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A common missense variant of \textit{LILRB5} is associated with statin intolerance and myalgia

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\textbf{Aims}  
A genetic variant in \textit{LILRB5} (leukocyte immunoglobulin-like receptor subfamily-B) (rs12975366: T > C: Asp247Gly) has been reported to be associated with lower creatine phosphokinase (CK) and lactate dehydrogenase (LDH) levels. Both biomarkers are released from injured muscle tissue, making this variant a potential candidate for susceptibility to muscle-related symptoms. We examined the association of this variant with statin intolerance ascertained from electronic medical records in the GoDARTS study.

\textbf{Methods and results}  
In the GoDARTS cohort, the \textit{LILRB5} Asp247 variant was associated with statin intolerance (SI) phenotypes; one defined as having raised CK and being non-adherent to therapy \textit{[odds ratio (OR) 1.81; 95% confidence interval (CI): 1.34–2.45]} and the other as being intolerant to the lowest approved dose of a statin before being switched to two or more other statins \textit{[OR 1.36; 95% CI: 1.07–1.73]}. Those homozygous for Asp247 had increased odds of developing both definitions of intolerance. Importantly the second definition did not rely on CK elevations. These results were replicated in adjudicated cases of statin-induced myopathy in the PREDICTION-ADR consortium \textit{[OR1.48; 95% CI: 1.05–2.10]} and for the development of myalgia in the JUPITER randomized clinical trial of rosuvastatin \textit{[OR1.35, 95% CI: 1.10–1.68]}. A meta-analysis across the studies showed a consistent association between Asp247Gly and outcomes associated with SI \textit{[OR1.34; 95% CI: 1.16–1.54]}.

\textbf{Conclusion}  
This study presents a novel immunogenetic factor associated with statin intolerance, an important risk factor for cardiovascular outcomes. The results suggest that true statin-induced myalgia and non-specific myalgia are distinct, with a potential role for the immune system in their development. We identify a genetic group that is more likely to be intolerant to their statins.

\textbf{Keywords}  
Statins • Pharmacogenetics • Immunogenetics • Precision medicine • Adverse drug reactions • Myalgia

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Introduction

Statins are first choice lipid-modifying medications for prevention and management of cardiovascular diseases (CVD).1-2 The UK is one of the largest users of statins worldwide,3 and with revised NICE guidelines approximately 12 million UK individuals will be prescribed statins.4,5 While statins are generally well tolerated, neurological,6 gastrointestinal,7 or muscle-based8 adverse drug reactions are reported. Adverse reactions to statins are likely to manifest as muscle aches (myalgia) along with elevated creatine phosphokinase (CK). Adherence to statin treatment is often negatively impacted in response to adverse reactions.9,10 The inability to adhere to statin treatment, whether due to statin-induced myalgia or more general forms of statin intolerance result in poor on-statin outcomes.11 Therefore, examining risk factors predisposing to statin intolerance is crucial from a public health perspective.

A genome-wide association study (GWAS) by Dubé et al.12 reported a missense variant Asp247Gly in the leukocyte immunoglobulin-like receptor subfamily B member 5 gene, LILRB5 on chromosome 19, base position 54759361 (Human Genome Build GRCh37), was associated with circulating serum CK levels. The mean CK levels of Asp247 homozygotes (T/T) were significantly higher. This association was found to be independent of statin use, however there is no known biological mechanism for the variant in determining CK levels. A GWAS by Kristjansson et al.13 of over 60 000 Icelanders replicated the association of the variant and CK levels. The same study also reported the association of the variant with serum lactate dehydrogenase (LDH) levels in a population of over 90 000 Icelanders.13 The LILRB5 variant showed the same direction of effect, i.e. Asp247 homoyzgotes had higher LDH and CK levels. LDH is often used in conjunction with CK as a marker of tissue damage. The findings suggest the variant might impart a statin independent susceptibility to muscle-based events. This makes LILRB5 a potential marker for susceptibility to the commonly noted muscle-based symptoms attributed to statin intolerance.

These discoveries warrant an investigation into the role of the LILRB5 variant in statin intolerance. Population-based studies use surrogate markers of intolerance, such as elevations in CK, trends in statin treatment, dose reductions, switching or the discontinuation of therapy. Therefore, a priori, we considered two definitions of statin intolerance, one dependent on and one independent of elevated CK levels. We hypothesize that carriers of variant associated with higher muscle enzyme levels (CK and LDH) will also be predisposed to forms of statin intolerance independent of CK levels.

The principal cohort used was the Genetics of Diabetes Audit and Research, Tayside Scotland (GoDARTS). GoDARTS has been previously used to establish pharmacogenetic associations of genes such as the hepatic influx transporter SLCO1B1 and statin intolerance.14 At present, GoDARTS contains 11 912 statin users and provides approximately 98 000 person-years of statin exposure, providing an ideal cohort to examine the association of this genetic variant with statin intolerance. Replication was examined in the Clinical Practice Research Datalink (CPRD) STAGE study,15 and clinically adjudicated cases of statin-induced myopathy (SIM) in the European PREDICTION-ADR consortium study.16 The interaction of this effect with statin use was then studied among participants who developed myalgia in the JUPITER (Justification for the Use of Statins in Prevention: an Intervention Trial Evaluating Rosuvastatin) randomized clinical trial (RCT) where individuals were allocated rosvastatin or placebo to assess the relative reduction in vascular events.16,17

Methods

GoDARTS cohort

Study population

Tayside Medical Ethics Committee approved the GoDARTS study and informed consent was obtained for all participants. The dataset contains complete electronic medical records (EMR), prescription information and laboratory results from 18 306 Scottish Caucasian individuals. Prescribing data were available from 1 January 1990 to 31 July 2013. In all, 10 149 study participants had type 2 diabetes (T2D) at recruitment and the remainder (8157) were recruited as non-diabetic controls. We performed a case-control study for statin intolerance in this population. We found 11 947 statin users from GoDARTS who had at least two prescriptions of statins. The prescription patterns indicating intolerance used in this study are similar to those used by Donnelly et al.17 to establish the association between statin intolerance and SLCO1B1 genotypes in the GoDARTS study. For features used to define statin intolerance and tolerance, see Supplementary Material online, Methods S1.

Statin intolerance in GoDARTS

General statin intolerance

Cases of general statin intolerance (GSI) were defined as users with CK raised above the ULN (Upper Limit of Normal), after start of statin therapy, who either switched statin therapies two or more times (not including systemic shifts to atorvastatin after patent expiration in the UK) or discontinued therapy ($n = 588$). Controls (statin tolerant individuals—ST1) had over 90% coverage with statin prescriptions, for a minimum of 5 years, at a minimum average daily dose of 40 mg of simvastatin (or equivalent dose of another statin), had consistently normal CKs while on statins, had never switched their statin therapy (except the systematic switch to atorvastatin) and had not discontinued therapy ($n = 356$).

Lowest approved daily starting dose statin intolerance

Since the LILRB5 Asp247Gly variant was known to be associated with CK levels, a phenotype independent of CK elevations was created in order to determine if the association of the variant with statin intolerance was confounded by the variant’s association with CK levels. The European Society of Cardiology and European Atherosclerosis Society joint recommendations on the management of dyslipidaemias suggest cessation of statin treatment if the user presents with normal CK, but persistent symptoms of intolerance.18 This intolerance definition was derived from the GAUSS-2 trial, the consensus definition based on recommendations by Banach et al. and recommendations of the National Lipid Association (NLA) in 2014.19-32

Cases of low dose intolerance (LDI) had used two or more different statins, and at least one statin that was discontinued would have to be at the lowest approved daily starting dose (NLA, 2014) before discontinuation, irrespective of their CK levels ($n = 591$). Controls (statin tolerant individuals—ST2) met all the criteria of the previous statin tolerant (ST1) group, except the definition was independent of the CK elevation criteria ($n = 443$). A higher proportion of controls had CK levels in the normal range, specifically, 354 of the 443 (80%) controls compared to 335 of 591 (57%) cases. Therefore, association tests for this phenotype were adjusted for (log-transformed) CK levels, in addition to other covariates.

For genotyping methods, see Supplementary material online, Methods S1.
Validation of statin intolerance phenotypes in GoDARTS

These phenotypic definitions of statin intolerance were validated against known SLC01B1 genotype risk score14 and the outcome of major adverse cardiovascular event (see Supplementary material online, Methods S2). They were significantly associated with both.

Replication studies

CPRD-STAGE study: statin-induced myopathy

Replication was sought from the CPRD-STAGE study.15 Data were available for 129 cases of SIM and 2501 population controls from the Wellcome Trust Case Control Consortium (WTCCC1).15 Cases of statin myopathy were identified using CPRD and tertiary muscle clinics and conformed to SIM classification standards.9 Analysis presented is unadjusted for covariates due lack of available data for the WTCCC population controls. For additional cohort information, see Supplementary material online, Methods S3.

PREDICTION-ADR: statin-induced myopathy

Cases and controls for SIM were contributed by the consortium’s study centres in Uppsala (Sweden), Dundee and Liverpool (UK). Cases met criteria for classification of SIM.9 Identification of SIM from population cohorts: GoDARTS, Genetics of Scottish Health Registry (GoSHARE) and CPRD using EMRs was based on on-statin CK levels raised ≥4 times ULN. Subsequently, clinical adjudication was undertaken by physicians and specialists. Factors considered were resolution of CK after de-challenge, post-event prescribing changes (e.g. switching or total discontinuation), medical history of kidney disease, trauma, falls, myocardial infarction, thyroid disease and tests for HMGCR (3-Hydroxy-3-Methylglutaryl-CoA Reductase) antibodies, muscle biopsy and physical activity, if available. Cases were also identified from CVD clinics, general practitioners (GP) practices, and muscle disease clinics where adjudication was performed directly by physicians. Swedish cases were selected from Swedegene Biobank, which recruits patients reported to the adverse drug reaction registry at Medical Products Agency, Uppsala. Statin tolerant controls were on therapy for a minimum of 1 year with no recorded adverse events. Analysis was performed on 229 cases of SIM and 432 adjudicated controls of Caucasian ethnicity. Whole-exome sequencing was undertaken in laboratories in Liverpool, Dundee and Uppsala. For details of sequencing methods, see Supplementary material online, Methods S4.

JUPITER trial: myalgia

The replication in JUPITER focused on 8749 study participants of verified European ancestry with available genetic data among whom 4381 were stable for 129 cases of SIM and 2501 population controls from the WTCCC1. Only one phenotype from GoDARTS could be selected since the two groups contained overlapping individuals. LDI phenotype was selected as the phenotype definition did not include the CK levels and the model was adjusted for CK measures. The analysis was performed using the metafor package in R26 and results are presented in a Forest plot (Figure 1).

The minor allele frequency in GoDARTS, CPRD, PREDICTION-ADR, and JUPITER study populations were 0.37, 0.39, 0.37, and 0.40, respectively. The effect of the LILRB5 variant was considered dominant based on large-scale analyses with serum CK in GoDARTS (see Supplementary material online, Results S1). Therefore all association tests compared those homozygous for Asp247T (T/T) with carriers of 247Gly (T/C or C/C).

Results

Baseline characteristics of general statin intolerance and low dose intolerance

Covariates associated with statin use or with the development of adverse drug reactions (ADR) were tested. Specifically, mean age at start and end of statin therapy, sex, diagnosis of T2D, first and last statin used, starting and ending doses, use of interacting co-medications and, by phenotype definition did not include the CK levels and the model was adjusted for CK measures. Analysis was performed on results from the discovery and replication cohorts was performed. Finally, a fixed-effects meta-analysis on results from the discovery and replication cohorts was performed. Only one phenotype from GoDARTS could be selected since the two groups contained overlapping individuals. LDI phenotype was selected as the phenotype definition did not include the CK levels and the model was adjusted for CK measures. The analysis was performed using the metafor package in R26 and results are presented in a Forest plot (Figure 1).

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Covariates associated with GSI included younger age at start and longer duration of therapy, female gender, lower incidence of simvastatin use at the start and end of therapy, lower starting and ending dose, the use of interacting co-medications and, by phenotype definition, CK levels at time of diagnosis.

Covariates associated with LDI included longer duration of statin therapy, lower frequency of simvastatin use at the start and end of...
The variant effect was observed in both unadjusted and adjusted models for both phenotypes (Table 2). Individuals homozygous for LILRB5 Asp247 genotype had 1.96 (95% CI: 1.25–3.07) times the odds of having GSI compared with carriers of the 247Gly variant, in a model adjusted for first statin on therapy, dose, age, sex, and concurrent use of interacting medications (Table 2). For LDI, individuals homozygous for LILRB5 Asp247 genotype had 1.43 (95% CI: 1.10–1.86) times the odds of being intolerant compared to carriers of the 247Gly variant, in a model adjusted for the first and last statin on therapy, CK levels and concurrent use of interacting medications (Table 2).

### Results of replication studies

Replication of the genotypic effect was noted in two out of three studies of statin-related adverse outcomes. In the CPRD-STAGE study, the association was found to be non-significant (odds ratio...
Asp247 homozygous genotype is associated with increased risk of outcomes associated with statin intolerance across observational, clinically adjudicated and clinical trial datasets. We observe a consistent relationship of increased risk of statin intolerance and the LILRB5 Asp247 genotype using two definitions of intolerance in the GoDARTS population. There was congruence between cases and controls of SIM in the PREDICTION-ADR study and with myalgia in the JUPITER trial, but no significant association in the CPRD-STAGE study.

A possible mechanism for the role of LILRB5 in muscle pathology is suggested by a recent study by Kuswanto et al. who highlight a role for the immune system in the repair and regeneration of skeletal muscles. They report that the presence and rapid accumulation of T regulatory (Treg) cells is crucial in the repair of damaged skeletal muscles. It is also reported that statins increase both the number and suppressive function of CD4+ Foxp3+ Treg cells. Foxp3 is a transcription factor that is the master regulator of Treg immune-suppressive activity. The same study shows sustained increased expression of Foxp3 with statin use. Therefore, mechanisms that induce Foxp3 expression and sustain Treg function are of great interest in understanding muscle homeostasis. We examined mRNA expression data from the GTex portal and found that the LILRB5 Asp247 variant is associated with FOX3 mRNA expression in the spleen (see Supplementary material online, Figure S6). FOX3 lies on the X chromosome, indicating a trans-eQTL effect, with the LILRB5 variant having an indirect immunomodulatory effect on FOX3 expression. These findings underscore a role for immunogenetics in understanding muscle damage and repair, with LILRB5 Asp247Gly being the first candidate to be found for common statin intolerance. An illustration of the potential mechanism is provided in Figure S7.

Discussion

We report that the LILRB5 Asp247 homozygous genotype is associated with increased risk of outcomes associated with statin intolerance across observational, clinically adjudicated and clinical trial datasets. We observe a consistent relationship of increased risk of statin intolerance and the LILRB5 Asp247 genotype using two definitions of intolerance in the GoDARTS population. There was congruence between cases and controls of SIM in the PREDICTION-ADR study and with myalgia in the JUPITER trial, but no significant association in the CPRD-STAGE study.

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Meta-analysis of results

A meta-analysis of the observed effects across GoDARTS, CPRD-STAGE, PREDICTION-ADR and JUPITER revealed that overall, Asp247 homozygotes have 1.34 (95% CI: 1.16–1.54) times the odds of having outcomes associated with statin intolerance compared with carriers of the 247Gly variant (P-value 7 × 10^{-5}) (Figure 1).

Table 3 Distribution of LILRB5 Asp247Gly genotypes by clinically adjudicated SIM status

<table>
<thead>
<tr>
<th>Group</th>
<th>Asp247Asp (T/T)</th>
<th>Gly247X (T/C or C/C)</th>
<th>Total</th>
<th>Association</th>
</tr>
</thead>
<tbody>
<tr>
<td>Statin-induced myopathy</td>
<td>96</td>
<td>133</td>
<td>229</td>
<td>Odds ratio = 1.48</td>
</tr>
<tr>
<td>Statin tolerant controls</td>
<td>161</td>
<td>271</td>
<td>432</td>
<td>95% CI: 1.05–2.10</td>
</tr>
<tr>
<td>Total</td>
<td>257</td>
<td>404</td>
<td>661</td>
<td>P-value 0.025</td>
</tr>
</tbody>
</table>

Cases and controls were selected from PREDICTION-ADR in Dundee, Liverpool and Uppsala. Model was adjusted for study center. CI, confidence interval.

Table 4 Odds ratios of developing myalgia in the JUPITER trial

<table>
<thead>
<tr>
<th>Variables</th>
<th>β</th>
<th>Odds ratio 95% confidence interval</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Main effects model</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp247Asp vs. 247GlyX Gly247X</td>
<td>0.16</td>
<td>1.17 (1.02–1.35)</td>
<td>0.03</td>
</tr>
<tr>
<td>Adjusted model</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp247Asp vs. 247GlyX</td>
<td>0.30</td>
<td>1.35 (1.07–1.71)</td>
<td>0.01</td>
</tr>
<tr>
<td>Rosuvastatin vs. placebo</td>
<td>-0.13</td>
<td>0.88 (0.68–1.13)</td>
<td>0.34</td>
</tr>
<tr>
<td>Final CK measure (log transformed)</td>
<td>0.19</td>
<td>1.21 (0.87–1.69)</td>
<td>0.26</td>
</tr>
<tr>
<td>Asp247GlyX/rosvustatin</td>
<td>-0.34</td>
<td>0.71 (0.51–0.99)</td>
<td>0.04</td>
</tr>
</tbody>
</table>

The adjusted model accounts for treatment allocation arm and final CK measures. CK, creatine phosphokinase.
Previously proposed mechanisms for SIM include an association between statins and reduced mitochondrial function, attenuated energy production, and altered muscle protein degradation contributing to muscle symptoms. Studies have shown evidence of structural perturbations in skeletal muscle cells associated with statin use. However, other studies failed to observe such abnormalities. There are other known immune-mediated forms of statin-related myopathies such as idiopathic inflammatory myositis or immune-mediated necrotizing myopathy, however these are very rarely observed. Overall, however, there remains a lack of clarity about the underlying pathophysiology of statin intolerance.

While the current variant results in an amino acid substitution, it is not clear that the phenotype results from this protein change. This is especially true as this variant is also associated with LILRB5 expression in certain tissues in the GTEx portal database (see Supplementary data are not biased. This demonstrates that the observed phenotypes are not associated with genetically driven variation in LILRB5 expression and therefore the association with the Asp247Gly variant would appear to be mediated by a functional change in the protein due to the amino acid substitution. However, this has to be confirmed by direct experimentation.

Previous studies have shown that CK levels were associated with LILRB5 variant and with all definitions of intolerance, including diagnoses of myalgia, making it a potential confounder. We have ruled out any artefactual associations by including CK measures as a covariate in analyses, where appropriate. Since the GSI phenotype in GoDARTS and diagnoses of myopathy in CPRD-STAGE and PREDICTION-ADR were entirely dependent on elevated CK, this adjustment was not possible. Additionally, the findings of this study could be impacted by confounders that were unmeasured in the cohorts used. Indeed, the non-significant finding in CPRD-STAGE might be due to the use of population controls with no available clinical or demographic information, limiting inclusion of important covariates in the analysis.

Another source of bias in non-randomized studies could be drug interactions that are known to increase risk of SIM. Inhibition of cytochrome P450 (CYP) 3A4 can increase exposure to simvastatin and atorvastatin several fold. On the other hand, inhibition of hepatic influx transporter OATP1B1 by drugs such as gemfibrozil can increase plasma concentrations of all statins. Due to the increased risk of muscle toxicity with combination therapy, fibrates are not generally recommended for concurrent use with statins for primary lipid control, but are co-prescribed to patients with T2D to control triglyceride levels. Since GoDARTS is primarily a population of T2 Diabetics, fibrates are widely prescribed in the study population. We observe comedication, especially fibrates consistently increased the risk of statin intolerance. However, in adjusted models, the association of the LILRB5 Asp247Gly variant was independent of the effect of these co-medications. Additionally, the effect is observed in the RCT setting, which confirms that the results from our observational data are not biased.

This finding, in addition to other previously reported genetic associations can facilitate the development of gene risk scores for the prevention of adverse outcomes to statin therapy. Preliminary analyses in GoDARTS reveal a significant interaction between the known SLC01B1 polymorphisms and LILRB5 Asp247Gly (see Supplementary material online, Results S4). This would suggest that we are making progress in dissecting the complex genetic architecture of statin intolerance, but future studies would be required to examine the corresponding pharmacokinetics of specific statins such as rosuvastatin that are not affected by SLC01B1.

The JUPITER trial allowed us to examine the association of the LILRB5 Asp247Gly variant in the presence and absence of statins, revealing that homozygosity of Asp247 is associated with increased odds of myalgia regardless of statin allocation. This supports the concept that LILRB5 Asp247 homozygous genotype modulates CK and LDH levels through statin-independent muscle damage. The association of 247Gly carriers with the development of myalgia in JUPITER is suggestive of a more complex biological gene–drug interaction. The observation that 247Gly carriers showed statin-specific myalgia, suggests a subpopulation of individuals who are inherently protected from myalgia, are susceptible to true ‘statin-induced’ myalgia. In observational data such as GoDARTS it is impossible to determine if intolerance to statins is occurring due to statin-specific or non-specific side effects. However, occurrence of intolerance is associated with increased risk of adverse CV outcomes (see Supplementary material online, Methods S2). We believe a recruit-by-genotype trial would be the ideal platform to examine the statin-dependency by LILRB5 Asp247Gly genotypes, and to further explore the underlying immune mechanisms.

Clinical trials have consistently found no evidence of statin-specific myalgia, just as there is no difference in incidence of myalgia between placebo and rosuvastatin arms of the JUPITER trial. The lack of association of statins with muscle pain in RCTs has led to a debate regarding the existence of statin-related muscle symptoms. Indeed the difficulty of ascribing causality in statin related muscle symptoms is highlighted by the Goal Achievement after Utilizing an anti-PCSK9 Antibody in Statin-Intolerant Subjects -3 (GAUSS-3) trial. Data from this trial were the first systematic evaluation of statin-specific myalgia with rechallenge and provided an estimate of 43% of individuals having statin-specific myalgia, and also demonstrated that 37% of intolerant individuals have statin-independent or non-specific myalgia. The LILRB5 Asp247Gly genotype presents a unique opportunity to probe the immune mechanisms behind the phenomena of muscle pain specific to statins compared to ‘constitutive’ muscle pain that appears in LILRB5 Asp247 homozygotes.

**Supplementary material**

Supplementary material is available at *European Heart Journal* online.

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References


24. Hsieh, J, MacFadyen JG, Morgan J, Ridker PM. Cardiovascular event reduction and adverse events among subjects taking low-density lipoprotein cholesterol <50mg/dl with rosuvastatin: the JUPITER trial justifications for the use of statins