HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials


Summary

Background Statins increase the risk of new-onset type 2 diabetes mellitus. We aimed to assess whether this increase in risk is a consequence of inhibition of 3-hydroxy-3-methylglutaryl-CoA reductase (HMGCR), the intended drug target.

Methods We used single nucleotide polymorphisms in the HMGCR gene, rs17238484 (for the main analysis) and rs12916 (for a subsidiary analysis) as proxies for HMGCR inhibition by statins. W

Findings Data were available for up to 223 463 individuals from 43 genetic studies. Each additional rs17238484-G allele was associated with a mean 0.06 mmol/L (95% CI 0.05–0.07) lower LDL cholesterol and higher body weight (0.30 kg, 95% CI 0.20–0.43), waist circumference (0.32 cm, 95% CI 0.16–0.47), plasma insulin concentration (1.62%, 95% CI 0.53–2.72), and plasma glucose concentration (2.23%, 95% CI 0.02–0.42). The rs12916 SNP had similar effects on LDL cholesterol, body weight, and waist circumference. The rs17238484-G allele seemed to be associated with higher risk of incident type 2 diabetes, Study-specific effect estimates per copy of each LDL-lowering allele were pooled by meta-analysis. These findings were compared with a meta-analysis of new-onset type 2 diabetes and bodyweight change data from randomised trials of statin drugs. The effects of statins in each randomised trial were assessed using standard care controlled trials and bodyweight: evidence from genetic analysis and randomised trials

Interpretation The increased risk of type 2 diabetes noted with statins is at least partially explained by HMGCR inhibition.

Funding The funding sources are cited at the end of the paper.

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Introduction

Statins reduce LDL cholesterol concentration by inhibiting 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR), leading to a proportionate reduction in cardiovascular disease (CVD) risk.14 Consequently, statins have become the most widely prescribed drug class: over 25% of US adults aged at least 45 years (30 million individuals) received these drugs from 2005 to 200815 and an estimated 56 million might be eligible for statin treatment under new guidelines.3 A meta-analysis of randomised controlled trials of statins recently identified a higher risk of type 2 diabetes mellitus from statin treatment compared with placebo or standard care,7 which was dose related.8 These findings prompted a US Food and Drug Administration Drug Safety Communication in 20129 and a change to statin safety labelling. Subsequently, observational studies have also reported a higher risk of type 2 diabetes with statin treatment compared with individuals not taking statins.10–12 Although type 2 diabetes is a cardiovascular risk factor, there remains a net benefit of statin treatment for prevention of CVD1 including among patients with diabetes.4

The mechanism underlying the glucose-raising effect of statins is of interest. A potential explanation in observational studies is that statin users adopt a less healthy lifestyle than individuals not taking statins, but this explanation is unlikely in masked treatment trials, which suggests that the effect is pharmacological. However, whether the glucose-raising effect of statins is explained by the same mechanisms as for LDL cholesterol lowering (ie, HMGCR inhibition) or by one of the proposed pleiotropic effects of statins13–15 (eg, mediated through isoprenoid intermediates and G-protein signalling16) is uncertain.

To investigate the mechanism underlying the glucose-raising effect of statins, we used the mendelian randomisation principle.17–19 with common variants in the gene encoding a drug target as unconfounded, unbiased proxies for pharmacological action on that target.18 We identified single nucleotide polymorphisms (SNPs) in the HMGCR gene and examined their associations with bodyweight, body-mass index (BMI), waist circumference, plasma glucose, and plasma insulin concentration.19–21 The primary disease outcome was type 2 diabetes, including prevalent (occurring before study baseline) as well as incident cases (occurring subsequently, appendix). In the mendelian randomisation paradigm, the intervention is the naturally randomised allocation of genotype, which occurs at conception and exerts its effect from that point through the lifetime of the individual. Therefore, events prevalent at the time of recruitment to genetic studies are nevertheless incident from the perspective of the time of the genotypic randomisation and can be included in the genetic analysis. Thus, for the genetic analysis, both prevalent and incident cases were included to maximise power.

All studies contributing data to these analyses were approved by their local ethics committees, as described in the published findings of each study (appendix).

Methods

Genetic studies

We selected as instruments two SNPs (rs17238484 and rs12916) in the HMGCR gene on the basis of genetic associations with LDL cholesterol in the Whitehall II study (n=46788) using the IBC HumanCVD BeadChip (Cardiochip; Illumina, San Diego CA, USA) (appendix).20 Both were subsequently associated with LDL cholesterol at a genome-wide level of significance,21 with strong associations in the largest genome-wide study of lipids so far (rs17238484 \( P<0.15 \times 10^{-21} \); rs12916 \( P<1.00 \times 10^{-30} \)).22 Data were available for the greatest number of individuals for the rs17238484 SNP, and this was used for the principal analysis; a subsidiary analysis used the rs12916 SNP. To investigate potential confounding by linkage disequilibrium between our lead SNPs and others in nearby genes, we assessed the association of the HMGCR SNPs with hepatic genome-wide expression data (appendix). If the lead SNPs were in strong linkage disequilibrium with nearby loci, those genes might confound the noted effects of HMGCR genotype on measured phenotypes.23
type 2 diabetes at baseline. Two trials (ALLHAT and A to Z) did not measure bodyweight sequentially, and bodyweight data were unavailable from the remaining three trials (appendix). Data were also analysed separately for participants not experiencing any cardiovascular events. Changes in LDL cholesterol in each treatment group at 1 year were available from the Cholesterol Treatment Trialists’ Collaboration meta-analysis for 18 trials, whereas data for mean changes in LDL cholesterol during two trials were taken from the primary publications. Information about plasma glucose and insulin concentrations, BMI, waist circumference, and waist:hip ratio was unavailable from the trials.

**Statistical analysis**

For the genetic studies, we assessed study-specific associations of rs17238484 and rs12916 with each continuous trait using univariate linear regression models.
Plasma glucose and insulin were analysed on the natural logarithmic scale because of their skewed distributions, and we present proportional differences in geometric means per allele. The rs17238484-G allele and rs12916-T allele were each associated with lower LDL cholesterol concentration and were designated the effect alleles, to facilitate direct comparison with statin treatment.

We assessed associations of the rs17238484 and rs12916 SNPs with type 2 diabetes risk using univariate logistic regression models to estimate the odds ratio (OR) per LDL-lowering allele. We combined within-study estimates using fixed-effects and random-effects meta-analyses, with heterogeneity quantified by the I² statistic. Heterogeneity between subgroups was assessed using meta-regression. All genetic analyses were done using a prespecified routine in Stata version 12.1, which was translated for use in SPSS, SAS, and R where necessary.

To corroborate our genetic findings, we examined the associations of the two lead SNPs in a large genome-wide association study of BMI, a Metabochip analysis of plasma insulin, and a genome-wide association study and Metabochip analysis of type 2 diabetes.

In the meta-analysis of statin trial data, we synthesised within-trial ORRs for type 2 diabetes during follow-up in participants free from type 2 diabetes at baseline and within-trial mean differences in bodyweight change between treatment groups, calculated as the difference from baseline to final visit, using random-effects and fixed-effects meta-analyses. We undertook meta-regression analyses of the associations of new-onset type 2 diabetes and bodyweight change with change in LDL cholesterol at 1 year and with follow-up duration. We assessed inter-study heterogeneity using the R² statistic and used Stata version 10.1 for trial-related analyses.

Role of the funding source
The funding sources had no role in study design, data collection, data analysis, data interpretation, the writing of the report, or the decision to submit for publication. DIS, DP, and AHN had full access to all the data in the study and had final responsibility for the decision to publish for publication.

Results
Of 38 Cardiochip SNPs within 55 kb of the HMGCR gene, seven met prespecified criteria for instrument selection (appendix), of which all but the two selected, rs17238484 and rs12916, were in strong linkage disequilibrium (r²>0.9; appendix). Gene expression data for rs17238484 were unavailable, but the T allele of rs12916 was associated with lower hepatic HMGCR expression (p=1.30 × 10⁻⁵) but not with expression of adjacent genes (appendix).

Data for up to 195 444 individuals (43 studies) for the HMGCR rs17238484 SNP and 94 652 individuals (21 studies) for the rs12916 SNP (or suitable proxies in studies in which these were not directly measured) contributed to the analysis of genetic associations with biomarkers and outcomes. The mean age of study participants was 59 years (range 26–75; appendix).

The association of the rs17238484 genotype with circulating concentrations of major lipid fractions followed an additive model in the meta-analysis of available data (figure 1A). Each additional rs17238484-G allele was associated with 0.06 mmol/L (95% CI 0.05–0.07) lower LDL cholesterol (p=1.34 × 10⁻¹⁵; 101 919 individuals, 26 studies), 0.07 mmol/L (0.06–0.08) lower total cholesterol (p=6.46 × 10⁻¹⁶; 117 545 individuals, 30 studies), and 0.07 mmol/L (0.06–0.08) lower non-HDL cholesterol (p=3.32 × 10⁻¹⁶; 103 375 individuals, 27 studies). The association of genotype with LDL cholesterol concentration was consistent between subgroups (data available in up to 29 studies, 116 327 individuals), with all meta-regression p values greater than 0.05 (appendix). Associations of rs12916 with plasma lipids were directionally concordant with rs17238484 and of similar magnitude (appendix).

The rs17238484-G allele was associated with 1.62% (95% CI 0.53–2.72; p=0.004) higher plasma insulin concentration (37 453 individuals, 12 studies) and with higher plasma glucose concentration (0.23%, 0.02–0.44; p=0.03; 73 490 individuals, 23 studies; figure 1B). Each rs17238484-G allele was also associated with 0.30 kg higher bodyweight (95% CI 0.18–0.43; p=3.15 × 10⁻⁶; 143 113 individuals, 30 studies) and 0.11 kg/m² higher BMI (0.07–0.14; p=1.77 × 10⁻⁶; 152 004 individuals, 32 studies; figure 1C), but not with height (p=0.23; 77 291 individuals, 23 studies; appendix). Each additional rs17238484-G allele was associated with greater waist circumference (0.32 cm, 95% CI 0.16–0.47; p=8.32 × 10⁻⁵; 69 163 individuals, 19 studies), hip circumference (0.21 cm, 0.10–0.32; p=1.67 × 10⁻⁴; 69 159 individuals, 19 studies), and waisthip ratio (0.001, 0.0003–0.002; p=0.01; 95 946 individuals, 23 studies; figure 1D). The rs12916 SNP showed directionally concordant associations with these biomarkers (appendix). Additive association patterns were noted with all these traits, and no differences in the rs17238484 SNP effect occurred between subgroups (all meta-regression p values >0.05; appendix). The appendix shows estimates from random-effects meta-analyses.

Public domain data from a meta-analysis of genome-wide association studies of BMI and an Illumina Metabochip-based analysis of plasma insulin revealed directionally concordant associations of the rs17238484 and rs12916 SNPs or suitable proxies with both these traits: log plasma insulin rs12916 β 0.007 (95% CI 0.002–0.012; p=4.72 × 10⁻⁵) and rs17238484 β 0.01 (0.004–0.016; p=5.92 × 10⁻⁴); and BMI rs17238484 p=0.09, 28 × 10⁻⁴ and rs12916 p=0.45, 10⁻⁴. Associations of both SNPs with fasting insulin were attenuated to the null after adjustment for BMI in the same datasets (rs17238484 p=0.74; rs12916 p=0.63).

In 26 236 cases and 164 842 controls in 35 population studies, the HMGCR rs17238484-G allele, which was associated with lower LDL cholesterol and higher
Data were analysed by fixed-effects meta-analysis. Figure 2: Meta-analyses of the associations of 3-hydroxy-3-methylglutaryl-CoA reductase variants rs17238484 and rs12916 with risk of type 2 diabetes.

![Figure 2](image_url)
Data from 129 170 participants free from type 2 diabetes at baseline were available from 20 statin trials (table). At 1-year of follow-up, mean LDL cholesterol reduction was 0·92 mmol/L (0·44–1·70) across all 20 trials, and 0·50 mmol/L (0·25–0·76) in the intensive-dose versus moderate-dose trials (32752 individuals).

Mean follow-up across all 20 trials was 4·2 years (range 1·9–6·7). Over this time, 3858 individuals allocated to statin...
Figure 3: Effect of statin treatment on new-onset type 2 diabetes

Data were analysed by random-effects meta-analysis. OR odds ratio. Case-developed type 2 diabetes. Non-case did not develop type 2 diabetes.

Table: Effect of statin treatment on new-onset type 2 diabetes

<table>
<thead>
<tr>
<th>Statin treatment</th>
<th>Placebo-controlled or standard care-controlled</th>
<th>Control</th>
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<tbody>
<tr>
<td></td>
<td>OR (95% CI) Weight (%)</td>
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</tr>
<tr>
<td></td>
<td>1.12 (1.03–1.22)</td>
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<tr>
<td>GISSI-HF</td>
<td>0.89 (0.79–1.00)</td>
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<tr>
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<td>0.89 (0.76–1.03)</td>
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<tr>
<td>ASCOT-LA</td>
<td>1.07 (0.90–1.28)</td>
<td>3.43</td>
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<tr>
<td>SPARCL</td>
<td>1.07 (0.90–1.25)</td>
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</tr>
<tr>
<td>MECA</td>
<td>1.15 (0.95–1.40)</td>
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</tr>
<tr>
<td>CORONA</td>
<td>1.14 (0.95–1.36)</td>
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<td>JUPITER</td>
<td>1.10 (0.95–1.27)</td>
<td>4.66</td>
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<tr>
<td>GEISS-HF</td>
<td>1.11 (0.93–1.30)</td>
<td>4.88</td>
</tr>
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</table>

Intensive vs moderate dose

| PROVE-IT TIMI22  | 1.01 (0.76–1.34) | 3.18 |
| A to Z           | 1.37 (0.94–1.99) | 1.87 |
| TNT              | 1.19 (0.92–1.52) | 1.42 |
| IDEAL            | 1.07 (0.95–1.22) | 1.39 |
| SEARCH           | 1.12 (0.94–1.32) | 1.34 |

Overall

| 3858 | 45741 |
| 6700 | 2181 |
| 6131 |

The appendix provides fixed-effects meta-analysis estimates. When limited to individuals not experiencing a cardiovascular event, estimates were similar (0.21 kg, 95% CI 0.08–0.35; 83 959 individuals). The effect on bodyweight change was noted only in trials comparing statin treatment with placebo or standard care (0.33 kg, 95% CI 0.25 to 0.42; P = 0.18), but not in trials comparing moderate-dose with intensive-dose statin treatment (0.15 kg, 95% CI 0.15 to 0.25; P = 0.63). No association was noted between relative LDL cholesterol reduction and within-trial bodyweight change (log-odds per 1 kg reduction in LDL cholesterol 0.004, 95% CI 0.19–0.159 to 0.107; p = 0.06), or after adjustment for trial type (ie, placebo-controlled and standard care-controlled or intensive vs moderate statin dose) and percent LDL cholesterol change (log odds 0.006, 0.051 to 0.039; p = 0.77).

The effect of statin treatment on bodyweight were available from 15 trials, including 93 939 participants free from type 2 diabetes at baseline. Mean follow-up was 3–9 years (range 1.9–3.9). Recipients of statin treatment or intensive-dose statin treatment were 0.24 kg (95% CI 0.10–0.38) heavier by the end of follow-up than were control recipients in a random-effects meta-analysis (figure 4), although there was substantial heterogeneity between trials (I² 78–6%, 95% CI 65–3.86–8). The appendix provides fixed-effects meta-analysis estimates.

Discussion

HMGCR genetic variants in population studies and statin treatment in trials were associated with higher bodyweight and higher risk of type 2 diabetes, suggesting that these effects are a consequence of HMGCR...
inhibition. The association of \textit{HMGCR} SNPs with risk of type 2 diabetes is new, as is the association of statin treatment and \textit{HMGCR} SNPs with increased bodyweight.

Increased bodyweight plays a causal part in the development of type 2 diabetes,\(^{35}\) suggesting a possible mechanism for the dysglycaemic effect of statin treatment. However, whether the relation between \textit{HMGCR} inhibition and type 2 diabetes is mediated exclusively by changes in body composition remains unknown. Statin treatment led to higher bodyweight and increased risk of type 2 diabetes, and both \textit{HMGCR} SNPs studied were associated with higher bodyweight and waist circumference, and one with higher plasma insulin and glucose concentrations. Insulin resistance might accompany bodyweight gain and a central distribution of adipose tissue. However, we were unable to identify a specific association of statin treatment with insulin resistance in these analyses because the relevant measures were unavailable from trials. One small trial\(^{36}\) that was ineligible for the present study reported 2 months of atorvastatin treatment led to higher glycated haemoglobin (HbA\(_1c\)) and insulin concentrations and lower insulin sensitivity than with placebo, and findings from a previous meta-analysis\(^{31}\) of statin trials suggested differential sensitivities on insulin sensitivity between statins. In \textit{JUPITER}\(^{37}\) and PROVE-IT TIMI 22,\(^{38}\) small increases in HbA\(_1c\) were noted in individuals randomly assigned to statin treatment compared with control individuals, and in \textit{AFORERD},\(^{39}\) HbA\(_1c\) also increased slightly in patients on atorvastatin compared with placebo after 4 months. Nevertheless, the association of one \textit{HMGCR} SNP with fasting insulin and glucose concentrations, and its attenuation to the null after adjustment for BMI, support a bodyweight-mediated association between \textit{HMGCR} inhibition and insulin resistance as a possible mechanistic explanation. Conversely, the magnitude of bodyweight gain we noted in both statin trials and genetic studies seems insufficient to account for the corresponding risk of type 2 diabetes. Intensive statin treatment also showed no greater effect on bodyweight than low-dose or moderate-dose treatment, although type 2 diabetes risk was greater with intensive statin treatment.

The anatomical site of the genetic and drug effects on energy metabolism that we report is not completely certain. The liver is a likely location, in view of its important involvement in lipid metabolism; however, the dysglycaemic phenotypes reported here might be caused by modulation of \textit{HMGCR} function in skeletal muscle. Additional, off-target effects of statins might also make a further contribution to bodyweight gain.\(^{39}\)

Inhibition of \textit{HMGCR} by statins impairs hepatocyte cholesterol synthesis, upregulates hepatic LDL receptor expression, and reduces circulating LDL cholesterol concentrations. Although the genetic findings provide evidence that the effect of statins on bodyweight and type 2 diabetes risk is caused by \textit{HMGCR} inhibition, whether this effect requires or is independent of reductions in circulating LDL cholesterol remains unclear. A meta-regression analysis of trial data did not provide evidence for an association between LDL cholesterol reduction and bodyweight or type 2 diabetes risk, but these analyses were done with summary-level data, which might have limited our ability to detect any such relation. Studies of genetic variants from other loci

<table>
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<th>Active</th>
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<td></td>
<td>Change in bodyweight</td>
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<tr>
<td></td>
<td>(kg 95% CI)</td>
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<tr>
<td>MEGA</td>
<td>0.18 (0.00 to 0.36)</td>
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<td>CORONA</td>
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<tr>
<td>JUPITER</td>
<td>0.40 (0.23 to 0.57)</td>
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<tr>
<td>Overall</td>
<td>0.33 (0.25 to 0.42)</td>
<td>79.32</td>
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Note: weights are from random-effects analysis.
slightly increase the risk of type 2 diabetes—an association
wide association studies, associations of the rs17238484
gene. In publicly available data from two genome-
HMGCR
-30 associations of the rs17238484 and rs12916 with BMI and plasma insulin concentration were noted at strong but sub-genome-wide levels of significance. This evidence, the consistent effect of both SNPs on LDL cholesterol, and a specific association with hepatocyte HMGCR mRNA expression for one of the SNPs (rs12916; appendix) supports their validity as genetic instruments in this analysis.

We used two HMGCR SNPs in the genetic analysis, one for the main (rs1238484) and another (rs12916) for a subsidiary analysis. Although the findings were broadly consistent, the small differences in effect estimates between the two variants could be caused by the different allele frequencies, available sample size for each, and the association of each with a functional variant or variants that were not identified.

This study has some limitations. Not all phenotypes measured in genetic studies were available in the statin trials—notably plasma glucose and insulin, waist and hip circumference, and waist/hip ratio. Moreover, not all studies in the genetic analysis measured glucose in fasting samples. In view of the wide age range of participants included in these analyses, survival bias might have affected our findings; however, this is unlikely and any such effect, if present, would probably have been limited. The HMGCR variants might affect the odds of being prescribed lipid-lowering drugs and thus introduce bias to the association between HMGCR and risk of type 2 diabetes. However, we found no evidence of an interaction between genotype, lipid-lowering drug use at study baseline, and risk of type 2 diabetes (appendix). The source of the heterogeneity between the statin trials that provided bodyweight data, particularly for dose-comparison trials, remains uncertain. Reductions in LDL cholesterol between arms in the dose-comparison trials was smaller than that achieved in the placebo-controlled trials. Our analysis was restricted to participants without type 2 diabetes at baseline. However, we did not have access to data on within-trial death, withdrawal, or loss to follow-up. Although observational pharmacoepidemiological studies have also examined the association of statin prescription with the development of type 2 diabetes, studies of this type can be prone to confounding and bias. For this reason, and to permit more direct comparison with the genetic analysis, we focused on data from randomised trials. Finally, trial analyses were done with summary-level data, which limited power for meta-regression.

Our findings pertain to the mechanism by which statins slightly increase the risk of type 2 diabetes—an association that has already been established. Findings from recent analyses of trials have shown that, although this association is robust, the absolute risk of developing type 2 diabetes is greatly offset by the benefits of statin treatment for CVD risk. Indeed, the efficacy of statin treatment to reduce the risk of CVD has been shown conclusively in several large primary and secondary prevention randomised controlled trials, including in individuals with type 2 diabetes, with a favourable risk/benefit profile. For this reason, our findings provide mechanistic insight, but should not alter present guidance on prescription of statins for prevention of CVD. Nevertheless, our results, including the new finding of increased bodyweight with statin treatment, suggest lifestyle interventions such as weight optimisation, healthy diet, and adequate physical activity should be emphasised as important adjuncts to prevention of CVD with statin treatment to attenuate risks of type 2 diabetes. The reason why bodyweight change does not seem to be greater with intensive statin treatment compared with moderate-dose treatment needs further investigation.

In conclusion, both statin treatment in randomised trials and carriage of common SNPs in the HMGCR gene in population studies were associated with bodyweight gain and higher risk of type 2 diabetes. Bodyweight gain is physiologically linked to insulin resistance and is one of the strongest risk factors for type 2 diabetes, which might partly explain the higher risk of type 2 diabetes in statin-treated patients.

Contributors

DIS, DP, ADH, and NS conceived the project, established and coordinated the consortium of studies, designed and executed the analysis, interpreted the findings, and wrote and revised the first and subsequent drafts of the manuscript. KBK contributed to analysis design and execution. MVH and FDs contributed to data analysis, interpretation of findings, and manuscript preparation. JELE, YG, AAin, YRL, MCW, SGB, RTM, US, PJS, MF, AW, LAL, and HH contributed to data collection and preparation. TS and RS contributed to analysis design. SS and AT-H contributed to data collection, data analysis, interpretation of findings, and manuscript preparation. PCDJ and SJS contributed to data analysis and analysis. RAS, ML, and NV contributed to data analysis and manuscript preparation. CG contributed to data analysis, interpretation of findings, and manuscript preparation. CC and JAC contributed to data collection, preparation, and analysis. APe, NGF, NCO-M, RBS, BS, IF, and OHK contributed to data collection and preparation, and manuscript preparation. KWL, JP, and PH contributed to genotyping, data collection, and preparation. GL contributed to data collection and interpretation of findings. JG, YtvdS, APA, SM, UdF, AAL, PAD, JK, JRD, ACK, GT, DDW, PA, WMV, SRP, TRG, and JC contributed to data collection and manuscript preparation. IT contributed to data collection and analysis, and interpretation of findings. DIvlaA, RK, Mba, AT, WS, DD, DFS, NRP, HN, CD, DK, RH, BAC, MGM, and MT contributed to data collection. JAH, JWJ, Gjdb, Padj, PFW, RWM, DAL, GDS, YB-S, DSS, MC, and MV contributed to data collection and preparation, interpretation of findings, and manuscript preparation. DB and ET contributed to data collection, preparation, and analysis, and manuscript preparation. Fv, RMs, and FE contributed to interpretation of findings. RCIKJ, AHM-mz, CBE, JGR, AMG, RM, TRP, JJVM, JLH, PMR, APM, LT, KKR, JEM, JFP, JCM, JAD, SK, and PvdH contributed to data collection, interpretation of findings, and manuscript preparation. AdB contributed to manuscript preparation. DIc contributed to data collection and preparation, data analysis, interpretation of findings, and manuscript preparation. SRS and RCh contributed to interpretation of findings and manuscript preparation.
Declaration of interests

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