

# Combined analysis of 19 common validated type 2 diabetes susceptibility gene variants shows moderate discriminative value and no evidence of gene–gene interaction

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## Abstract

**Aims/hypothesis** The list of validated type 2 diabetes susceptibility variants has recently been expanded from three to 19. The variants identified are common and have low penetrance in the general population. The aim of the study is to investigate the combined effect of the 19 variants by applying receiver operating characteristics (ROC) to demonstrate the discriminatory value between glucose-tolerant individuals and type 2 diabetes patients in a cross-sectional population of Danes.

**Methods** The 19 variants were genotyped in three study populations: the population-based Inter99 study; the ADDITION study; and additional type 2 diabetic patients and

glucose-tolerant individuals. The case–control studies involved 4,093 type 2 diabetic patients and 5,302 glucose-tolerant individuals.

**Results** Single-variant analyses demonstrated allelic odds ratios ranging from 1.04 (95% CI 0.98–1.11) to 1.33 (95% CI 1.22–1.45). When combining the 19 variants, subgroups with extreme risk profiles showed a threefold difference in the risk of type 2 diabetes (lower 10% carriers with  $\leq 15$  risk alleles vs upper 10% carriers with  $\geq 22$  risk alleles, OR 2.93 (95% CI 2.38–3.62,  $p=1.6 \times 10^{-25}$ ). We calculated the area under a ROC curve to estimate the discrimination rate between glucose-tolerant individuals and type 2 diabetes patients based on the 19 variants. We found an area under

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the ROC curve of 0.60. Two-way gene–gene interaction showed few nominal interaction effects.

**Conclusions/interpretation** Combined analysis of the 19 validated variants enables detection of subgroups at substantially increased risk of type 2 diabetes; however, the discrimination between glucose-tolerant and type 2 diabetes individuals is still too inaccurate to achieve clinical value.

**Keywords** ADDITION · Bootstrap · Case–control study · Genetic association · Inter99 · Polymorphism · ROC · Receiver operating characteristic · SNP · Type 2 diabetes

### Abbreviations

GWA Genome-wide association  
MAF Minor allele frequency  
ROC Receiver operating characteristic  
SNP Single-nucleotide polymorphism

### Introduction

Type 2 diabetes is a rapidly growing public health problem and although environmental factors are of major importance, genetic risk factors also predispose to the disease. Until recently, only three gene loci, *PPARG* [1], *KCNJ11* [2, 3] and *TCF7L2* [4], had convincingly shown replicated association with type 2 diabetes. However, within the last 2 years results of genome-wide association studies (GWA) have revolutionised the field of research and identified 14 new susceptibility type 2 diabetes variants [5–15]. Together with *WFS1* [16] and *TCF2* (also known as *HNF1B*) [17, 18], identified by a candidate gene approach, the total number of validated type 2 diabetes susceptibility loci now reaches 19. All identified alleles associated with type 2 diabetes risk are common (minor allele frequency [MAF]>5%) and have a low penetrance (OR<1.5) in the general population. Little is known about the molecular mechanisms by which these variants increase diabetes risk; however, physiological studies have demonstrated that the majority may mediate their pathogenic effect through an abnormal beta cell function, which seems to be the case for *CDKAL1*, *SLC30A8*, *HHEX*, *CDKN2A*, *IGF2BP2*, *TCF7L2*, *KCNJ11*, *WFS1*, *CDC123*, *JAZF1*, *MTNR1B* and *TSPAN8* [3, 8, 14, 19–23]. As for the remaining susceptibility variants, a predisposing effect through obesity affecting an increase in fat accumulation has been demonstrated for variation in *FTO* [24, 25] and variation in *PPARG* has shown a potentially pathogenic effect on type 2 diabetes through an impairment of insulin sensitivity [26].

An important question is, to what extent do the combined effect of these variants predict which individuals are at risk of developing type 2 diabetes. Indeed, if the discrimination is

successful, the prospect of prediction and application of genotype-based early and individualised prevention and treatment strategies for type 2 diabetes would be of major clinical importance.

The issue of combining the known available type 2 diabetes susceptibility variants has been addressed before in case–control settings. Before the release of GWA studies, Weedon et al. [27] demonstrated that the combined effect of three common genetic variants only moderately enabled discrimination between type 2 diabetes patients and glucose-tolerant individuals (AUC of the receiver operating characteristics [ROC] 0.58). With the recent release of GWA studies and thus the expansion of the number of validated type 2 diabetes susceptibility variants, three studies have investigated the combined effect of 17 independent loci on type 2 diabetes risk and although subgroups of carriers of several risk alleles were considered to be at high risk of developing type 2 diabetes, the overall conclusion pointed towards a low discriminative ability between cases and controls assessed by the AUC of an ROC curve [28–30]. Also, two prospective studies estimated the predictive value of 16 and 18 type 2 diabetes susceptibility variants, respectively. The studies demonstrated that even though the discriminatory power of genetic testing is limited, it increases with duration of follow up [31, 32], suggesting that even genetic risk factors with moderate effects may, on a life-long basis, contribute considerably to diabetes risk.

Recently, two new type 2 diabetes candidate genes were discovered. A Japanese study reported the result of a genome-wide scan of 268,068 single-nucleotide polymorphisms (SNPs) and identified *KCNQ1* as a type 2 diabetes susceptibility gene [11, 12]. The rs2237895 variant—located in the intronic region of *KCNQ1*—showed an OR 1.23 (95% CI 1.18–1.29,  $p<1\times 10^{-16}$ ). Additionally, three recent papers reported that variants in the *MTNR1B* locus strongly associate with type 2 diabetes risk and a meta-analysis of *MTNR1B* rs10830963 demonstrated OR 1.09 (95% CI 1.05–1.12,  $p=3.3\times 10^{-7}$ ) [13–15].

Here we present an updated study evaluating the combined effect of 19 validated type 2 diabetes susceptibility variants; it includes the newly discovered *KCNQ1* and *MTNR1B* variants that in the Danish population showed to be the fifth and second strongest type 2 diabetes-associated variants, respectively. By applying ROC curves in a large sample of Danes we demonstrate how well the 19 variants discriminate between glucose-tolerant individuals and type 2 diabetes patients alone and in combination with known type 2 diabetes risk factors such as BMI, age and sex. In addition, we investigate whether the combined effect from the variants is explained additively or whether a synergistic effect on diabetes risk (two-way gene–gene interaction) exists between the variants.

## Methods

**Study population** The 19 type 2 diabetes susceptibility variants were genotyped in 9,395 Danes involving: (1) the population-based Inter99 sample (ClinicalTrials.gov NCT00289237) of middle-aged individuals sampled at the Research Centre for Prevention and Health ( $n=4,928$ ) [33]; (2) type 2 diabetes patients and glucose-tolerant individuals sampled through the outpatient clinic at Steno Diabetes Center ( $n=2,107$  and  $n=734$ , respectively); and (3) screen-detected type 2 diabetes patients from the Danish ADDITION screening cohort (ClinicalTrials.gov NCT00237549) sampled through Department of General Practice at University of Aarhus ( $n=1,626$ ) [34]. Study group 1 and glucose-tolerant individuals from study group 2 underwent a standard 75 g oral glucose tolerance test. Informed written consent was obtained from all participants before participation. The study was approved by the Ethical Committee of Copenhagen and Aarhus Counties and was in accordance with the principles of the Helsinki Declaration. Glucose-tolerant individuals and type 2 diabetes patients were defined according to World Health Organization 1999 criteria [35]. Individuals with type 2 diabetes had increased BMI and age (mean BMI  $30.6\pm 5.5$  kg/m<sup>2</sup>, mean age  $60\pm 10$  years) compared with glucose-tolerant individuals (mean BMI  $25.6\pm 4.0$  kg/m<sup>2</sup>, mean age  $47\pm 9$  years).

**Statistical analysis** For each variant we estimated the multiplicative effect on type 2 diabetes risk as well as the two-way gene–gene interaction by applying logistic regression with adjustment for sex and age. The two-way interaction was performed by comparing one model including only the main effect (SNP) with an alternative model including a SNP–SNP interaction variable in addition to the main effect. The covariate for each SNP was denoted as the number of disease alleles (i.e. coded as 0, 1 or 2 according to the number of risk alleles) and the pair-wise interaction as the product of the pairs of SNPs (i.e. multiplicative interaction).

When estimating the combined effect of the 19 susceptibility SNPs, each risk allele was defined as the allele associated with increased risk of type 2 diabetes in previous studies [5–18], hence each individual is assigned a risk score ranging from zero to 38. For each risk score the numbers of glucose-tolerant individuals and type 2 diabetic patients were calculated. Fisher's exact test was applied to test whether the distribution of glucose-tolerant individuals and type 2 diabetes patients was different for subgroups with multiple risk scores and few risk scores.

**Receiver operating characteristics** We estimated the discriminatory power between glucose-tolerant individuals and type 2 diabetes patients of the 19 susceptibility variants by applying ROC. We used logistic regression including all

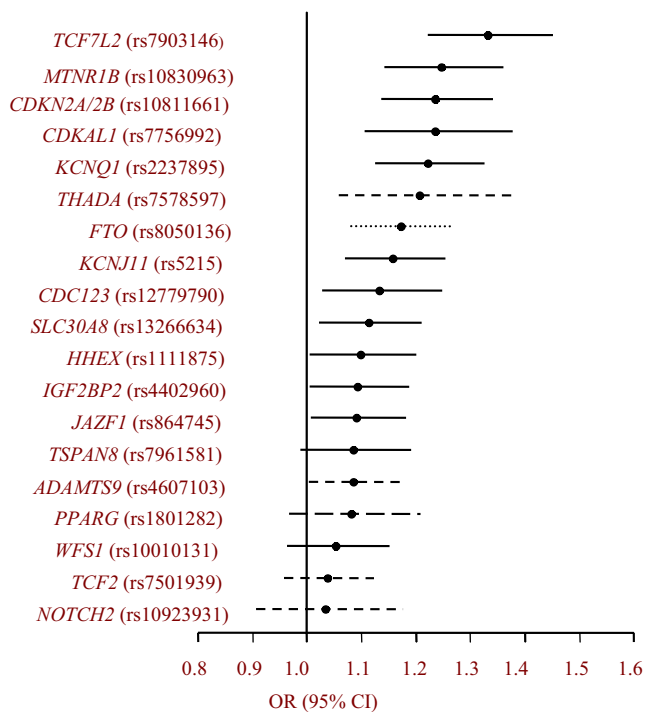
variants coded as 0, 1 or 2 according to the number of risk alleles. In order to cross-validate the results, bootstrapping ( $n=50$ ) was applied. Cross-validation works by fitting the same model in different bootstraps (subsets of the original data). The remaining subsets (out-of-bag data) are used for the selectivity of the fitted model. For each ROC, an area under the curve is used as a measure of the predictive power of the method. Each ROC curve in the present paper consists of the result of all bootstraps, the mean ROC estimated from the bootstrap samples by taking the mean of the bootstrap sample at each 1–selectivity point and the apparent ROC curve which are estimated from the entire dataset. All analyses were performed using RGui version 2.7.0, applying the *per* package (<http://www.r-project.org>, accessed 1 May 2008).

## Results

The clinical characteristics of all participants in the three study samples are reported in Electronic supplementary material (ESM) Table 1. We estimated the association of each of the 19 validated variants on type 2 diabetes risk by applying a multiplicative genetic model. Results of the risk of susceptibility variants adjusted for sex, age and BMI can be found in ESM Fig. 1. However, here we focus on results adjusted for sex and age as BMI is an effect modifier compared with sex and age, which are considered confounders (Fig. 1).

The minor alleles of *CDKN2A*, *THADA*, *JAZF1*, *HHEX* and *SLC30A8* variants were associated with a decreased risk of developing type 2 diabetes, whereas the minor alleles of *TCF7L2*, *CDKAL1*, *KCNQ1*, *FTO*, *KCNJ11*, *TSPAN8*, *CDC123*, *MTNR1B*, and *IGF2BP2* variants were associated with an increased risk of type 2 diabetes. As for the remaining loci, no association was observed although the directions were consistent with previous reports. The OR for each individual variant ranged from 1.04 (95% CI 0.98–1.11; *NOTCH2*; i.e. no association) to 1.33 (95% CI 1.22–1.45) for *TCF7L2*, so far the largest risk effect of all common type 2 diabetes loci. As for the result of the single-variant analysis all data have been published previously [8, 12, 13, 21–23, 36–38].

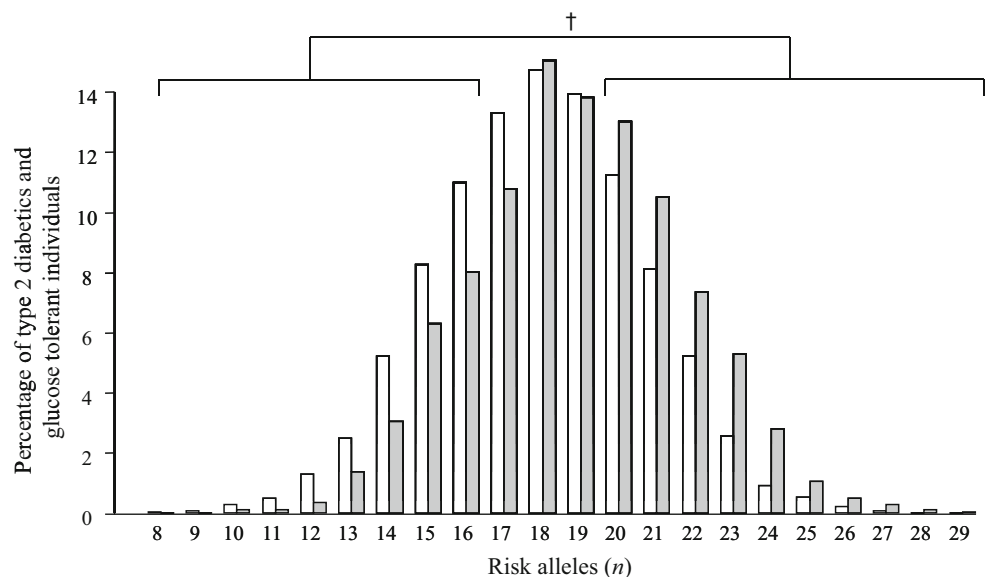
The combined effect of the 19 variants was estimated by calculating the percentage of glucose-tolerant individuals and type 2 diabetic patients stratified according to the number of risk alleles (Fig. 2). We demonstrate that, on average, type 2 diabetic patients carry more risk alleles and thus the curve is shifted right compared with the curve of glucose-tolerant individuals (Fig. 2). By stratifying the number of risk alleles into quartiles we estimated OR 2.13 (95% CI 1.85–2.47,  $p=4.91\times 10^{-26}$ ) between the lowest quartile (number of risk alleles  $\leq 16$ ,  $n=1,404$ ) and the



**Fig. 1** ORs and 95% CIs of the 19 validated variants for type 2 diabetes using a genetic multiplicative model adjusted for sex and age. The risk alleles of the 19 variants are defined as the alleles associated with type 2 diabetes in accordance with the literature [5–18]. The 19 variants may exert their diabetogenic effects through: beta cell dysfunction (solid line); altered BMI (dotted line); changes in insulin sensitivity (dashed/dotted line); and unknown mechanisms (dashed line)

uppermost quartile (number of risk alleles  $\geq 20$ ,  $n=1,927$ ). In addition, if we stratify the individuals into subgroups of extreme risk allele profiles by comparing the lower 10% (carriers of eight to 15 risk alleles) with the upper 10%

**Fig. 2** The percentage of glucose-tolerant individuals (white bars) and type 2 diabetes patients (grey bars) stratified according to number of risk alleles of the 19 validated type 2 diabetes variants. The OR is calculated using Fisher’s exact test as number of glucose-tolerant individuals and type 2 diabetes patients carrying  $\leq 16$  risk alleles (the lowest quartile) vs the number of glucose-tolerant individuals and type 2 diabetes patients carrying  $\geq 20$  risk alleles (uppermost quartile). †OR 2.13,  $p=4.0 \times 10^{-26}$



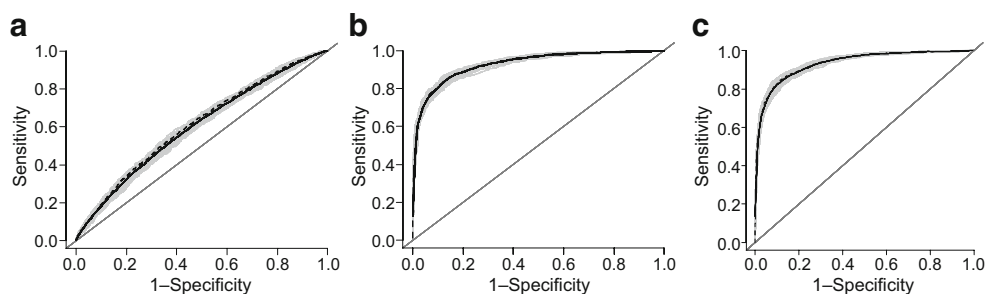
(carriers of 22 to 29 risk alleles) we estimate OR 2.93 (95% CI 2.38–3.62,  $p = 1.6 \times 10^{-25}$ ).

The discriminatory value of a genetic test based on the 19 type 2 diabetes susceptibility variants was calculated as the area under the ROC, which is a graphical plot of the sensitivity vs (1–specificity). The area under the ROC was estimated to 0.60 (Fig. 3a). We also tested whether the 19 susceptibility variants added to the discriminatory power when accounting for known type 2 diabetes risk factors such as BMI, age and sex (Fig. 3b). A model that includes only BMI, age and sex has an AUC of 0.92 and after applying the 19 susceptibility variants an AUC of 0.93 was achieved (Fig. 3c).

Finally we estimated the two-way interaction between each combination of the 19 variants (171 combinations) (ESM Table 1) and the result demonstrated few, probably spurious, associations ( $p < 0.05$ ). As none of the associations was significant after Bonferroni correction we believe that an additive model between each variant is acceptable. Additionally, we calculated the AUC under an ROC curve in which a model including all variants (additive) is compared with a model including a two-way interaction term in addition to the variants (interaction). The results showed that if interaction is included an AUC of 0.56 is reached, which indicates reduced discriminatory value (ESM Fig. 2).

**Discussion**

In our analyses, in which we applied ROC to demonstrate the discriminatory value between 5,302 glucose-tolerant individuals and 4,093 type 2 diabetes patients of the combined effect of 19 validated type 2 diabetes suscepti-



**Fig. 3** ROC curves for the discrimination between glucose-tolerant individuals and type 2 diabetes patients. The grey shadow represents ROC curves obtained in the process of bootstrap cross-validation ( $n=50$ ). The mean of the bootstrapping ROC curves is presented as a thin solid line. The dotted line represents the apparent ROC curve estimated from the original data. **a** The mean AUC of the bootstrap

samples (thick solid line) based on the 19 type 2 diabetes susceptibility variants (AUC 0.60). **b** The mean AUC of the bootstrap samples when including conventional type 2 diabetes risk factors (BMI, age and sex) (AUC 0.92). **c** The mean AUC of the bootstrap when including the 19 susceptibility variants and clinical type 2 diabetes risk factors (BMI, age and sex) (AUC 0.93)

bility variants, we were able to identify subgroups with substantial increases in risk of type 2 diabetes. For instance, in a subgroup of individuals carrying more than 22 risk alleles we estimated an odds ratio of 2.93 (95% CI 2.38–3.62,  $p=1.6 \times 10^{-25}$ ) compared with individuals carrying fewer than 15 risk alleles. However, when evaluating the general ability to discriminate between glucose-tolerant individuals and type 2 diabetes patients, assessed by the area under an ROC curve, we estimated an AUC of 0.60. The ROC analyses in the same study samples of the corresponding discriminatory value of conventional risk factors such as BMI, age and sex resulted in an AUC of 0.92 and when the 19 susceptibility variants were included an AUC of 0.93. Thus, although tremendous progress in finding type 2 diabetes susceptibility genes has recently taken place, the discriminatory value of the common genetic variations is still too limited to be of clinical importance. For illustration, if we screen a sample of individuals for the 19 type 2 diabetes susceptibility genes and we want to detect 80% of the type 2 diabetic patients, we have to account for the fact that 70% of the healthy individuals are misclassified as type 2 diabetic patients (Fig. 3a).

Our results are in line with the conclusions from recent cross-sectional and longitudinal studies assessing the combined impact of several risk alleles on type 2 diabetes risk [27–32]. In the recent prospective study by Lyssenko et al., it was demonstrated that the addition of 16 type 2 diabetes susceptibility variants to clinical risk factors improved the prediction of future type 2 diabetes assessed by the area under an ROC curve from 0.74 to 0.75 [31].

A major limitation in the current and previous comparable cross-sectional studies is the fact that case–control designs are used that comprise approximately equal numbers of glucose-tolerant individuals and type 2 diabetic patients. As a result, the discriminatory value is overestimated as the prevalence rate at the population level constitutes approxi-

mately 6% compared with a case–control design which often includes equal numbers of cases and controls. Another limitation when calculating the OR between carriers of multiple risk alleles and few risk alleles is the fact that each risk allele is assigned the same effect. This limitation, however, is overcome when calculating ROC curves where each SNP is assigned an individual effect size. Also, when we run the ROC analyses with age included we introduce an overestimation of the discriminatory value as the majority of the type 2 diabetic patients in most studies are older than the glucose-tolerant individuals.

Gene–gene interaction, the fact that one gene variant masks or enhances the effect of another variant significantly affecting a disease association, has been discussed as one of the promising tools to explain the variation in type 2 diabetes risk. A recent study suggested a significant interaction between variants in *IGF2BP2* and *LOC38776*, *SLC30A8* and *HHEX* on risk of type 2 diabetes [28]; these variants are all known to mediate the pathogenic effect through an abnormal beta cell function. Indeed we also attempted to replicate such findings by estimating the two-way interaction between the 19 variants. The result demonstrated sporadic nominally significant interactions which are most likely to be due to type 1 errors and are not consistent with any of the previous findings [28]. A possible explanation may be a lack of statistical power, as the 19 susceptibility variants investigated here confer a modestly increased risk of type 2 diabetes. Based on 95% confidence interval estimates of the effect size, we can in the current study exclude a gene–gene interaction OR above 2.6 between two variants on type 2 diabetes risk (data not shown). The suggestion that only additivity between the examined type 2 diabetes variants appears to exist is also emphasised in ESM Fig. 2 where the discrimination value is reduced when including possible two-way genetic interaction terms. The results seem to be in line with previous studies [29, 30].

In the present paper we have investigated common variants with a low penetrance in the general population and demonstrated limited success in the discrimination of glucose-tolerant individuals and type 2 diabetes patients based on the genetic profile. Janssens et al. [39] investigated the usefulness of genomic profiling in the general population by simulating a population of 1 million individuals carrying 40 genotypes under different scenarios. The study demonstrated that common variants with low penetrance have little predictive power as we also show in the present paper. In contrast, it has been proposed that accumulation of rare variants with a mildly deleterious effect may substantially increase the relative risk at the individual level [40]. Indeed, with the next generation of sequencing technologies enabling gene-specific re-sequencing of the entire human genome, rare variants may be identified that in combination may contribute substantially to the risk of type 2 diabetes. Such results together with the known common susceptibility variants may increase the discriminative value of genetic risk factors and push the limit towards a threshold acceptable for clinical utility.

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