history, physical examination and electrocardiography. Hypertension, diabetes, dyslipidemia and family history of CHD were self-reported or confirmed by treatment. Subjects were classified as current smokers if they had reported having smoked during the previous year. Barefoot weight and height measurements were used to calculate body mass index (BMI; weight in kg divided by height in m²). The study was approved by the local Ethics Committee and all participants gave written informed consent. All subjects were of European descent.

The rs2234693 variant was genotyped in these individuals by TaqMan Assay (ABI PRISM 7900HT; Applied Biosystems, Foster City, CA), using previously described primers and probes [12]. Deviation from Hardy–Weinberg equilibrium (HWE) among controls was assessed using a chi-square (χ²) test with one degree of freedom (df). The distributions of clinical variables in each genotype group were compared using a χ² test or Fisher exact test for categorical variables, and analysis of variance for normally distributed continuous variables. Genotype frequencies in cases and controls were compared using a 1 df χ² test (two separate tests: common homozygotes (TT) versus heterozygotes (CT); common homozygotes (TT) versus rare homozygotes (CC)). Our sample had 80% power to detect an odds ratio (OR) of 1.37 at a significance level of *p* < 0.05, given the minor allele frequency among controls (MAF = 0.45). Statistical analysis was carried out using SPSS v12 (SPSS Inc. Chicago, IL), and power calculation was carried out using the *bpower* function from the R package *Hmisc*. A *p*-value of <0.05 was considered statistically significant.

2.2. Qualitative assessment of previous evidence

To assess the quality of current evidence regarding the association between rs2234693 and CHD (including fatal and non-fatal acute MI, angina, angiographic CHD), we searched the published literature for studies addressing this question, and evaluated these

![Flow chart of the procedures carried out in this study.](image-url)
studies collectively and individually according to published guidelines on the reporting and interpretation of association studies [7,8] (flow chart in Fig. 1).

To identify studies of interest, we performed structured literature searches in PubMed and reviewed the bibliographies of topical review articles. To further ensure the inclusion of all relevant studies, we also performed retrospective bibliography searches and prospective cited-reference searches for all articles encountered during this process. The search strategy used is described in detail in Supplementary Data. Data of interest was extracted from these articles by three independent reviewers (CL, GL, RE). This information was used to assess the quality of reported evidence for association, and also to perform a meta-analysis of these studies.

The quality of the evidence for association between rs2234693 and CHD risk was assessed cumulatively and also for each individual article.

The quality of the cumulative evidence for this association was assessed according to the classification system proposed by Ioannidis et al. [7]. Briefly, this classification consists of a 3-letter code, which describes (i) the quantity of evidence for a given association in terms of the total number of carriers of the rare allele from all reported studies, (ii) the extent of independent replication, and (iii) the likelihood of an important bias in the studies reported. The quality of evidence for the association can then be ranked as “strong”, “moderate” or “weak”.

Assessment of the quality of evidence at the individual article/study level was performed according to guidelines proposed by the NCI-NHGRI Working Group on Replication in Association Studies [8], a set of recommended best practices for the design, conduct and publication of studies that report an association or attempt to replicate a reported association. These guidelines identify a set of attributes that an association study should ideally possess, and are presented in the form of 55 conditions/questions related to experimental design, demography, quality control, etc. For each of these conditions, data was extracted from the articles identified in the literature searches mentioned above, and each study was scored as 1 when the requirement was met and 0 otherwise. In order to provide as objective an assessment as possible, we considered only the first 43 questions/conditions, since the reminder (44–55) were related to the subjective view of the author/reviewer. Thus we assigned a quality score (QS) from 0 to 43, since the reminder (44–55) was not taken into account.

3. Results

3.1. Candidate gene association study

Demographic characteristics, distribution of clinical variables and genotype counts and frequencies for all individuals are shown in Table 1, and stratified by sex in Supplementary Table 6. No significant association was observed between genotype frequencies and demographic and clinical variables in cases compared to controls (p > 0.05). No significant difference in genotype frequencies was observed among cases compared to controls (CT vs. TT: OR 1.19, 95% CI 0.92–1.54, p = 0.185; CC vs. TT: OR 0.98, 95% CI 0.71–1.37, p = 0.915).

Table 1

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Cases (N = 423)</th>
<th>Controls (N = 1269)</th>
<th>p-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>61.21 ± 11.16</td>
<td>60.72 ± 10.05</td>
<td>0.416</td>
</tr>
<tr>
<td>Sex (men/women)</td>
<td>318/105</td>
<td>954/315</td>
<td>1</td>
</tr>
<tr>
<td>Hypertension</td>
<td>230 (54.4)</td>
<td>437 (34.4)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Diabetes</td>
<td>96 (22.7)</td>
<td>270 (21.3)</td>
<td>0.08</td>
</tr>
<tr>
<td>Dyslipemia</td>
<td>218 (51.5)</td>
<td>559 (44.1)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Smoking</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never smokers</td>
<td>108 (25.5)</td>
<td>619 (48.8)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Current smokers</td>
<td>176 (41.6)</td>
<td>253 (19.9)</td>
<td></td>
</tr>
<tr>
<td>Ex-smokers &gt;1 year</td>
<td>81 (19.3)</td>
<td>371 (29.2)</td>
<td></td>
</tr>
<tr>
<td>Body mass index (kg/m²)</td>
<td>27.70 ± 4.57</td>
<td>28.18 ± 4.12</td>
<td>0.102</td>
</tr>
<tr>
<td>Family history of CHD*</td>
<td>60 (14.2)</td>
<td>134 (10.6)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>rs2234693 (PvuII)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>117 (27.7)</td>
<td>383 (30.2)</td>
<td>0.276</td>
</tr>
<tr>
<td>CT</td>
<td>231 (54.6)</td>
<td>636 (50.1)</td>
<td></td>
</tr>
<tr>
<td>CC</td>
<td>75 (17.7)</td>
<td>250 (19.7)</td>
<td></td>
</tr>
<tr>
<td>MAF</td>
<td>0.450</td>
<td>0.450</td>
<td></td>
</tr>
<tr>
<td>OR (95% CI)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>1</td>
<td>1.19 (0.92–1.54)</td>
<td>0.185</td>
</tr>
<tr>
<td>CC</td>
<td>0.98 (0.71–1.37)</td>
<td>0.915</td>
<td></td>
</tr>
<tr>
<td>rs9340799 (XbaI)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>175 (41.4)</td>
<td>544 (42.9)</td>
<td>0.387</td>
</tr>
<tr>
<td>AG</td>
<td>202 (47.8)</td>
<td>563 (44.4)</td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>46 (10.8)</td>
<td>162 (12.7)</td>
<td></td>
</tr>
<tr>
<td>MAF</td>
<td>0.348</td>
<td>0.349</td>
<td></td>
</tr>
<tr>
<td>OR (95% CI)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>1</td>
<td>1.26 (0.86–1.85)</td>
<td>0.208</td>
</tr>
<tr>
<td>CC</td>
<td>1.13 (0.78–1.64)</td>
<td>0.507</td>
<td></td>
</tr>
</tbody>
</table>

Results are expressed as mean ± SD for normally distributed variables or n (%) for categorical variables. MAF, minor allele frequency; SD, standard deviation. Both polymorphisms were in HWE.

* Self-reported history or treatment.

† To test differences between cases and controls, a Pearson χ² test was performed for categorical variables and a Student’s t-test for continuous-normally distributed variables.
The quality of cumulative evidence reported to date regarding this association was assessed according to the guidelines proposed by Ioannidis et al. [7]. In terms of the amount of evidence (first letter), the total number of individuals reported in the least common genetic group of interest (rare homozygote, CC) was 6964, 2163 cases, and 4801 controls (Supplementary Table 5), corresponding to classification A. In terms of the extent of replication, (second letter), this association has been extensively replicated, but without between-study consistency corresponding to classification B. Finally, in terms of potential biases in reported studies (third letter), there were no obvious biases in the studies reported, but there was considerable missing information regarding the generation of evidence, corresponding to classification B. Therefore, the cumulative evidence presented in all previously reported studies achieves a classification of ABB, corresponding to “moderate” evidence [7].

For each of these 12 articles, the quality of the evidence presented was assessed using a scoring process based on 43 of the 55 conditions cited in the NCI-NHGRI guidelines [8]. A grid of the full results of this exercise (43 conditions by 12 articles), and the resulting QSs are presented in Supplementary Table 4; the QS for each article is also shown in Table 2 and Fig. 2. The mean number of conditions met was 11.06 (median 10; range 6–19). Studies with a relatively small total sample size, e.g. <1000 subjects [11,15–18,20,21], generally met fewer conditions (mean QS 9; range 6–13). Moreover, the smaller studies generally showed more extreme, non-mutually concordant results (Fig. 2). The five larger studies [11,12,19,26,27] generally performed better (mean QS 13.7; range 7–19), and concordantly, these studies reported generally less extreme, non-significant results and narrower confidence intervals.

These results generally show broad variability in quality between studies, and a negative relationship between the reported OR and the QS, consistent with no association in the high quality, generally larger and better powered studies, and a false-positive association in the smaller, lower quality studies.

### 3.3. Quantitative assessment of all evidence to date, meta-analysis

A meta-analysis was performed using data from the 15 studies identified in the literature searches and the REGICOR data reported here (32,783 individuals; Table 2). No significant association between this variant and CHD was observed (pooled OR 1.06, 95%CI 0.96–1.18, p = 0.243 (CT vs. TT test) and 1.17, 95%CI 1.00–1.32, p = 0.055 (CC vs. TT test), nor when the analysis was stratified by gender (Fig. 2a and Supplementary Fig. 2) or by phenotype (MI/CAD) (data not shown).

The meta-analysis showed substantial between-study heterogeneity ($\chi^2 = 29.04, p = 0.0159$ and $\chi^2 = 47.24$, $p = 0.0000337$, for the CT vs. TT and CC vs. TT tests, respectively). Meta-regression analysis showed that most of this heterogeneity was explained by QS (heterogeneity, after adjusting for QS: $\chi^2 = 24.37$, $p = 0.0413$ and $\chi^2 = 35.21, p = 0.0014$, for CT vs. TT and CC vs. TT, respectively). Heterogeneity could not be accounted for by clinical outcome (MI/CAD), study design, gender or sample size, either individually or in combination.

Having identified QS as accounting for the majority of between-study heterogeneity, we stratified the meta-analysis by the mean QS ($\overline{QS}$; 11.06; Fig. 2b). A significant association was observed (CC vs. TT test) for studies with QS $< \overline{QS}$ (pooled OR 1.37, 95%CI 1.08–1.74, $p = 0.01$), while no association was observed for studies with QS $> \overline{QS}$ (pooled OR 0.93, 95%CI 0.82–1.05, $p = 0.248$). Between-study heterogeneity persisted for studies with QS $< \overline{QS}$, but disappeared for studies with QS $> \overline{QS}$. The results for the CT vs. TT test remained non-significant after stratification by QS.

In the sensitivity analysis (Fig. 2a), the pooled OR for the CC vs. TT meta-analysis (range 1.10–1.22) was most strongly affected by the removal of the Shearman study [11] (pooled OR (95%CI) reduced from 1.17 (1.00–1.32) to 1.10 (0.95–1.27)). The results of the CT vs. TT meta-analysis were not significantly affected by the removal of any study.

Results of these analyses carried out for the rs9340799 (Xbal) variant are shown in the Supplementary Data. No significant association was found for any of the tests performed.

### 4. Discussion

In this study, we performed a qualitative and quantitative evaluation of all reported evidence regarding a widely studied putative association between the rs2234693 variant in Intron 1 of the ESR1 gene and CHD. We also present data from the REGICOR study to address this question in our population. We have updated and
Fig. 2. Meta-analysis results for the association between rs2234693 and coronary heart disease. (a) Forest plot showing meta-analysis results. Data presented in a logarithmic scale for two genotypic tests (CC vs. TT and CT vs. TT). The pooled OR is shown as a diamond (♦), where the width of the diamond corresponds to the 95% CI. Studies in italics were included in the most recent meta-analysis [12]. The data for the gender-stratified analysis was performed using data for studies that provided gender-stratified data. OR (95% CI) sensitivity was calculated by excluding one study at a time and calculating the OR for the remaining studies.

(b) Crude meta-analysis results and stratified by QS. Using meta-regression, QS was found to account for most of the between-study heterogeneity. Stratifying by QS, the pooled odds ratio remained significant and between-study heterogeneity disappeared in the meta-analysis of studies with QS > 11.06, while both the association and the between-study heterogeneity disappeared in the meta-analysis of studies with QS < 11.06.
extended two previous meta-analyses of association studies, and we observe no evidence of association between rs2234693 and CHD in >32,000 individuals. We observe significant heterogeneity between the ORs reported in previous studies and show that much of this heterogeneity can be explained by study quality. In our qualitative analysis we conclude that previous evidence in favour of this association is moderate. We observe that the reported OR is associated with both study sample size and a descriptive measure of study quality. Similar results were observed for the rs9340799 (Xbal) variant (Supplementary Data).

Neither rs2234693 nor rs9340799 was associated with MI in the REGICOR study (men/women tested separately or together), which is consistent with the results observed for higher quality studies in the meta-analyses (OR ∼ 1).

The qualitative assessment showed considerable variation in quality of evidence between previous studies. While several of the criteria proposed in the guidelines used [8] might not be strictly necessary for a candidate gene association study, some studies lacked a number of important attributes, indicating that further efforts are required to standardise the design, and reporting of genetic association studies. The cumulative evidence [7] available is moderate for the rs2234693 variant and weak for the rs9340799 variant.

We have also updated previous meta-analyses regarding the putative association between rs2234693 and CHD [11,12]. As noted by Kjaergaard et al. [12], it was not possible to perform the covariate adjustment used by Shearman et al. [11] because they did not describe which covariates they adjusted for. For this reason, and since the inheritance model tested was not consistent across studies, we meta-analysed the crude results from each study. We have extended the previous meta-analyses in a number of ways: (a) expanding the phenotype definition to include both fatal MI and chronic CHD, (b) extending the meta-analysis to women, (c) adding data from 8 additional studies, including the results from the REGICOR project, increasing the total sample size from 16,706 to 32,783 samples, and most importantly (d) we show that differences in the quality of previous studies provide a convincing explanation for the lack of consistency between these studies. Using meta-regression, we found that much of the heterogeneity in our meta-analysis could be explained by study quality, and that this heterogeneity was mainly restricted to lower quality studies. Moreover, the higher quality studies showed consistently non-significant results [28]. This highlights the utility of quality assessment frameworks, such as those used in this study, for the interpretation of genetic association studies, and the motivation or design of follow-up studies.

We feel that our results now allow investigators who are interested in the role of ESR1 variation in relation to MI/CHD to confidently accept the null hypothesis for this variant.

Although we confirm the lack of association between CHD and the widely studied rs2234693 variant, this does not eliminate the possibility that other ESR1 variation may be involved in CHD risk. A large number of variants have been reported in this gene (∼2700, dbSNP Build 129, April 08), but less than 10 have been studied. The majority of studies have focused on the rs2234693 variant, which may reflect the tendency for early studies to examine the same variant as had previously been studied in relation to other complex phenotypes (e.g. cancer [29] and bone mineral density [30]).

In conclusion, this study refutes the hypothesis that the ESR1 rs2234693 variant is involved in CHD risk. We observe significant heterogeneity between the results of previous studies, which is mainly related to their quality. Moreover, study quality is inversely associated with the magnitude of the reported OR. Further studies analyzing a broader range of variants may be better described the relationship, if any exists, between variation in this gene and risk of CHD.

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