PCS\(\text{K}\) genetic variants and risk of type 2 diabetes: a mendelian randomisation study


Summary

Background Statin treatment and variants in the gene encoding HMG-CoA reductase are associated with reductions in both the concentration of LDL cholesterol and the risk of coronary heart disease, but also with modest hyperglycaemia, increased bodyweight, and modestly increased risk of type 2 diabetes, which in no way offset their substantial benefits. We sought to investigate the associations of LDL cholesterol-lowering PCS\(\text{K}\) variants with type 2 diabetes and related biomarkers to gauge the likely effects of PCS\(\text{K}\) inhibitors on diabetes risk.

Methods In this mendelian randomisation study, we used data from cohort studies, randomised controlled trials, case control studies, and genetic consortia to estimate associations of PCS\(\text{K}\) genetic variants with LDL cholesterol, fasting blood glucose, HbA\(_1c\), fasting insulin, bodyweight, waist-to-hip ratio, BMI, and risk of type 2 diabetes, using a standardised analysis plan, meta-analyses, and weighted genetic centile scores.

Findings Data were available for more than 550 000 individuals and 51 623 cases of type 2 diabetes. Combined analyses of four independent PCS\(\text{K}\) variants (rs11583680, rs11591147, rs2479409, and rs11206510) scaled to 1 mmol/L lower LDL cholesterol showed associations with increased fasting glucose (0·09 mmol/L, 95% CI 0·02 to 0·15), bodyweight (1·03 kg, 0·24 to 1·82), waist-to-hip ratio (0·006, 0·003 to 0·010), and an odds ratio for type diabetes of 1·29 (1·11 to 1·50). Based on the collected data, we did not identify associations with HbA\(_1c\) (0·03%, –0·01 to 0·08) fasting insulin (0·00%, –0·06 to 0·07), and BMI (0·11 kg/m\(^2\), –0·09 to 0·30).

Interpretation PCS\(\text{K}\) variants associated with lower LDL cholesterol were also associated with circulating higher fasting glucose concentration, bodyweight, and waist-to-hip ratio, and an increased risk of type 2 diabetes. In trials of PCS\(\text{K}\) inhibitor drugs, investigators should carefully tolerate these safety outcomes and quantify the risks and benefits of PCS\(\text{K}\) inhibitor treatment, as was previously done for statins.

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Introduction The benefit of statins in reducing LDL cholesterol and coronary heart disease (CHD) risk is well established. More recently, and only after completion of numerous randomised controlled trials, was it discovered that statins increase risk of type 2 diabetes, although this effect is modest and greatly outweighed by the benefits of this drug class. Genetic studies based on common variants in the gene encoding the target of statins, HMG-CoA reductase (HMGCR), suggest the effect is mechanism-based (ie, on-target). Genetic studies assessing the effects of variants in a broader range of
Research in context

Evidence before this study


Randomised trials of treatment with statins and carriage of corresponding genetic variants in HMGCR that lower LDL cholesterol both show and increase in the risk of type 2 diabetes. More recently, genetic predisposition to lower LDL cholesterol concentrations has been linked to an increased risk of diabetes, suggesting that dysglycaemia might be a consequence of lowering LDL cholesterol in general. Whether lowering of LDL cholesterol by PCSK9 inhibitors results in increased risk of diabetes is currently unknown. Clinical trials of PCSK9 inhibitors to assess their effect on cardiovascular outcomes are ongoing, but reliable evidence for a possible association between PCSK9 inhibition and risk of diabetes could take longer to accru.

Added value of this study

Mendelian randomisation is an established approach that uses randomly allocated variants in the encoding gene to infer mechanism-based efficacy and safety outcomes from pharmacological perturbation of a drug target. We used four genetic variants in PCSK9 in more than 50,000 individuals (including about 50,000 diabetes cases) and showed that PCSK9 genetic variants associated with lower LDL cholesterol concentrations were associated with increased concentration of fasting glucose, bodyweight, and risk of diabetes. This finding adds robust new evidence to previous research that identified weak associations of PCSK9 with risk of diabetes.

Implications of all the available evidence

Similar to statin therapy, treatment with PCSK9 inhibitors is likely to increase the risk of diabetes. Patients treated with PCSK9 inhibitors should be carefully monitored for dysglycaemia, including within ongoing and future clinical trials.
effect estimates from the participating studies were then meta-analysed with pooled summary estimates from the public domain data repositories of relevant genetic (genome-wide association study [GWAS]) consortia, but only if the study-level estimates had not previously contributed to consortia results, to prevent double counting. All studies contributing data to these analyses were approved by their local ethics committees.

Data were collected for LDL cholesterol, insulin (fasting and non-fasting), glucose (fasting and non-fasting), HbA₁c, insulin resistance and secretion via basal homeostatic model assessments (HOMA-IR and HOMA-B), bodyweight, height, BMI, waist-to-hip ratio, and history or incidence of type 2 diabetes.

Publicly available summary-level data were available on blood lipids from the GLGC, type 2 diabetes-related biomarkers (plasma insulin, glucose, HbA₁c, HOMA-IR, and HOMA-B) from the Meta-Analyses of Glucose and Insulin-related traits Consortium (MAGIC), bodyweight, height, BMI, and waist-to-hip ratio from the Genetic Investigation of Anthropometric Traits consortium (GIANT), and type 2 diabetes from the Diabetes Genetics Replication and Meta-analysis consortium (DIAGRAM) and Exome chip 80K. Additionally, cross-sectional data were obtained for adiposity traits and the prevalence of type 2 diabetes from UK Biobank.

Statistical analyses
In all analyses we assumed an additive allele effect with genotypes coded as 0, 1, and 2, representing the number of minor alleles. We analysed continuous biomarkers using linear regression models; the composite endpoint of prevalent or incident type 2 diabetes was analysed with logistic regression. Study-specific associations were pooled for each SNP by use of the inverse-variance weighted method for fixed-effect and random-effects meta-analysis. We assessed between-study heterogeneity using the Q-test and the \( I^2 \) statistic with a one-sided upper 97·5% CI. Study-specific associations were excluded if the SNP was not in Hardy-Weinberg equilibrium (appendix).

Our approach to SNP selection was designed to prune the number of SNPs at PCSK9 used in the analysis, without loss of information. We decided a priori to combine the four approximately independent SNPs in a weighted gene-centric score (GS) using the inverse-variance weighted method for fixed and random effects. The GS provides a more precise estimate of the downstream effects of variation at PCSK9 by incorporating maximum biological variation. Furthermore, if the four SNP effects are homogeneous (assessed by the heterogeneity measures Q-test and \( I^2 \)), the GS estimates will be more powerful and precise compared with individual SNPs in isolation. If, however, the SNP effects are heterogeneous (meaning that the PCSK9 effects are different according to which part of the gene is assessed), the GS method will be less powerful than the individual SNP tests (depending on the degree of heterogeneity). Our aim was to estimate the effect of the PCSK9 locus as a whole, but SNP-specific estimates are also reported. Other important assumptions of the GS approach are (approximate) independence of the included SNPs (assessed by pairwise linkage disequilibrium (r²) and use of multivariable regression models) and the additivity of allele effects. We also investigated whether the association of individual SNPs with diabetes risk was in proportion to the association with LDL cholesterol lowering.

Estimates are presented as mean differences or odds ratios (ORs) with 95% CIs, presented either per LDL-cholesterol-decreasing allele or, in the case of GS, per 1 mmol/L (38·67 mg/dl) lower LDL cholesterol. The per 1 mmol/L GS effect estimates were derived by multiplying point estimates and their variances by the multiplicative inverse of the estimated SNP-LDL cholesterol effects. Similar to most genetic studies, missing data were excluded in an available case manner, assuming a missing-completely-at-random mechanism. To avoid potential bias due to population stratification and non-modelled ancestry interactions, analyses excluded individuals of non-European ancestry. Differences in ancestry can be a potential source of confounding bias (ie, population stratification bias) when environment is related to both the genes and the outcome of interest. Analyses were done with the statistical programme R (version 3.3.0).

Sensitivity analyses
We assumed that the allele effects were additive, which we assessed in available individual participant data by comparing an additive model to a non-additive model (allowing for dominance or recessiveness) using a likelihood ratio test (meta-analysed by Fisher’s method). Because measurement error might be larger in prevalent cases (ascertained, for example, from hospital records) we did a further sensitivity analysis in which we separately analysed incident and prevalent type 2 diabetes. This sensitivity analysis was done not because we expect the true associations of PCSK9 to be different with respect to prevalent and incident case status, but merely reflected a quality-control check. Although SNPs were selected to be independent, there was some degree of residual dependency (appendix; maximum r² 0·26). To explore the effect of this residual correlation between the four study SNPs (appendix), we compared results from a (correcting for this correlation) to pairwise results (ignoring any between-SNP correlation) based on the same data.

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The funder of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report. The corresponding author (AFS) had full access to all the data in the study and had final responsibility for the decision to submit for publication.
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prescribed a lipid-lowering drug.\textsuperscript{44} We were unable to account for this effect in the analysis because prescription data for these treatments were often not available, and when they were recorded they were only available for a single follow-up point. For lipid-lowering treatments, one record of treatment does not properly reflect the time-varying therapy received, and adjusting for only a single record when in fact treatment varies over follow-up might increase bias.\textsuperscript{35} Typically, diabetes drug analyses cannot predict off-target effects of treatments. We refer to on-target effects as those that are due to a drug effect on the intended target (in this case PCSK9). Although monoclonal antibody therapeutics are often highly specific, perhaps more so than small molecule therapeutics, they retain the potential for off-target effects. Hence, in the presence of off-target effects, results from ongoing randomised controlled trials could differ from the genetic associations reported here.

Our main findings are based on four PCSK9 SNPs in combination and scaled to 1 mmol/L lower LDL-cholesterol. This approach assumes additive effects across the SNPs, an assumption that held well in sensitivity analyses. A potentially unobserved non-additive effect might explain why we identified a genetic association with fasting glucose and a concordant (although non-significant) association with HbA\textsubscript{c}, whereas fasting

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**Figure 2: Association of genetic variants in PCSK9 with glycaemic and anthropometric biomarkers**

Effect estimates are presented as mean difference with 95% CIs. Associations were scaled to a 1 mmol/L reduction in LDL cholesterol. SNP-specific results are pooled by use of a fixed-effect model; weighted gene-centric score (GS) models combining all four SNP-specific estimates are presented as fixed-effect and random-effects estimates. The size of the black dots representing the point estimates is proportional to the inverse of the variance. Between-SNP heterogeneity was measured as a two-sided Q-test ($\chi^2$) and an $I^2$ with one-sided 97.5% CI. Note that results from individual participant data are supplemented by repository data from the Global Lipids Genetics Consortium, the Meta-Analyses of Glucose and Insulin-related traits Consortium, and the Genetic Investigation of Anthropometric Traits consortium.

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<td>30781</td>
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<td>337818</td>
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<td>n=11591147</td>
<td>185131</td>
<td>1.027 (-0.029 to 2.084)</td>
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$\chi^2=0.49$, $p=0.92$, $I^2=0$ (97.5% CI 0 to 0)

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$\chi^2=4.92$, $p=0.011$, $I^2=39.07$ (97.5% CI 0 to 60.23)

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<td>0.09 (-0.34 to 0.80)</td>
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<td>n=2479409</td>
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<tr>
<td>n=11583860</td>
<td>55271</td>
<td>0.02 (-0.006 to 0.11)</td>
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$\chi^2=2.23$, $p=0.53$, $I^2=0$ (97.5% CI 0 to 0)

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$\chi^2=53.91$, $p=0.09$, $I^2=54.59$ (97.5% CI 0 to 71.72)

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<tr>
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<td>98709</td>
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$\chi^2=3.96$, $p=0.07$, $I^2=24.18$ (97.5% CI 0 to 45.68)
Figure 3: Association of genetic variants in PCSK9 with risk of type 2 diabetes, individually (A) and as weighted gene-centric score (B)

Effect estimates are presented as odds ratios (ORs) for the incidence or prevalence of type 2 diabetes, with 95% CIs. Associations were scaled to a 1 mmol/L reduction with risk of type 2 diabetes, individually (A) and as weighted gene-centric score (B). The size of the black dots representing the point estimates is proportional to the inverse of the variance. Between SNP heterogeneity was measured as a two-sided Q-test ($\chi^2$) and an $I^2$ with one-sided 97.5% CI. Results from individual participant data are supplemented by repository data from the Diabetes Genetics Replication and Meta-analysis consortium.
insulin seemed unaffected. Conflicting evidence exists about a possible role of PCSK9 and PCSK9 monoclonal antibodies in disruption of pancreatic islet function.8,41 Although concordant with fasting glucose, the HbA1c association was non-significant in the collected data, which might be related to the large amount of heterogeneity between the four SNPs (upper-bound P = 72%). Interestingly, the association of the PCSK9 GS with BMI was smaller than that with bodyweight, which might be (partially) explained by a slightly greater average height among individuals with PCSK9 variants associated with lower LDL cholesterol concentrations. A further potential reason for the slight discrepancy between the BMI and bodyweight associations could be the greater heterogeneity in the associations of PCSK9 SNPs with BMI than with weight. Notably, the GS effect estimates were often driven by a large effect of SNP rs11591147; as our dose-response analysis shows (figure 4), the larger influence of this SNP appropriately reflects the proportionally larger LDL cholesterol effect of this SNP. Finally, we did not have access to measures of PCSK9 concentration in this analysis, but others46 have shown associations between common and rare PCSK9 alleles (including some of the same SNPs used here) and circulating PCSK9 concentrations.

Setting aside associations with glycaemia and weight, risk of type 2 diabetes could also be increased because lifelong exposure to genetic variation in PCSK9 may reduce mortality, making it conceivable that individuals with these variants survive longer and hence have more time to develop type 2 diabetes. However, whether PCSK9 genotype reduces mortality has not been conclusively shown.46,47 Irrespective of the nature of the PCSK9 association with type 2 diabetes, large randomised trials should determine whether this relation also holds for PCSK9 monoclonal antibodies.

In a recent study,13 investigators used a single SNP in PCSK9 and also reported evidence of an association with type 2 diabetes (OR 1·19, 95% CI 1·02 to 1·38; per 1 mmol/L reduction in LDL cholesterol). In the present study, we incorporated data from four SNPs, instead of a single SNP, in a PCSK9 gene score with participant data from 50 studies supplemented by large genetic consortia and are able to confirm their results, and also show this increase in type 2 diabetes risk is likely to be related to PCSK9-related increases in bodyweight and glucose. Previous studies of LDL cholesterol lowering HMGCR1 and NPC1L1 variants (encoding pharmacological targets of statins and ezetimibe, respectively) and more widely on LDL cholesterol-lowering variants from multiple GWAS-associated loci, as well as analyses of patients with monogenic hypercholesterolaemia, have provided evidence of a link between LDL cholesterol and type 2 diabetes, compatible with the findings from the present study. However, it is far from certain that all LDL cholesterol-lowering interventions will increase risk of type 2 diabetes, as not all share the same mechanism of action. The major site of both statins and PCSK9 inhibitors is thought to be the liver, through increased cellular membrane expression of the LDL receptor. The liver is also the site of action of the investigational apolipoprotein B antisense oligonucleotide mipomersen, whereas ezetimibe, the other licensed LDL cholesterol lowering drug, acts in the intestine to limit LDL cholesterol absorption. A potential unifying mechanism might be pancreatic β cell LDL receptor upregulation, increased lipid accumulation, and β cell dysfunction, but this suggestion will need to be tested experimentally.

In conclusion, genetic variants in PCSK9 that associate with lower concentrations of LDL cholesterol are also associated with a modestly higher risk of type 2 diabetes and with associated differences in measures of glycaemia and bodyweight. Investigators of ongoing and future randomised controlled trials of PCSK9 inhibitors should carefully monitor changes in metabolic markers, including bodyweight and glycaemia, and the incidence of type 2 diabetes in study participants. Genetic studies of the type used here could be more widely used to interrogate the safety and efficacy of novel drug targets.

Contributors
AFS, DIS, MVH, RSP, FWA, J-PC, BJK, ADH, DP, and NS contributed to the conception and design of the study. AFS, DIS, and MVH designed the analysis scripts shared with individual centres. AFS did the meta-analysis and had access to all the data. AFS, DIS, and MVH drafted the report. RSP, ZF-H, DML, FPH, BLH, EHY, CP, MM, EVI, GKH, ID, KNN, ES-T, JD, LB, TL, SC, JW, SK, KW, DM, JW, RM, GW, PW, YB-S, SMc, JFP, MKi, CW, AS-G, PM-V, AN, AGP, NCO-M, YTM85, GM, GF, SGua, CS, NJW, CI, RS, JL, MBo, SmA, AP, RR, Ata, HP, LLNH, NG, OP, TH, AL, KSS, JC, SEH, MBr, TK, HH, DSC, CAM, Medicine, University of Regensburg, Regensburg, Germany (S Baumsteiner); Department of Non-Communicable Disease Epidemiology, London School of Hygiene & Tropical Medicine, London, UK (T Meadle RFS); Division of Pharmacogenomics and Clinical Pharmacology, Utrecht Institute of Pharmaceutical Sciences, Faculty of Science, Utrecht University, Utrecht, Netherlands (AH Matallan-van der Zee, EV Baranova MSc); CNRS UMR 8199, European Genomic Institute for Diabetes (EGID), Institut Pasteur de Lille, University of Lille, Lille, France (F Frouge, D Thullier MSc, A Bonnefond); Renal and Cardiovascular Epidemiology, Centre de Recherche en Epidemiologie et Sante des Populations (CESEP), INSERM U1018, Villejuif, France (B Balkau PhD, FInstitut du Thorax, INSERM, CNRS, University of Nantes, CHU de Nantes, Nantes, France (Prof B Caron MD); Institute for Social and Economic Research, University of Essex, Colchester, Essex, UK (M Smart PhD, Y Baow PhD, Prof M Kumar PhD); Harvard Medical School Center for Cardiovascular Disease Prevention, Brigham and Women’s Hospital, Boston, MA, USA (Prof PA M Ridker MD, D I Changman PhD); Department of Epidemiology, Fred Hutchinson Cancer Research Center, University of Washington, Seattle, WA, USA (A P Reiner MD); Anschutz Medical Campus, University of Colorado Denver, Denver, CO, USA (Prof A Lange PhD); Biomedical and Translational Informatics, Gettsinger Health System, Danville, PA, USA (M D Ritchie PhD); Department of Biochemistry and Molecular Biology, Huck Institutes of the Life Sciences, Pennsylvania State University, University Park, PA, USA (M D Ritchie); and Department of Surgery, University of Pennsylvania, Philadelphia, PA, USA (B Keating PhD)

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Decleration of interests

KH or his institution have received honoraria for consultancy, Advisory board participation, or conduct of clinical trials from AMGEN, Aegerion, Pfizer, AstraZeneca, Sanofi, Regeneron, KOWA, Ionis Pharmaceuticals, and Cerenis. GKH has received research support from Aegerion, AMGEN, Sanofi, AstraZeneca, and Synageva. BC has received research funding from Pfizer and Sanofi, and has received personal fees for lectures from AstraZeneca, Pierre Fabre, Janssen, Eli Lilly, MSD Merck & Co, Novo Nordisk, Sanofi, and Takeda, and has acted as a consultant or advisory panel member for Aegerion, Eli Lilly, Novo Nordisk, Sanofi, and Regeneron. DP has consulted for Sanofi on two occasions in previous employment (related to PCSK9 inhibitors) and was an investigator on clinical trials of PCSK9 inhibition funded by Aegerion. NS has consulted for Amgen and Sanofi (related to PCSK9 inhibitors) and was an investigator on clinical trials of PCSK9 inhibition funded by Aegerion. He has also consulted for MSD, Boehringer Ingeheim, Janssen, and Novo Nordisk. DJH has consulted for Pfizer for work unrelated to this report. AP has been a consultant and a member of an advisory panel for Amgen. EI is a scientific advisor and consultant for Precision Wellness Inc and a scientific advisor for Cellink, for work unrelated to this paper. All other authors declare no competing interests.

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References


