Large-scale meta-analysis of interleukin-1 beta and interleukin-1 receptor antagonist polymorphisms on risk of radiographic hip and knee osteoarthritis and severity of knee osteoarthritis

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IL-1
Interleukin
Gene
Association
Polymorphism

Objective: To clarify the role of common genetic variation in the Interleukin-1β (IL1B) and Interleukin-1R antagonist (IL1RN) genes on risk of knee and hip osteoarthritis (OA) and severity of knee OA by means of large-scale meta-analyses.

Methods: We searched PubMed for articles assessing the role of IL1B and IL1RN polymorphisms/haplotypes on the risk of hip and/or knee OA. Novel data were included from eight unpublished studies. Meta-analyses were performed using fixed- and random-effects models with a total of 3595 hip OA and 5013 knee OA cases, and 6559 and 9132 controls respectively. The role of ILRN haplotypes on radiographic severity of knee OA was tested in 1918 cases with Kellgren–Lawrence (K/L) 1 or 2 compared to 199 cases with K/L 3 or 4.

Results: The meta-analysis of six published studies retrieved from the literature search and eight unpublished studies showed no evidence of association between common genetic variation in the IL1B or IL1RN genes and risk of hip OA or knee OA (P > 0.05 for rs16944, rs1143634, rs419598 and haplotype C-G-C (rs1143634, rs16944 and rs419598) previously implicated in risk of hip OA). The C-T-A haplotype formed by rs419598, rs135952 and rs2905, previously implicated in radiographic severity of knee OA, was associated with reduced severity of knee OA (odds ratio (OR) = 0.71 95%CI 0.56–0.91; P = 0.006, Open access under the Elsevier OA license.
Introduction

Osteoarthritis (OA) is a multifactorial disease of the musculoskeletal system primarily involving the joints of the knee, hip, hand and spine. The prevalence of OA increases with age and is estimated to affect 40% of people over the age of 70 years1. There is a large body of evidence that synovial inflammation is implicated in many of the signs and symptoms of OA, including joint swelling and effusion2. This synovitis is cytokine-driven and there is convincing evidence that chondrocytes contribute to cytokine production leading to cartilage matrix degradation and in fact a number of variants in genes encoding for cytokines, in particular Interleukin-1 (IL-1), IL-6 and IL-10 involved in inflammation, have been reported to be associated with risk of OA as shown in a recent review3,4. Chondrocytes are known to respond to IL-1 beta and alpha (IL1B, IL1A) by decreasing synthesis of matrix components and increasing synthesis of matrix metalloproteinases3. The IL-1 receptor antagonist (IL1RN gene) could antagonise the effects of both IL1A and IL1B. In addition, it was recently shown that carriers of the IL1RN C-T-A haplotype had significantly lower synovial fluid levels of IL-10 and trends towards lower levels of IL-6 and IL-1B5. It is therefore expected that carriers of this haplotype are able to antagonise the effects of IL-1 and therefore reduce the risk of OA.

Several studies have investigated the role of polymorphisms in the IL-1 gene on knee and hip OA, in particular IL1B C +3954T (rs1143634), IL1B A-511G (rs16944) and the IL1RN 86 bp intron two variable number tandem repeat (VNTR) (tagged by rs419598), but results are conflicting6-15. One haplotype, C-G-C (rs1143634, rs16944 and rs419598), was associated with an increased risk of hip OA in two studies (in total 144 cases and 1501 controls)10,14. However, this could not be replicated by another study (370 cases, 544 controls)6. Recently, a small meta-analysis (n = 1238 hip, knee and hand OA cases and 1260 controls) has been published on the IL-1 region and OA, but remained inconclusive16. In that meta-analysis, some studies (n = 4) with data available on allele frequencies of single nucleotide polymorphisms (SNPs) rs16944, rs419598 or rs1143634 (or SNPs/VNTR in linkage disequilibrium (LD) with these three SNPs) and knee and/or hip OA data were not included in the final analysis.

In 2009, Attur and colleagues explored the role of IL1RN variants on radiographic severity7. It was shown in two studies (n total = 130) that carriers of the C-T-A haplotype (rs419598/rs319592/rs9005) had a significantly decreased risk for severe knee OA (odds ratio (OR) 0.14, 95%CI 0.05–0.37, P < 0.0001 for the haplotype analysis). The C/C genotype at rs419598, was also reported in the same study to be significantly associated with radiographic severity (OR 0.22 95%CI 0.10–0.49).

Our scope was to clarify the role of rs1143634, rs16944 and rs419598 IL1B and IL1RN polymorphisms on risk of knee and hip OA. To do so, we have carried out a large meta-analysis of both published data (n = 6) and unpublished new studies (n = 8), comprising a total 3595 hip OA cases and 6559 controls and 5013 knee OA cases and 9132 controls. Because one of these variants has also been implicated in severity of knee OA, a meta-analysis on severity of knee OA with rs419598 was also carried out in eight new studies plus the original report. To detect association between severity of knee OA and the C-T-A haplotype, three studies and the original report were meta-analysed.

Subjects and methods

Study subjects

Unpublished studies with novel data

A full detailed description of each study cohort on recruitment, radiographic and clinical assessment is presented in the Supplementary methods section. In this meta-analysis, five studies are available with data on common genetic variation in the IL-1 region for hip OA and eight studies for knee OA. The baseline characteristics and sample size of these studies are shown in Table 1a. In total seven cohort studies originating from three countries were included. We included studies from the United Kingdom (UK): the Chingford Study (CS)17,18, TwinsUK19 and the Hertfordshire Cohort Study (HCS)20, the Netherlands: Rotterdam Study I and III (RSI, RSSI)21 and the Genetics osteoArthritis and Progression Study (GARP Study)22 and Estonia: Estonia Cohort Study (ECS)23. Also, one case-control study from Nottingham osteoArthritis (NCCS) (UK) is included24. All studies were approved by the relevant Ethics Committee and informed consent was obtained from all study participants (see Supplementary methods section). In addition, severity of knee OA was studied in seven of these studies and in one additional study (CS, GARP, HCS, NCCS, RSI, RSSI, TwinsUK and GOAL).

Published studies

We searched PubMed for relevant articles assessing the relationship between genetic variation in the IL-1 region and knee and hip OA. In Table 1b the baseline characteristics and sample size of six studies identified by our search are given. Since not all studies published allele and/or haplotype counts we contacted the authors if necessary to obtain haplotype and allele counts to perform a meta-analysis with a minimum amount of bias. We were not able to retrieve allele counts for the controls of one Japanese study23 and for the London samples published by Smith et al. excluding participants from the CS15. Therefore, these samples were not included in the meta-analysis. In addition, in the study of Meulenbelt et al. a subset of the RSI was used25. For this study we have now included the complete RSI and therefore results of Meulenbelt et al. are not shown separately.

Meta-analysis

For the meta-analysis we were able to include 14 studies on knee OA for one or more variants and eight studies on hip OA with a total number of up to 3595 hip OA cases and 6559 controls and 3013 knee OA cases and 9132 controls. In addition, one study (n = 130 knee radiographic osteoarthritis (ROA) cases from two cohorts) published data on radiographic severity of knee OA and common genetic variation in the IL-1 region25. We included this study in the meta-analysis of severity of knee OA. One study with already published data on the relationship between knee and hip OA and common genetic variation in the IL-1 region, provided also unpublished data on severity of knee and hip OA (GOAL Study)5 and was therefore also included in the meta-analysis on severity of knee OA.

Laboratory methods

GARP study

The genotypes of rs1143634, rs16944 and rs419598 were determined by mass spectrometry (homogeneous Mass ARRAY
### Table Ia
Baseline characteristics of unpublished studies assessing the relationship between common genetic variation in the Il-1 region and risk of hip and knee OA

<table>
<thead>
<tr>
<th>Study</th>
<th>Type of study</th>
<th>Origin</th>
<th>Number</th>
<th>Age mean (range)</th>
<th>BMI mean (range)</th>
<th>% women</th>
<th>Definition</th>
<th>Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Cohort UK</strong></td>
<td>Case-control</td>
<td>UK</td>
<td>547/671</td>
<td>63.6 (54–76)</td>
<td>24.8 (17–42)</td>
<td>100%</td>
<td>No ROA</td>
<td>Rotterdam study I</td>
</tr>
<tr>
<td><strong>Cohort Netherlands</strong></td>
<td>Case-control</td>
<td>Netherlands</td>
<td>772</td>
<td>64.9 (59–71)</td>
<td>27.7 (15–45)</td>
<td>70%</td>
<td>No ROA</td>
<td>Rotterdam twin study</td>
</tr>
<tr>
<td><strong>TwinsUK</strong></td>
<td>Case-control</td>
<td>UK</td>
<td>2115/2777</td>
<td>66.4 (43–93)</td>
<td>26.6 (17–42)</td>
<td>51%</td>
<td>No ROA</td>
<td>Rotterdam study II</td>
</tr>
<tr>
<td><strong>Rotterdam study III</strong></td>
<td>Case-control</td>
<td>Netherlands</td>
<td>1514</td>
<td>66.1 (55–89)</td>
<td>25.7 (16–60)</td>
<td>54%</td>
<td>No ROA</td>
<td>Rotterdam study III</td>
</tr>
<tr>
<td><strong>Cohort Netherlands</strong></td>
<td>Case-control</td>
<td>Estonia</td>
<td>750</td>
<td>66.1 (55–89)</td>
<td>25.7 (16–60)</td>
<td>54%</td>
<td>No ROA</td>
<td>Copenhagen study</td>
</tr>
<tr>
<td><strong>TwinsUK</strong></td>
<td>Case-control</td>
<td>UK</td>
<td>708 (722)</td>
<td>66.1 (55–89)</td>
<td>25.7 (16–60)</td>
<td>54%</td>
<td>No ROA</td>
<td>Chingford study</td>
</tr>
</tbody>
</table>

**Notes:**
- ROA = radiographic osteoarthritis; COA = clinical osteoarthritis; THR = total hip replacement; TKR = total knee replacement.
- Knee OA controls and hip OA controls respectively if both phenotypes are present in one study.
- Controls of the RSI are used as controls for the GARP Study.
- Average for hip and knee controls.

### Table Ib
Baseline characteristics of published studies assessing the relationship between common genetic variation in the Il-1 region and risk of hip and knee OA

<table>
<thead>
<tr>
<th>Study</th>
<th>Type of study</th>
<th>Origin</th>
<th>Number</th>
<th>Age mean (range)</th>
<th>BMI mean (range)</th>
<th>% women</th>
<th>Definition</th>
<th>Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Case-control</strong></td>
<td>Case-control</td>
<td>UK</td>
<td>267</td>
<td>62*</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unrelated healthy blood donors</td>
<td>Healthy controls</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>Case-control</td>
<td>China</td>
<td>271</td>
<td>58</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unrelated healthy blood donors</td>
<td>Healthy controls</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>Czech Republic</td>
<td>Czech Republic</td>
<td>135</td>
<td>54.1</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unrelated healthy blood donors</td>
<td>Healthy controls</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>UK</td>
<td>UK</td>
<td>143</td>
<td>66.5 (45–86)</td>
<td>29.3 (17–58)</td>
<td>49%</td>
<td>Unaffected spouses</td>
<td>Healthy individuals</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>Turkey</td>
<td>Turkey</td>
<td>1174</td>
<td>73 (56–90)</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unaffected spouses</td>
<td>Healthy individuals</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>Turkey</td>
<td>Turkey</td>
<td>866</td>
<td>61.3 (41–83)</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unaffected spouses</td>
<td>Healthy individuals</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>Turkey</td>
<td>Turkey</td>
<td>151</td>
<td>29.9 (19–48)</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unaffected spouses</td>
<td>Healthy individuals</td>
</tr>
<tr>
<td><strong>Case-control</strong></td>
<td>Turkey</td>
<td>Turkey</td>
<td>104</td>
<td>29.9 (19–48)</td>
<td>29.3 (17–58)</td>
<td>50%</td>
<td>Unaffected spouses</td>
<td>Healthy individuals</td>
</tr>
</tbody>
</table>

**Notes:**
- Mean age in cases.
- Median age in cases.
- Percentage women in cases.
- Healthy controls from the Center at Physical Examination.
- Knee OA controls and hip OA controls respectively if both phenotypes are present in one study; ROA = radiographic osteoarthritis; COA = clinical osteoarthritis; THR = total hip replacement; TKR = total knee replacement.
system; Sequenom Inc., San Diego, CA), using standard conditions. Genotypes were analysed by using Genotyper 3.0 software (Sequenom Inc.). Control subjects of the RSI were used as controls for the GARP study.

RSI and III

Genotypes were subtracted from the genome-wide association (GWAS) dataset of the RSI and III. Genotyping of the samples with the Illumina HumanHap550v3 Genotyping BeadChip was carried out at the Genetic Laboratory of the Department of Internal Medicine of Erasmus Medical Center, Rotterdam, the Netherlands. The Bead-studio GenCall algorithm was used for genotype calling and quality control procedures were as described previously. Missing genotypes for RSI and III were imputed as described previously. Subsequently, genotypes of rs1143634, rs16944, rs419598, rs315952 and rs9005 were subtracted using PLINK software V1.07. All five polymorphisms were in HWE in controls (P > 0.05, data not shown).

TwinsUK Study

Genotypes were subtracted from the GWAS dataset of the TwinsUK study using the same methods as for RSI and RSIll. All polymorphisms were in HWE in controls (P > 0.05, data not shown).

Other studies

For the NCCS, HCS, CS and ECS study participants, genomic DNA was extracted from peripheral blood leukocytes of affected individuals and controls using standard protocols. Genotyping was carried out by Kbioscience Ltd, Hertfordshire UK. The IL-1 SNPs were genotyped using the KASPar chemistry, which is a competitive allele-specific PCR SNP genotyping system; Sequenom Inc., San Diego, CA), using standard conditions. Genotypes were subtracted from the GWAS dataset of the RSI and III using the same methods as for RSI and RSIll. All polymorphisms were in HWE in controls (P > 0.05, data not shown).

Haplotype estimation

In Supplementary Fig. 1 we show the LD plot for II-1. LD is low between the rs16944, rs1143634 and rs419598 (lowest D' = 0.38 and r² = 0.02). In addition, as in Supplementary Table I we show D' and r² values between rs16944, rs1143634 and rs419598 for all studies contributing novel data to this meta-analysis. For all new studies as well as for GOAL we estimated haplotypes on a population level using the program Haploview v 4.1. In all studies, seven common haplotypes were present for hip OA (rs1143634, rs16944 and rs419598). For the remainder of published studies the haplotype frequencies reported by authors were used and the reader is referred to the original studies (see Table Ia and Ib and Supplementary Table II).

Statistical analysis

Allele and genotype ORs were calculated by comparing the allele and genotype frequencies between cases and controls. Three SNPs, previously implicated in risk of hip and knee OA, rs16944, rs1143634 and rs419598, were tested for association with knee and hip OA. In addition, the haplotype C-G-C or 1-1-2 which was reported as significantly associated with hip OA in two previous studies (rs1143634, rs16944 and rs419598), was tested for association with hip OA.

To be consistent with the previously published study by Attur et al. we classified patients as severe knee OA case if the K/L score of the knee was 3 or 4 and as mild to moderate knee OA with a K/L score of 1 or 2. The studies with data for this type of analysis are CS, GARP, GOAL, HCS, NCCS, RSI, RSIll and TwinsUK, totalling 3297 individuals with K/L 1 or 2, and 2243 with K/L 3 or 4 (Table III). These were combined to 130 individuals with K/L 1 or 2 from the original US study and individuals with K/L 3 or 4. In addition, for TwinsUK, RSI and RSIll were able to estimate the C-T-A haplotype consisting of respectively rs419598, rs315952 and rs9005. A meta-analysis was performed for both the C allele of rs419598 and for the C-T-A haplotype with severity of knee OA. We carried out both fixed-effects and random-effects meta-analyses as follows:

Meta-analyses

We synthesized the effect estimates in each study using fixed- and random-effects models. In fixed-effects calculations it is assumed that the true effect of risk allele is the same value in each study, whereas in random-effects calculations the risk allele effects for the individual studies are assumed to vary around some overall average effect. We assessed the presence of heterogeneity using the Cochran's Q-statistic. The heterogeneity was quantified by using the I². In the absence of at least moderate inter-study heterogeneity within samples (I² < 25%) we conducted a Mantel–Haenszel meta-analysis of data from the samples to assess the overall evidence of association. For the random-effects models we used the DerSimonian–Laird method which incorporates the heterogeneity between studies. The overall treatment effect is estimated by a weighted average of the individual effects with weights inversely proportional to the variance of the observed effects. The statistical significance of the DerSimonian–Laird OR was estimated using the Z-statistic (the point estimate to its standard error). If evidence of heterogeneity existed, defined as either P < 0.10 for the Q-statistic and/or I² > 25%, a random-effects model was applied for the meta-analysis.

<table>
<thead>
<tr>
<th>SNP/Haplotype</th>
<th>Phenotype</th>
<th>N cases</th>
<th>N controls</th>
<th>Association results</th>
<th>Heterogeneity statistics</th>
<th>Statistical power</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>OR  95%CI P-value</td>
<td>I² Q df P-value (Q)</td>
<td>Minimal OR for 80%</td>
</tr>
<tr>
<td>rs1143634</td>
<td>Knee OA</td>
<td>4429</td>
<td>8549</td>
<td>1.03 ± 0.95−1.12</td>
<td>0.43 21% 12.7 10 0.24</td>
<td>1.088</td>
</tr>
<tr>
<td>rs16944</td>
<td></td>
<td>4761</td>
<td>8770</td>
<td>1.02 ± 0.96−1.08</td>
<td>0.57 0% 6.4 10 0.78</td>
<td>1.078</td>
</tr>
<tr>
<td>rs419598</td>
<td></td>
<td>4900</td>
<td>9195</td>
<td>1.05 ± 0.97−1.14</td>
<td>0.24 32% 17.5 12 0.13</td>
<td>1.082</td>
</tr>
<tr>
<td>rs1143634</td>
<td>Hip OA</td>
<td>3634</td>
<td>7918</td>
<td>0.97 ± 0.90−1.04</td>
<td>0.40 0% 3.7 6 0.72</td>
<td>1.096</td>
</tr>
<tr>
<td>rs16944</td>
<td></td>
<td>3605</td>
<td>7725</td>
<td>1.04 ± 0.95−1.14</td>
<td>0.35 36% 9.4 6 0.16</td>
<td>1.088</td>
</tr>
<tr>
<td>rs419598</td>
<td></td>
<td>3619</td>
<td>7897</td>
<td>1.00 ± 0.93−1.08</td>
<td>0.97 0% 5.7 6 0.46</td>
<td>1.093</td>
</tr>
<tr>
<td>C-G-C haplotype</td>
<td></td>
<td>3654</td>
<td>8131</td>
<td>1.04 ± 0.93−1.17</td>
<td>0.52 44% 12.4 7 0.09</td>
<td>1.148</td>
</tr>
</tbody>
</table>

All association results are fixed-effects ORs unless indicated otherwise; OA – osteoarthritis; df – degrees of freedom.
C-G-C haplotype – rs1143634-rs16944-rs419598.
* Random-effects model.
Table III

<table>
<thead>
<tr>
<th>Genotype and haplotype frequencies for knee severity replication studies</th>
</tr>
</thead>
<tbody>
<tr>
<td>study</td>
</tr>
<tr>
<td>--------------------------</td>
</tr>
<tr>
<td>K/L score 1–2</td>
</tr>
<tr>
<td>N</td>
</tr>
<tr>
<td>rs419598 CC/CT haplotype</td>
</tr>
<tr>
<td>C-T-A haplotype</td>
</tr>
<tr>
<td>K/L score 3–4</td>
</tr>
<tr>
<td>N</td>
</tr>
<tr>
<td>rs419598 CC/CT haplotype</td>
</tr>
<tr>
<td>C-T-A haplotype</td>
</tr>
</tbody>
</table>

Results for the C-T-A haplotype refer to: rs419598-rs315952-rs9005 C-T-A haplotype; n = number of subjects. N/A = not applicable.

Statistical power

Statistical power was computed using Quanto 1.2.4 (University of Southern California, USA, http://hydra.usc.edu/gxe).

Results

For the statistical power for each meta-analysis, given the frequency of the minor allele and the sample sizes available, it was estimated that we had 80% power to find associations with an OR = 1.09–1.15 (depending on the allele frequency and on the number of studies with data for each SNP) for hip OA and OR = 1.08–1.09 for knee OA with P < 0.05 (Table II).

The allele and haplotype frequencies for cases and controls in each study are presented in Supplementary Table Ia and b respectively for unpublished and published studies. The summary results of the hip and knee OA meta-analyses for rs1143634, rs16944 and rs419598 and haplotype C-G-C for hip OA are presented in Table II. No significant associations were observed between rs16944, rs1143634 or rs419598 and hip or knee OA (P > 0.05). No association was seen between the C-G-C haplotype and hip OA OR = 1.06 (95%CI 0.90–1.24 P = 0.52) (Fig. 1).

The genotype and haplotype frequencies for severe knee OA cases (K/L 3 and 4) and controls (K/L 1 or 2) in each study are presented in Table III. No evidence of association between risk of severe knee OA and rs1143634-rs16944-rs419598 C-G-C haplotype on risk of hip OA, (P² = 0%) and the effect of this genotype became OR = 1.00 (95%CI 0.87–1.15; P = 0.97) indicating no role for this genotype in severity of knee OA. When a fixed-effects meta-analysis were performed for the haplotype reported to be associated with OA radiographic severity [Fig. 2(B)] a trend was observed in the same direction in all three replication studies and combined with the initial report from Attur and co-workers16 a summary effect of OR = 0.71 (95%CI 0.56–0.91; P = 0.006) was observed. Nevertheless, the extremely strong effect reported by the first study introduces significant heterogeneity (P² = 74% Q = 0.008) and a random-effects meta-analysis resulted in OR = 0.61 (95%CI 0.35–1.06 P = 0.08) [Fig. 2(B)].

Fig. 1. Study specific estimates and summary association (random-effects) between risk of hip OA and rs1143634-rs16944-rs419598 “C-G-C” haplotype on risk of hip OA.

Fig. 2. Study specific estimates and summary association (random-effects) between severity of knee OA defined as K/L 1 or 2 vs K/L 3 and 4 and (A) rs419598 CC/CT genotype, (B) haplotype rs419598, rs315952 and rs9005 “C-T-A”.
Discussion

This meta-analysis on common genetic variation in the IL-1 region and risk of hip and knee OA is the largest to date, including all available published studies \( n = 6 \) and unpublished novel data \( n = 8 \), and shows no evidence for a consistent association with knee or hip OA. In this study we had 80% power to detect OR \( = 1.09-1.15 \) for hip OA and OR \( = 1.08-1.09 \) for knee OA with \( \alpha = 0.05 \). Therefore it is not likely that we have observed false-negative associations with regards to risk. Nevertheless, we find that the IL1RN C-T-A haplotype may indeed have a role in severe knee OA which is consistent with the well known IL1’s established role as a regulator of cartilage degradation\(^{1,3} \). Since there is a limited sample size of subjects of a non-Caucasian origin, we cannot exclude that there might be evidence of association between the SNPs studied and OA in subjects from a different ethnic origin.

So far, the literature has been inconclusive on the role of IL-1 polymorphisms and/or haplotypes in risk of knee and hip OA, probably due to low sample sizes of individual studies. An attempt was made by Moxley and colleagues to perform a meta-analysis, but the results remained inconclusive\(^{16} \). One of the reasons for this could be that they did not include all published studies on genetic variation in the IL-1 region. More importantly the authors did not add unpublished novel data. This approach resulted in not only low power to detect statistically significant associations, but could potentially also lead to publication bias.

There were not enough published studies examining the same genetic variant in relation to OA to study presence of publication bias.

In two previous publications the C-G-C haplotype was associated with an increased risk of hip OA, although this could not be replicated by another larger study\(^{10} \). In this meta-analysis, which had 25 bias. associations, but could potentially also lead to publication bias.

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Conflict of interest

Dr RA Maciewicz is employed by, owns stock and has patent applications for AstraZeneca.

Dr Abramson and Dr Attur have a patent application in the field of IL-1 family gene polymorphisms for determining the risk of OA incidence, severity and progression.

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Supplementary data

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References