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Stratified genome-wide association analysis of type 2 diabetes reveals subgroups with genetic and environmental heterogeneity

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Abstract

Type 2 diabetes (T2D) is a heterogeneous illness caused by genetic and environmental factors. Previous genome-wide association studies (GWAS) have identified many genetic variants associated with T2D and found evidence of differing genetic profiles by age-at-onset. This study seeks to explore further the genetic and environmental drivers of T2D by analyzing subgroups on the basis of age-at-onset of diabetes and body mass index (BMI). In the UK Biobank, 36 494 T2D cases were stratified into three subgroups, and GWAS was performed for all T2D cases and for each subgroup relative to 421 021 controls. Altogether, 18 single nucleotide polymorphisms were significantly associated with T2D genome-wide in one or more subgroups and also showed evidence of heterogeneity between the subgroups (Cochrane's $Q P < 0.01$), with two SNPs remaining significant after multiple testing (in *CDKN2B* and *CYTIP*). Combined risk scores, on the basis of genetic profile, BMI and age, resulted in excellent diabetes prediction [area under the ROC curve (AUC) = 0.92]. A modest improvement in prediction (AUC = 0.93) was seen when the contribution of genetic and environmental factors was evaluated separately for each subgroup. Increasing sample sizes of genetic studies enables us to stratify disease cases into subgroups, which have sufficient power to highlight areas of genetic heterogeneity. Despite some evidence that optimizing combined risk scores by subgroup improves prediction, larger sample sizes are likely needed for prediction when using a stratification approach.

Introduction

Diabetes is a metabolic disease characterized by high blood glucose resulting primarily from either insufficient insulin production or insulin resistance. Incidence of diabetes is increasing due to both lifestyle factors, such as increasing levels of obesity, and longer life expectancy (1). Among minority ethnic communities in the UK, the prevalence is up to four times higher than in White populations (2). Diabetes represents a significant health burden because of the increased rates in individuals with diabetes of physical disability, including blindness and limb amputation, and comorbidities, such as kidney disease, cardiovascular disease and cancer (3).

Glucose homeostasis involves many distinct mechanisms, and genetic susceptibility to diabetes arises from gene variants affecting different gene networks. A complex pattern of genetic susceptibility and environmental exposures by individual leads to significant heterogeneity in the pathogenesis of type 2 diabetes (T2D) between individuals. Better understanding of these heterogeneous drivers may aid in predicting both susceptibility to diabetes in individuals, and its downstream complications and thus

enable targeted treatments depending on whether, for example, the driver was related to insulin signalling, beta cell function or a combination of both. Accounting clinically for heterogeneity in diabetes is likely to lead to personalized treatment with correspondingly more reliable control of blood sugar levels. Diabetic complications are strongly related to the level of exposure to uncontrolled blood sugar levels, highlighting the importance of treatments that enable individuals to manage their blood sugar levels well.

A clear genetic component to T2D has been identified through population, family and twin-based studies, with heritability estimates ranging from 26% genetic heritability to 50% MZ twin concordance (4). Many genome-wide association studies (GWAS) of T2D have been carried out, with a large recent meta-analysis including 62 892 diabetic cases and 596 424 controls identifying 139 loci associated with T2D (5). However, these loci only explain around 20% of T2D heritability (6). It is becoming increasingly clear that T2D is a disease that has different pathogenic pathways. Most GWAS do not consider the underlying heterogeneity between cases, but studies that stratify cases have found evidence for

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Table 1. Participant characteristics of T2D cases and controls and characteristics of the three subgroups

	Diabetes cases	Controls	Group 1	Group 2	Group 3
Number	38 481	421 021	20 588	6328	9344
BMI (mean, SD)	31.6 (5.7)	27.0 (4.5)	35.2 (4.7)	26.8 (2.7)	26.8 (2.3)
Age-at-onset (mean, SD)	58.6 (11.1)	n/a	59.0 (10.0)	51.6 (7.2)	68.1 (5.7)
Age (at 1/1/21)	71.5 (7.0)	68.0 (8.1)	70.7 (7.1)	75.1 (4.4)	68.5 (7.4)
Sex					
Female	39%	56%	41%	31%	40%
Male	61%	44%	59%	69%	60%
Smoking status					
Never	42%	54%	42%	43%	41%
Ex-smoker	45%	35%	46%	41%	45%
Current	13%	10%	12%	16%	14%

different genetic profiles between subgroups of T2D cases. Perry *et al.* (7) stratified T2D cases by body mass index (BMI) in a meta-analysis of previous GWAS findings and found a difference in the genetic profile of lean individuals compared with obese. Stratification has also been explored by age-at-onset (8), which showed evidence for different genetic profiles by age. In addition, previous work clustering adult-onset diabetes patients showed five clusters of patients from six variables, each with distinct characteristics and risk of complications (5). GWAS carried out on these five clusters identified three single nucleotide polymorphisms (SNPs), which reached genome-wide significance in at least one cluster (9). However, the small sample size, with 9486 individuals divided over five clusters, suggests that with greater power further heterogeneity is likely to be detected.

In this study, we aimed to identify differences in the genetic profiles of T2D in European-ancestry individuals, using larger subgroups, which broadly captured genetic and environmental drivers of diabetes. We derived three subgroups of T2D cases in the UK Biobank, on the basis of BMI and age-at-onset of diabetes. In GWAS, we identified diabetes-associated SNPs in each subgroup and tested for heterogeneous SNP-effects across the groups. We explored the genetic correlation between subgroup-derived genetic risk profiles and diabetes traits, including beta cell function and insulin resistance. Finally, we investigated whether this BMI- and age-subgroup approach improved T2D prediction from genetics or with an integrated risk model across genetic and environmental factors.

Results

In the UK Biobank, 36 494 European-ancestry individuals with T2D were grouped according to BMI and age-at-onset of diabetes into three subgroups. Group 1 consisted of individuals with BMI >30, Group 2 with BMI <30 and age-at-onset <60 and Group 3 with BMI <30 and age-at-onset >60. The characteristics of study participants and subgroups are summarized in Table 1. GWAS were conducted for all individuals and by subgroup using the same 421 021 controls to ascertain whether there were differences in the genetic profiles of these three subgroups.

GWAS overall and by subgroup

GWAS with T2D cases in all subgroups (36 494 cases and 421 021 controls) identified 267 lead SNPs as genome-wide significant associations. An additional 10 SNPs showed genome-wide significant associations in subgroup-specific GWAS. Of the 277 lead SNPs, 25 were novel with no previous evidence of association

with T2D, either at these SNPs or at SNPs in linkage disequilibrium (LD) (Table 2), excluding SNPs from genes with known associations with diabetes. Many of the lead SNPs had been found previously to have suggestive associations with T2D, which did not meet genome-wide significance. Thirteen of the novel SNPs had previously been associated with metabolic measures, eight were associated with other non-metabolic traits and the remaining four were not previously associated with any traits. Two of the novel SNPs not previously associated with metabolic traits were annotated to genes, which have been associated with chronic inflammatory diseases (PKIG and SBNO2). In addition, one further SNP, rs9934018, was annotated to *CLCN7* encoding a chloride channel protein with previous work indicating a relationship between chloride channels and beta cell health (10). Three novel SNPs were found to be significant only in subgroup 1, defined by BMI > 30 (1:168960001, rs17153738, rs76798800). Results for all 277 SNPs are given in Supplementary Material, Table S1. There was no evidence of genomic inflation for either the combined or subgroup analysis with $\lambda_{1000} \sim 1$.

Given these indicators of heterogeneity, we further explored differences in association across subgroups. Eighteen of the 277 lead SNPs significantly associated with diabetes also showed significant heterogeneity between the subgroups using a threshold of Cochran's Q with $P < 0.01$ (Fig. 2); two SNPs (rs72655474 in *CDKN2B*, rs10166720 in *CYTIP*) remained significant after a Bonferroni correction for multiple testing.

Genetic differences between groups

Manhattan plots illustrating the genetic associations of each subgroup and all T2D cases are shown in Figure 1. The genetic correlations between the groups were high, partly driven by the common set of controls across all GWAS analyses. The correlation between Groups 1 and 2 was the highest at $r^2 = 0.97$ [standard error (SE) 0.05]. The correlations between Group 3 and both Groups 1 and 2 were similar (Groups 1–3, $r^2 = 0.88$, SE 0.05; Groups 2–3, $r^2 = 0.85$, SE 0.05). SNP heritability for each subgroup was $h^2 = 0.02$ – 0.03 (Supplementary Material, Table S2).

In genetic correlation analysis with 15 predefined phenotypes related to T2D, 11 phenotypes evaluated had significant nonzero genetic correlations with one or more subgroups (Supplementary Material, Table S3, Fig. 2B). Groups 1 and 2 had significant correlations with fasting insulin (Group 1: $r^2 = 0.49$; Group 2: $r^2 = 0.31$) and insulin resistance (Group 1: $r^2 = 0.52$; Group 2: $r^2 = 0.38$), with lower, nonsignificant correlations in Group 3. The only group showing a significant correlation with beta cell function was Group 3 ($r^2 = -0.31$). Longevity only showed a genetic correlation with Group 1 ($r^2 = -0.39$).

Table 2. Novel SNPs that were either significant in the analysis including all groups or significant in a subgroup analysis

ID	Chrom	Position	Gene	Effect allele	Effect allele freq	Beta	se	P-value	Previous associations
1:168960001	1	168960001		AT	0.978861	0.118722	0.030362	9.22E-05	Unrelated
rs17153738	7	106658309		T	0.654342	-0.03904	0.008896	1.14E-05	Unrelated
rs76798800	1	154994978	DCST2	G	0.733766	0.037472	0.009505	8.08E-05	BMI/WHR
rs371649660	7	74353884	GTF2I	C	0.890097	0.095554	0.014636	6.63E-11	BMI/WHR
rs2821226	1	203517292		A	0.472495	0.048463	0.008491	1.15E-08	BMI/WHR
rs199679345	6	34234953		C	0.951861	-0.13681	0.019876	5.85E-12	Related
20:43246633	20	43246633	PKIG	CACAA	0.952468	0.126113	0.02029	5.11E-10	None
rs201458438	12	123801250	SBNO1	C	0.320434	-0.06178	0.00955	9.84E-11	BMI/WHR
rs38169	7	15893300		C	0.244283	0.061601	0.009802	3.28E-10	Related
rs10823909	10	73989184	ANAPC16	T	0.911994	-0.08372	0.014924	2.03E-08	BMI/WHR
rs72752197	5	44627323		C	0.780923	0.057415	0.010266	2.23E-08	Unrelated
rs11057368	12	124309574	DNAH10	G	0.633135	0.048748	0.008813	3.18E-08	BMI/WHR
rs11187152	10	94500111		G	0.923309	0.098068	0.016017	9.21E-10	Unrelated
rs1916334	12	122484294	BCL7A	G	0.804831	-0.06304	0.010707	3.93E-09	BMI/WHR
rs56218834	2	25520857	DNMT3A	G	0.572974	0.062063	0.008558	4.12E-13	BMI/WHR
rs556132116	17	17931884	ATPAF2	C	0.689899	-0.05928	0.0108	4.04E-08	BMI/WHR
6:19809493	6	19809493	RP1-167F1.2	TA	0.689373	0.050394	0.009156	3.71E-08	None
10:114673015	10	114673015		GGT	0.856163	0.071575	0.012742	1.94E-08	None
rs142201902	3	185153047	MAP3K13	C	0.92574	-0.09285	0.016139	8.76E-09	BMI/WHR
rs34636896	10	114647936		G	0.183938	-0.10405	0.011741	7.84E-19	Unrelated
19:1149092	19	1149092	SBNO2	GC	0.638361	0.053763	0.009113	3.65E-09	Unrelated
rs876475	9	81545012		G	0.599162	-0.04786	0.008595	2.57E-08	Unrelated
rs59521405	2	112264989		T	0.752715	0.060811	0.009975	1.09E-09	BMI/WHR
rs78535155	13	49435399		A	0.985318	0.198544	0.036376	4.81E-08	None
rs9934018	16	1504934	CLCN7	T	0.593146	0.046978	0.00857	4.22E-08	Unrelated

P-values are shown for the all group analysis.

Genetic and environmental contributions

To determine whether the subgroups provided better prediction of diabetes case status, polygenic scores from each subgroup were generated and their predictive ability compared with the full dataset. The polygenic risk scores (PRSs) calculated using the GWAS summary statistics from the full dataset were more predictive of diabetes than those from each subgroup (Fig. 3).

As diabetes risk is a combination of genetic and environmental factors including ageing, a combined risk score (CRS) was optimized for the training set using both an overall and subgroup approach. This combined risk score included the genetic risk (GR) score, a BMI score and a smoothed age score (Fig. 4). CRSs based on the optimized parameters were calculated in the test set, and diabetes was predicted using the R predict function and an area under the ROC curve (AUC) determined.

The AUC prediction including all subgroup components for the full dataset, which included 7300 test cases, was 0.92. Also in the full dataset, a model utilizing only the PRS component had an AUC of 0.87 compared with an AUC of 0.74 for a model using only BMI and an AUC of 0.78 when both BMI and age were included. Further analysis was then undertaken to assess the impact of using subgroup-specific GR scores and subgroup optimization of the contribution to the risk score of genetics, BMI and Age (Table 3). We found an increase in prediction when using the GR score calculated on the full group but with the weighting of genetic and environmental factors by subgroup. For Group 1, this increased the AUC from 0.92 to 0.93.

Discussion

In this study, we explored the different genetic profiles amongst individuals with T2D on the basis of 457 515 European-ancestry

participants from the UK Biobank (36 494 diabetes cases and 421 021 controls). Individuals with T2D were grouped on the basis of age-at-onset and BMI, where Group 1 comprised all individuals with BMI ≥ 30 (Group 1), then Groups 2 and 3 had BMI < 30 with an age-at-onset < 60 (Group 2) or age-at-onset over 60 (Group 3). Our study builds on Noordam *et al.* (8), which found that the genetic profile of individuals with diabetes varies by age, and previous studies have found differences between lean and obese individuals and have identified distinct groups in terms of patient characteristics and risk of complications when clustering adult-onset diabetes (5). Our study found novel SNPs associated with T2D in the overall dataset, differing genetic profiles among the subgroups and SNPs with high heterogeneity between subgroups. The study further found that the contribution to overall risk between genetic and environmental factors varied by subgroup.

This study analyzed a larger sample size than previous UK Biobank Diabetes GWAS, by including related individuals using a mixed model implemented in regenie. Case-control studies with a small number of cases relative to the number of controls can suffer from bias that regenie addresses using the Firth correction method. This improved power enabled the identification of 25 novel SNPs. Four of the novel SNPs were annotated to genes with no annotated SNPs previously associated with diabetes including genes associated with chronic inflammatory diseases (PKIG and SBNO2) and CLCN7 encoding a chloride channel protein. PKIG is a protein kinase inhibitor, blocking protein kinases from phosphorylating proteins, which affects the level of activity and function. Specifically, it inhibits cAMP-dependent protein kinase (PKA) and the cAMP/PKA signalling pathway is important for regulating glucose homeostasis in a wide range of processes including both insulin and glucagon secretion and glucose uptake (11). SBNO2 regulates inflammatory processes (12) and has been found to be differentially methylated with BMI (13). Finally, CLCN7 is part of

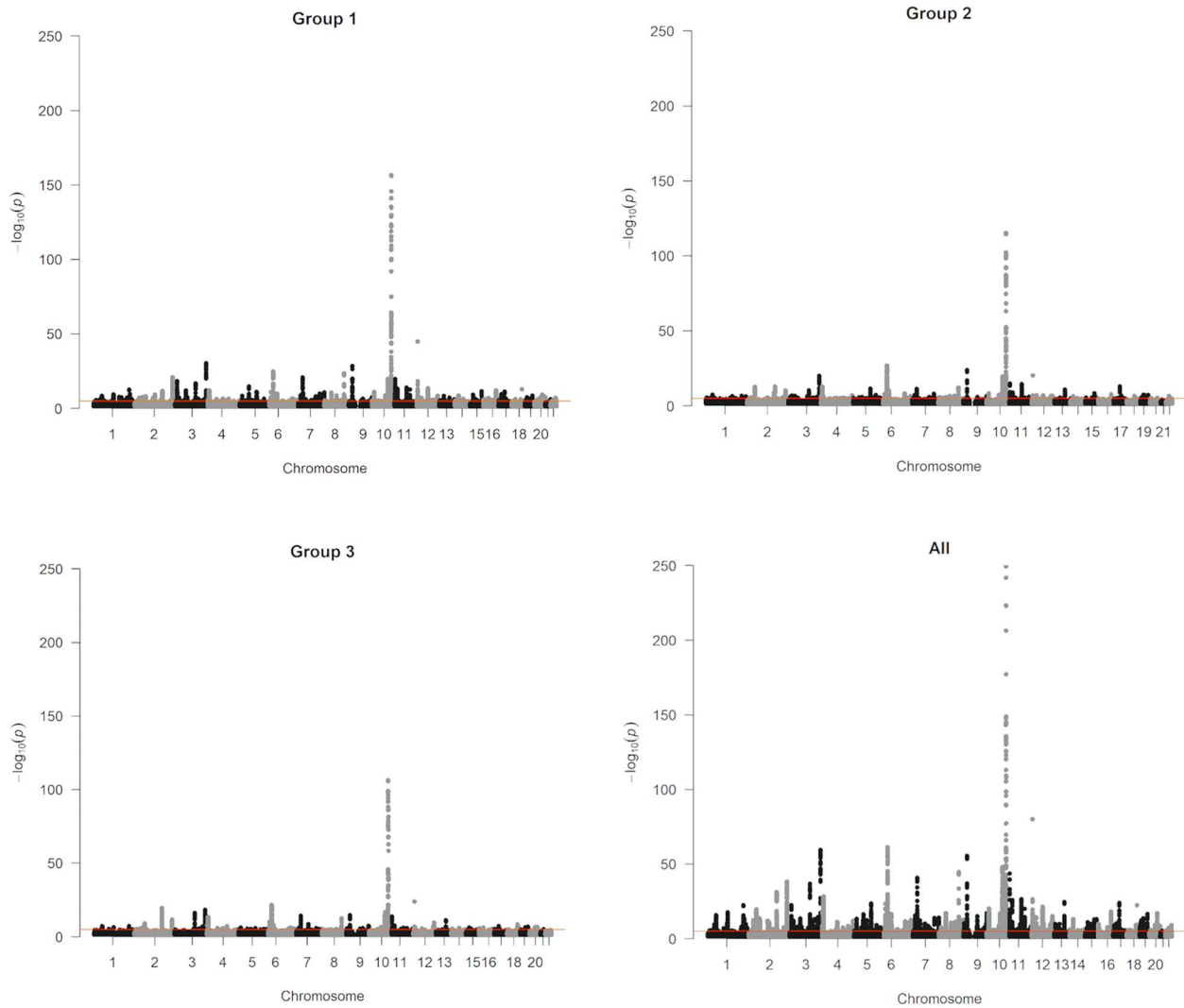


Figure 1. Genome wide association study results by subgroup. Manhattan plots GWAS results from T2D cases and controls from (A) Group 1, (B) Group 2, (C) Group 3 and (D) all groups combined.

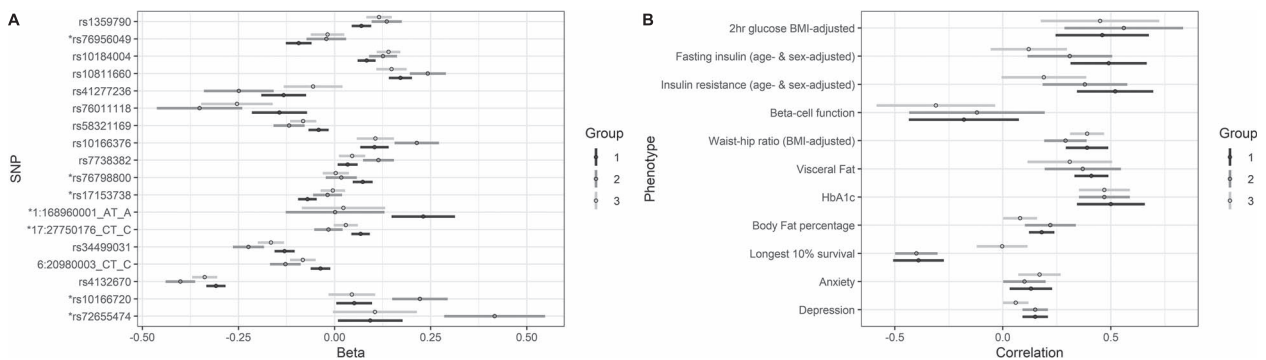


Figure 2. Genetic differences between subgroups. (A) Heterogeneity between SNPs showing SNPs with Cochran's $Q P < 0.01$. SNPs which are genome-wide significant in a subgroup but not genome-wide significant overall marked with an asterisk. (B) Genetic correlations between subgroups and genetic profiles of other phenotypes.

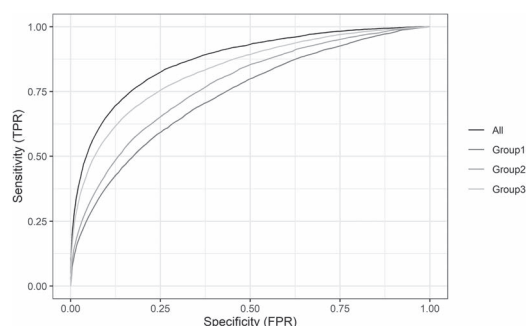
the family of chloride channel proteins. Beta cells contain chloride channels, which respond to glucose concentration and, in turn, lead to insulin secretion (14).

The three subgroups of T2D cases differed in size, which makes comparisons of the number of significant SNPs detected difficult. However, Group 3, despite being around half the size of Group

1, showed a greater predictive GR score ($AUC = 0.83$) than Group 1 ($AUC = 0.74$). This may indicate that the pathogenesis of diabetes in the obese group has a greater environmental component than the nonobese group. A high degree of genetic correlation was seen between groups but with statistically significant differences for individual SNPs. This observation is in line with

Table 3. Predicting diabetes using CRSs within groups and across groups

Training and test set	Genetic risk population	AUC (95% CI)
All groups	All groups	0.921 (0.918–0.924)
Group 1	All groups	0.932 (0.929–0.934)
Group 1	Group 1	0.883 (0.880–0.882)
Group 2	All groups	0.915 (0.912–0.918)
Group 2	Group 2	0.825 (0.820–0.829)
Group 3	All groups	0.916 (0.913–0.919)
Group 3	Group 3	0.894 (0.890–0.898)

**Figure 3.** ROC curves for PRSs by subgroup. All group analysis AUC = 0.87, Group 1 AUC = 0.74, Group 2 AUC = 0.78, Group 3 AUC = 0.83.

the results obtained by stratifying by age (8), which found different genetic profiles between older age-at-onset and younger age-at-onset. *TCF7L2* that contained SNPs more strongly associated with different age of diagnosis in the previous study also contained SNPs heterogeneous between the three groups in the current study. *Aly et al.* (9) also identified a variant in *TCF7L2* (rs7903146) as being significantly associated with only three of their five clusters, finding it not to be associated with severe insulin-resistant patients (characterized by late onset and obesity) or severe autoimmune diabetes. In this study, rs4917644 was not even nominally significantly associated with T2D in Group 3, but it was with Groups 1 and 2. In addition, 17 further SNPs had significant heterogeneity between the groups with four of these significant only in a subgroup and not genome-wide significant overall. Two SNPs met a multiple testing threshold for significance for heterogeneity. An SNP in *CDKN2B*, a gene that previous work has suggested plays a role in beta cell physiology and diabetes risk (15), and an SNP in *CYTIP*, a gene that has been found in animal models to have significantly different expression in mice deficient in insulin receptor substrate-2 (16). These links to physiological processes suggest that the underlying genetic heterogeneity may be reflected in the variation in disease pathogenesis by individual.

There were differences between the groups in their genetic correlation with other traits. Only Groups 1 and 2 had significant genetic correlations with insulin resistance and fasting insulin with the older age-at-onset group showing no significant correlation. This group instead showed a significant negative genetic correlation with beta cell function, which neither Group 1 or 2 did. This suggests that older age-at-onset diabetes for those who are not obese has a different pathogenesis from those whose diabetes develops at a younger age or who are obese. Previous work by *Udler et al.* (17) clustered individuals on the basis of previously identified GWAS variants and diabetic traits, identifying five clusters (Beta cell, Proinsulin, Obesity, Lipodystrophy and Liver). In the current study, we found differences between the subgroups in

loci identified by *Udler et al.* in their Proinsulin and Lipodystrophy clusters; there were also differences with *ARAP*, *CCND2*, *HNF4A*, *PPARG* and *FAF1* only significant in Group 1 and *ARAP*, *HNF4A* and *CMP* only significant in Group 2.

T2D is a complex disease driven by both genetic and environmental factors. The study sought to assess the contribution by subgroup of genetic and environmental factors to the overall risk by computing CRSs for a training dataset and assessing their predictive ability in a test dataset. Genetic risk was determined using polygenic risk scores, and the study found that the most predictive GR scores for each subgroup were those that were calculated on all T2D cases, rather than by subgroup. PRSs were calculated using all nominally significant SNPs, but the power may be too low within subgroups given the modest sample sizes. The CRS using all subgroups had an excellent level of prediction with an AUC of 0.92, but this was improved for Group 1 by using only Group 1 to optimize the balance between genetic and environmental risk factors. Group 1 consists of obese individuals, and the GR score prediction for this group is not strong (AUC 0.74), suggesting a greater environmental component to the pathogenesis. However, by utilizing the power of the significantly larger overall group, the improvement in GR score prediction combined with the weighting for BMI leads to an improvement in the prediction for this group.

Although the study had a relatively large discovery sample, the clustering process meant that each subgroup contained around 10 000 individuals with diabetes. This results in a lower statistical power for analyses within subgroups. The process used to group individuals also resulted in different sized groups leading to differing statistical power, making it harder to compare the resulting genetic profiles. Because of the low numbers of diverse ancestry participants in the UK Biobank, analyses were restricted to individuals of European-ancestry. Diabetes incidence varies substantially by ethnicity both in terms of the level and age of incidence, and results may therefore not be generalizable to other ancestries.

In summary, by stratifying T2D cases by age-at-onset and BMI, we found subgroup-specific genetic variation and furthermore differing contributions to disease pathogenesis from genetic and environmental risk by subgroup. However, larger sample sizes than those currently available are likely needed to optimize prediction of T2D in a stratification approach.

Materials and Methods

Study participants

This study included participants from the UK Biobank, which includes over 500 000 individuals aged 40–69 at the time of recruitment. Participants were recruited from across the UK between 2006 and 2010 (18), and genotype data are available for all individuals (19). Data up until 1 January 2021 were included in the study.

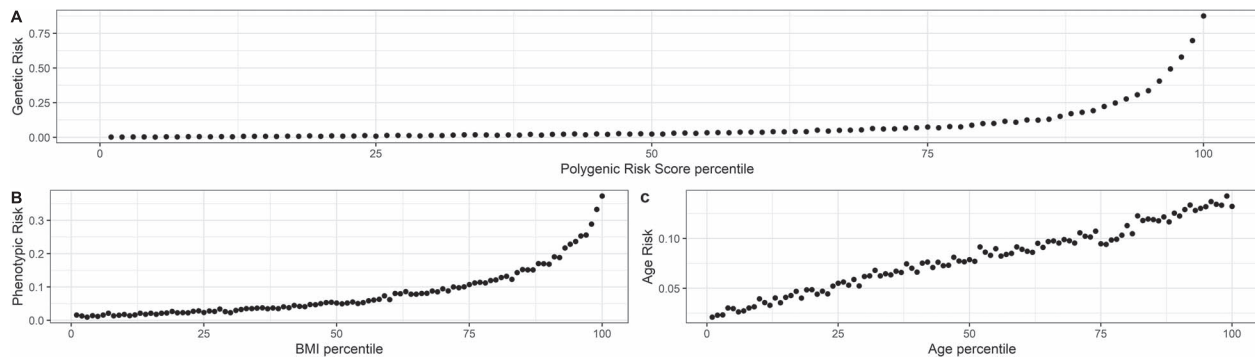


Figure 4. CRS components. (A) Genetic risk at each percentile category for polygenic risk calculated for the combined group. (B) Diabetes risk due to BMI calculated at each percentile category. (C) Diabetes risk due to age calculated at each percentile category.

Ethical approval was provided by the Research Ethics Committee (REC reference 20/NW/0382).

Data on participants' diabetes status were based primarily on hospital admission data but also included primary care data and self-reported status. A combination of data fields was used to determine diabetes status including self-reported 'Diabetes diagnosed by a doctor' (data field #2443) and the existence of the first reported date in data fields #130706 (insulin-dependent diabetes mellitus), #130708 (non-insulin-dependent diabetes mellitus), #130710 (malnutrition-related diabetes mellitus) and #130712 (other specified diabetes mellitus). For age-at-onset, self-reported responses to 'Age diabetes diagnosed' (data field #2976) were used along with the first occurrence of diabetes reporting in data fields #130706, #130708, #130710 and #130710. Individuals with missing BMI were not included in the study. Two further exclusions were made to remove type 1 diabetes (T1D) cases and individuals of non-European ancestry. The exclusions made for T1D were as follows: all cases with an age-at-onset of 18 or younger in recognition that cases arising at these ages are predominantly T1D (20) and those cases where the individual progressed to insulin treatment within 1 year identified in data field #2986. Previous work by Thomas *et al.* (21) indicates that 90% over T1D cases can be identified by this indicator. Individuals with no records of diabetes were used as controls. The same group of controls was used for all subgroup analyses for consistency to ensure results arising were due only to differences in cases. Individuals with non-European ancestry were identified through 4-means clustering of the first two genetic principal components (PCs) as supplied by the UK Biobank and excluded from analysis. Of the remaining individuals, 96% identified as white in data field #21000.

Subgroups

Individuals were put into groups on the basis of BMI and age-at-onset. Given the number of overweight T2D cases, the BMI threshold for grouping was chosen as obesity (BMI > 30 kg/m²). Group 1 included all individuals who had a BMI ≥ 30. To establish the differences between onset as age-related disease and onset at earlier ages, the age-at-onset was set to be 60. Groups 2 and 3 consisted of the remaining individuals divided by age-at-onset with Group 2 individuals having an age-at-onset < 60 and Group 3 with an age-at-onset ≥ 60.

Genetic data

UK Biobank profiled the genotypes using Affymetrix UK BiLEVE Axiom and Affymetrix UK Biobank Axiom arrays (<https://biobank>.

ndph.ox.ac.uk/showcase/label.cgi?id=263). UK Biobank also carried out genotype imputation and preliminary QC on the resulting genetic data (see Supplementary Note). The first 20 PCs were recalculated for the individuals to be included in the genome-wide association study (following exclusions for ancestry, juvenile diabetes and QC) using FlashPCA v2.0 (22).

Genome-wide association analyses

GWAS was conducted using logistic regression models using regenie, a C++ program for whole-genome regression modelling of large GWAS (23). Covariates included the first 20 PCs to account for population structure, sex and batch. In addition, further covariates were included to account for risk factors of diabetes including age, BMI and smoking. Analysis was restricted to SNPs on the autosomes, with a minimum allele frequency (MAF) > 1% and an imputation information score > 0.6. FUMA, a platform to annotate, prioritize, visualize and interpret GWAS results (24), was used to identify independent lead SNPs on the basis of a P-value threshold of 5×10^{-8} , $r^2 < 0.6$ and LD < 0.1. LDlink software program (25) was used to check for novel sites that were not in linkage disequilibrium (LD) with sites previously associated with diabetes or measures of blood glucose. For SNPs not in LDlink, a manual check of the GWAS catalogue (26) was carried out for all sites with LD < 0.2 within a 0.5 MB window. Lead SNPs were determined to be significant only in one subgroup if the P-values for that SNP in the GWAS of the other subgroups and combined analysis were all greater than 5×10^{-8} .

Analyzing genetic differences in the subgroups

To assess the heterogeneity of each SNP across the GWAS results for the subgroups, we used a fixed effects meta-analysis implemented through GWAMA (Genome-Wide Association Meta-Analysis) software (27) to calculate heterogeneity statistics. Heterogeneity was determined on the basis of Cochran's Q P-value at a threshold of 1% with $I^2 > 50\%$ and further with adjustment for multiple testing at a Bonferroni threshold 1.9×10^{-4} . Genetic correlations and SNP heritability were calculated using the LDSC software (28), on the basis of LD score regression. This is in line with previously reported subgroup GWAS (8), and LDSC has been reported to be unbiased with sample overlap (28). Genetic correlations between the subgroups were calculated to determine the extent to which genetic profiles for each group overlapped. Correlations were also calculated between GWAS results from each subgroup and 15 other phenotypes (Supplementary Material, Table S4), including five related to diabetes (2-h glucose, fasting insulin, HbA1c, insulin resistance and beta cell function), four metabolic phenotypes (waist-hip ratio adjusted for BMI, Visceral

Fat, Body Fat percentage), a longevity measure (longest 10% survival), four psychiatric phenotypes (anxiety, depression, Alzheimer's disease, autism) and two inflammatory phenotypes (inflammatory bowel disease and rheumatoid arthritis). GWAS summary statistics for these phenotypes were accessed from LD hub (29). A 95% confidence interval was constructed to test the significance between the correlations observed.

PRSs

PRSs for the combined groups and each individual diabetes subgroup were calculated on the basis of GWAS results after first rerunning the GWAS using a split training/test (80%/20%) set approach. GWAS were carried out as above in the training set. PRSs were calculated overall and for each diabetes subgroup using Polygenic Risk Score software, PRSice v2 (30,31). This software utilized the GWAS summary statistics from the training set analysis, including clumping ($r^2 < 0.1$ and 500 kb window) and a *P*-value threshold of 0.05 [on the basis of a previous study in UK Biobank (32)].

CRSs

CRSs were calculated using methodology described in Moldovan *et al.* (33), on the basis of the three risk factors of PRS, BMI and age. Each of these risk factors was transformed to account for the nonlinear relationship between diabetes risk across risk factor percentiles. After transformation of each risk factor, each individual then had an assigned GR score, a BMI risk score (BR) and an age risk score (AR). CRSs were then calculated as in the formula below with regression model parameters estimated as described in Moldovan *et al.* (33).

$$\text{CRS} = \alpha \text{ GR} + \beta \text{ BR} + \gamma \text{ AR}$$

The ability of the CRSs to predict diabetes was then assessed in the test set using the AUC. The AUC was calculated using the pROC package in R (34). The CRSs were calculated twice for each subgroup. Once using GR scores on the basis of the subgroup PRS with optimization by subgroup for α , β and γ and once using the GR scores on the basis of the overall data set also with optimization by subgroup. The AUC was determined using PRS alone, BMI alone and BMI and age to assess the impact of including genetics in the score.

Supplementary Material

Supplementary Material is available at HMG online.

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Conflict of Interest statement. None declared.

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Data Availability

This research has been conducted using the UK Biobank Resource under Application Number 65912. Data are available from UK Biobank subject to standard access procedures (www.ukbiobank.ac.uk). The code for carrying out GWAS using regenie has been added to Github (https://github.com/applyfun/gwas_methods).

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