CLINICAL STUDY

Two common genetic variants near nuclear-encoded OXPHOS genes are associated with insulin secretion in vivo

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Abstract

Context: Mitochondrial ATP production is important in the regulation of glucose-stimulated insulin secretion. Genetic factors may modulate the capacity of the β-cells to secrete insulin and thereby contribute to the risk of type 2 diabetes.

Objective: The aim of this study was to identify genetic loci in or adjacent to nuclear-encoded genes of the oxidative phosphorylation (OXPHOS) pathway that are associated with insulin secretion in vivo.

Design and methods: To find polymorphisms associated with glucose-stimulated insulin secretion, data from a genome-wide association study (GWAS) of 1467 non-diabetic individuals, including the Diabetes Genetic Initiative (DGI), was examined. A total of 413 single nucleotide polymorphisms with a minor allele frequency ≥0.05 located in or adjacent to 76 OXPHOS genes were included in the DGI GWAS. A more extensive population-based study of 4323 non-diabetics, the PPP-Botnia, was used as a replication cohort. Insulinogenic index during an oral glucose tolerance test was used as a surrogate marker of glucose-stimulated insulin secretion. Multivariate linear regression analyses were used to test genotype-phenotype associations.

Results: Two common variants were identified in the DGI, where the major C-allele of rs606164, adjacent to NADH dehydrogenase (ubiquinone) 1 subunit C2 (NDUFC2), and the minor G-allele of rs1323070, adjacent to cytochrome c oxidase subunit VIIa polypeptide 2 (COX7A2), showed nominal associations with decreased glucose-stimulated insulin secretion (P = 0.0009, respective P = 0.003). These associations were replicated in PPP-Botnia (P = 0.002 and P = 0.05).

Conclusion: Our study shows that genetic variation near genes involved in OXPHOS may influence glucose-stimulated insulin secretion in vivo.

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Introduction

Type 2 diabetes is a heterogeneous disease where multiple genes and environmental factors combine to cause the disease. Genetic factors may directly affect the risk of type 2 diabetes by modulating the capacity of the β-cells to secrete insulin and/or by inducing insulin resistance in target tissues. Mitochondrial dysfunction has been suggested to contribute to both impaired insulin secretion and insulin resistance (1, 2). In pancreatic β-cells, mitochondria play a key role in regulating insulin secretion. Oxidative phosphorylation (OXPHOS) by the respiratory chain, which contains five enzyme complexes embedded in the mitochondrial inner membrane, is coupled to conversion of ADP into ATP. Elevated plasma glucose levels will cause a rise in the β-cell ATP/ADP ratio, which is a main trigger for insulin secretion (3). Mitochondrial dysfunction could thereby lead to impaired insulin secretion from the β-cells and subsequently to an increased risk of type 2 diabetes. The multi-protein complexes in the OXPHOS system contain ~90 protein subunits encoded by both the nuclear and mitochondrial genomes (4), where the mitochondrial genome encodes 13 of the subunits present. A previous study from our group has shown the mRNA expression of peroxisome proliferator-activated receptor gamma coactivator 1 alpha (PPARGC1A), a master regulator of mitochondrial genes, to be reduced in islets from patients with type 2 diabetes and this reduction correlates with impaired glucose-stimulated insulin secretion (5). In addition, a common polymorphism (rs8192678) influences PPARGC1A mRNA expression and insulin secretion in the human islets. Even though a mutation in mitochondrial DNA has been found in a rare but specific form of diabetes (maternally inherited diabetes and diabetes), even though a mutation in mitochondrial DNA has been found in a rare but specific form of diabetes (maternally inherited diabetes and
Subjects and methods

Study populations

The DGI is a case–control-based study, where patients with type 2 diabetes, geographically matched controls and discordant sibships were selected from Finland and Sweden (13). Patients with type 2 diabetes were classified according to WHO (1999) criteria with fasting plasma glucose ≥7.0 mmol/l or a 2 h glucose ≥11.1 mmol/l during an oral glucose tolerance test (OGTT) and 1464 patients were included in the DGI. Non-diabetic subjects were defined as normal glucose tolerant, with fasting plasma glucose <6.1 mmol/l and 2 h glucose <7.8 mmol/l. Population-based non-diabetic subjects had no first-degree relatives with type 2 diabetes and included 1467 individuals (Table 1) (13). Only non-diabetic subjects were included in the current study.

Table 1 Clinical characteristics of non-diabetic participants in the DGI and the PPP-Botnia. Data are expressed as mean ± s.d. or median (IQR). Insulinogenic index: calculated as ((insulin at 30 min−insulin at 0 min)/(glucose at 30 min−glucose at 0 min)). HOMA-IR: calculated as ((glucose at 0 min × insulin at 0 min)/22.5).

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>DGI</th>
<th>PPP-Botnia</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (male/female)</td>
<td>1467 (707/760)</td>
<td>4323 (2043/2280)</td>
</tr>
<tr>
<td>Age (years)</td>
<td>58.8 ± 10.1</td>
<td>47.6 ± 15.2</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>26.6 ± 3.7</td>
<td>26.3 ± 4.3</td>
</tr>
<tr>
<td>Fasting glucose (mmol/l)</td>
<td>5.3 ± 0.5</td>
<td>5.3 ± 0.6</td>
</tr>
<tr>
<td>Glucose 30 min (mmol/l)</td>
<td>8.3 ± 1.5</td>
<td>8.3 ± 1.6</td>
</tr>
<tr>
<td>Glucose 120 min (mmol/l)</td>
<td>5.6 ± 1.3</td>
<td>5.2 ± 1.6</td>
</tr>
<tr>
<td>Fasting insulin (μU/l)</td>
<td>5.2 (4.3)</td>
<td>5.3 (4.2)</td>
</tr>
<tr>
<td>Insulin 30 min (μU/l)</td>
<td>50.2 (48.9)</td>
<td>50.4 (38.3)</td>
</tr>
<tr>
<td>Insulin 120 min (μU/l)</td>
<td>36.2 (29.7)</td>
<td>23.7 (26.2)</td>
</tr>
<tr>
<td>Insulinogenic index</td>
<td>14.1 (14.8)</td>
<td>15.9 (16.1)</td>
</tr>
<tr>
<td>HOMA-IR</td>
<td>1.46 (1.08)</td>
<td>1.28 (1.04)</td>
</tr>
</tbody>
</table>

Prevalence, Prediction and Prevention of diabetes (PPP-Botnia) is a population-based study in the Botnia region of Western Finland (14). The participants were aged 18–75 years (mean age 48.4 ± 15.6 years). Diagnosis of type 2 diabetes was confirmed from subject records or on the basis of fasting plasma glucose concentration ≥7.0 mmol/l and/or 2 h glucose ≥11.1 mmol/l. Only non-diabetic subjects (n=4323) were included in the current study, where 612 (14%) had fasting plasma glucose levels between 6.1 and 6.9 mmol/l (Table 1).

All participants gave written informed consent for the studies and the local ethics committees approved the protocols.

Assays and measurements

Blood samples for measurements of plasma glucose and serum insulin concentrations were drawn at 0, 30 and 120 min of the 75 g OGTT in both DGI and PPP-Botnia.

Plasma glucose was measured in DGI with a glucose oxidase method (Beckman Glucose Analyzer, Beckman Instruments, Fullerton, CA, USA) and in PPP-Botnia with a glucose dehydrogenase method (HemoCue, Ängelholm, Sweden). Three different methods for measurement of insulin concentrations were used in both DGI and PPP-Botnia: RIA (Pharmacia), enzyme linked immunooassay (DAKO Diagnostics Ltd, Cambridgeshire, UK) and fluoroimmunoassay (Delphia, Perkin-Elmer Finland, Turku, Finland). The Pharmacia and Delphia values were transformed into ‘Dako’ values using validated correction coefficients.

β-cell function and glucose-stimulated insulin secretion were assessed as insulinogenic index during an OGTT ((insulin at 30 min−insulin at 0 min)/(glucose at 30 min−glucose at 0 min)) (15). Insulin resistance estimated by the homeostasis model assessment (HOMA-IR) was calculated as ((glucose at 0 min × insulin at 0 min)/22.5). β-Cell function was also assessed in PPP-Botnia as disposition index, insulin secretion adjusted for insulin resistance (insulinogenic index/HOMA-IR).

Identification of single nucleotide polymorphisms in the DGI GWAS

We aimed at identifying single nucleotide polymorphisms (SNPs) situated in a region 25 kb upstream and 25 kb downstream of nuclear-encoded OXPHOS genes with a minor allele frequency (MAF) ≥0.05, showing nominal associations (P ≤ 0.01) with insulinogenic index in non-diabetic subjects in the DGI GWAS (13). Identified polymorphisms were ranked based on the P values of genotype–phenotype association. The GeneChip Human Mapping 500K Array Set (Affymetrix, Inc., Santa Clara, CA, USA) used in the DGI GWAS has coverage in the CEU HapMap population (r² ≤ 0.8) of 67%, based on single marker test. In the DGI GWAS,
413 SNPs within or near 76 OXPHOS genes fulfilled the MAF criteria (Supplementary Table 1, see section on supplementary data given at the end of this article) and nine of these SNPs were also nominally associated with insulinogenic index ($P \leq 0.01$). The two top hits were selected for follow-up in an independent cohort.

Genotyping

In the DGI GWAS, genotyping was performed using Affymetrix 500K chip array (13). In PPP-Botnia, rs606164 and rs1323070 were genotyped using allelic discrimination assays on the ABI 7900 platform (C__2983373_10 and C__3073719_10, Applied Biosystems, Foster City, CA, USA). The genotyping success rates were >95.5% and the concordance rate was 100% based on 4.2% duplicate comparisons.

Statistical analyses

Linear regression analyses were performed to test genotype–phenotype associations, assuming additive genetic models in both DGI and PPP-Botnia. Phenotype values were logarithmically transformed to fit a normal distribution in both cohorts before analyses.

In DGI, $z$-scores of insulinogenic index were prepared separately by gender and recruiting region (Botnia, Skara, Malmö or Helsinki) and regressed against genotype adjusted for age, log body mass index (BMI) and type of insulin measurement. Unrelated individuals and siblings were included in this analysis. To correct for inflation caused by inclusion of related individuals, the genomic control inflation factor based on the median test statistic was estimated, and $P$ values based on the test statistic adjusted by this factor are reported (13).

In PPP-Botnia, the log-transformed phenotype values were regressed against genotype adjusted for age, sex and BMI.

All analyses were carried out in non-diabetic individuals. Results are presented as median (inter-quartile range) or $\beta$ coefficient (s.e.m.). Statistical analyses were performed using SPSS version 17 for Windows (SPSS, Chicago, IL, USA) or using STATA/SE 10.0 (STATA Corp. LP, College Station, TX, USA).

Results

Identification of genetic loci associated with insulin secretion

To find genetic loci associated with insulin secretion in or adjacent to nuclear-encoded genes of the respiratory chain, we examined data from the DGI GWAS (13) (Table 1). Nine SNPs representing six genes were identified based on a MAF $\geq 0.05$, nominal associations to insulinogenic index with $P \leq 0.01$ and they are located in regions of 25 kb upstream or downstream of OXPHOS genes (Table 2). Region plots of the six identified OXPHOS genes are presented together with $-\log_{10} P$ values of all SNPs within these regions from the DGI GWAS as well as Haploview presentations of the LD-structure based on HapMap data (Supplementary Figure 1A–F, see section on supplementary data given at the end of this article). Based on the lowest $P$ values, two SNPs were selected for follow-up: rs606164, 12 kb upstream of NDUF2, and rs1323070, 24 kb downstream of COX7A2. The major C-allele of rs606164 and the minor G-allele of rs1323070 are nominally associated with decreased glucose-stimulated insulin secretion during an OGTT (insulinogenic index) in non-diabetic subjects of DGI (rs606164: $\beta = -0.21 \pm 0.062$, $P = 0.0009$ and rs1323070: $\beta = -0.14 \pm 0.046$, $P = 0.003$). The common variant rs606164 was not in LD with any of the other two SNPs identified in DGI located adjacent to NDUF2 (Table 2 and Supplementary Figure 1A, see section on supplementary data given at the end of this article). None of the variants

Table 2 SNPs identified from DGI GWAS located in a region of $\sim 25$ kb upstream or downstream of OXPHOS genes with an association to insulinogenic index in non-diabetic individuals of DGI with $P \leq 0.01$ and MAF $\geq 0.05$. In DGI $P$ values are based on linear regression to test association between genotype and insulinogenic index $z$-score with the covariates gender, recruiting region, age, BMI and type of insulin measurement. A genomic control inflation factor was used to adjust for related individuals.

<table>
<thead>
<tr>
<th>SNP</th>
<th>Chromosome</th>
<th>Nearest OXPHOS gene</th>
<th>Alleles$^a$ (major/minor)</th>
<th>MAF</th>
<th>$\beta$ (s.e.m.)</th>
<th>$P$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs606164</td>
<td>11</td>
<td>$\sim 12$ kb upstream NDUF2</td>
<td>C/G</td>
<td>0.16</td>
<td>$-0.21 (0.062)$</td>
<td>$9 \times 10^{-4}$</td>
</tr>
<tr>
<td>rs1323070</td>
<td>6</td>
<td>$\sim 24$ kb downstream COX7A2</td>
<td>A/G</td>
<td>0.36</td>
<td>$-0.14 (0.046)$</td>
<td>$3 \times 10^{-3}$</td>
</tr>
<tr>
<td>rs10793285</td>
<td>11</td>
<td>$\sim 20$ kb upstream NDUF2</td>
<td>T/G</td>
<td>0.36</td>
<td>$-0.12 (0.044)$</td>
<td>$6 \times 10^{-3}$</td>
</tr>
<tr>
<td>rs1133322</td>
<td>15</td>
<td>$\sim 0.3$ kb downstream COX5</td>
<td>A/G</td>
<td>0.49</td>
<td>$-0.13 (0.045)$</td>
<td>$7 \times 10^{-3}$</td>
</tr>
<tr>
<td>rs2643338</td>
<td>8</td>
<td>Intron UOCR6</td>
<td>A/G</td>
<td>0.47</td>
<td>$-0.12 (0.045)$</td>
<td>$1 \times 10^{-2}$</td>
</tr>
<tr>
<td>rs7827095</td>
<td>8</td>
<td>$\sim 3$ kb downstream UOCR6</td>
<td>T/C</td>
<td>0.47</td>
<td>$-0.12 (0.045)$</td>
<td>$1 \times 10^{-2}$</td>
</tr>
<tr>
<td>rs10734905</td>
<td>12</td>
<td>Intron ATP6OA2</td>
<td>G/T</td>
<td>0.32</td>
<td>$-0.13 (0.049)$</td>
<td>$1 \times 10^{-2}$</td>
</tr>
<tr>
<td>rs1264913</td>
<td>1</td>
<td>$\sim 15$ kb upstream ATP5F1</td>
<td>A/G</td>
<td>0.11</td>
<td>$-0.18 (0.071)$</td>
<td>$1 \times 10^{-2}$</td>
</tr>
<tr>
<td>rs2845556</td>
<td>11</td>
<td>$\sim 20$ kb upstream NDUF2</td>
<td>C/T</td>
<td>0.49</td>
<td>$-0.12 (0.046)$</td>
<td>$1 \times 10^{-2}$</td>
</tr>
</tbody>
</table>

MAF: minor-allele frequency.

$^a$Allele denoted in bold associated with decreased insulinogenic index.
were associated with type 2 diabetes in the case-control-based study of DGI GWAS or insulin resistance (HOMA-IR) in non-diabetic subjects of DGI (13) (Supplementary Table 1, see section on supplementary data given at the end of this article).

**Insulin secretion in vivo**

We next investigated whether the NDUFC2 variant, rs606164, and COX7A2 variant, rs1323070, were associated with insulin secretion in a more extensive replication cohort, the PPP-Botnia Study (14) (Table 1). In line with the findings in DGI, C-allele carriers of rs606164 showed decreased insulinogenic index in the PPP-Botnia study (β = -0.070 ± 0.022, P = 0.002) (Table 3). Moreover, G-allele carriers of rs1323070 showed a nominal association with insulinogenic index in PPP-Botnia (β = -0.040 ± 0.021, P = 0.05) (Table 3). Disposition index is an additional assessment of β-cell function that considers the insulin resistance–secretion relationship. When analysing disposition-index, C-allele carriers of rs606164 and G-allele carriers of rs1323070 also showed a decreased insulin secretion adjusted for insulin resistance in PPP-Botnia (rs606164: β = -0.066 ± 0.023, P = 0.007; rs1323070: β = -0.040 ± 0.019, P = 0.03). Neither rs606164 nor rs1323070 was associated with HOMA-IR in PPP-Botnia (P = 0.79 and P = 0.57, respectively).

**Discussion**

In this study, we have demonstrated that two common polymorphisms, rs606164 adjacent to NDUFC2 and rs1323070 adjacent to COX7A2, are associated with insulin secretion in vivo. Insulin secretion was measured as insulinogenic index at 30 min, a well-known measure of early-phase insulin secretion during an OGTT (15, 16).

Mitochondrial ATP production by OXPHOS in the respiratory chain is necessary for glucose-stimulated insulin release by β-cells (17). Insulin secretion is impaired in pancreatic islets from patients with type 2 diabetes partially due to impaired hyperpolarization of the inner mitochondrial membrane and a failure to respond with a rise in ATP levels (18), but the number of identified polymorphisms in genes of the OXPHOS process associated with type 2 diabetes and its risk factors are limited.

Recent GWAS have focused on identifying genes associated with type 2 diabetes and, today, more than 35 common variants have been identified that affect the risk of the disease (13, 19–28). Although many of these variants seem to affect the β-cell function and insulin secretion (29, 30), only a few GWAS have included measurements of glucose-stimulated insulin secretion (31). Due to the importance of OXPHOS in the regulation of insulin secretion, we examined if common variants near nuclear-encoded genes of the respiratory chain affect glucose-stimulated insulin secretion, using data from a GWAS, the DGI. The identification of variants was based on one trait and for variants in genes of one specific molecular pathway. Among variants near genes of the respiratory chain, rs606164 and rs1323070 showed the strongest associations with insulinogenic index in DGI. Although these associations were not genome-wide significant in the DGI, one should keep in mind that the study was underpowered for these associations, as they could only reliably be assessed for non-diabetic individuals. We therefore used a lower threshold for selection of SNPs for replication in an independent study, PPP-Botnia. Our inclusion criterium was to identify SNPs near nuclear-encoded OXPHOS genes, which are associated with insulinogenic index with P ≤ 0.01 and a MAF ≥ 0.05. Nine variants fulfilled the criterium.

To confirm the association of the two top hits, we replicated the results in a more extensive population-based cohort, the PPP-Botnia study from Western Finland (14). In accordance with DGI, C-allele carriers of rs606164 showed decreased insulin secretion and there was a nominal association between rs1323070 and insulin secretion in PPP-Botnia. This effect was maintained when adjusting for insulin resistance by using disposition index. The inclusion of individuals with impaired fasting glucose (IFG) in PPP-Botnia did not affect our findings, since an association between rs606164 and insulinogenic index as well as a trend towards association for rs1323070 was observed even when individuals with IFG were excluded.

The common variant rs606164 is located 12 kb upstream of the NDUFC2 gene, a position where genetic

**Table 3** Effects of rs606164 and rs1323070 on insulinogenic index in non-diabetic individuals of the PPP-Botnia study. Data are expressed as median (IQR). β coefficients (s.e.m.) are from linear regression analyses adjusted for age, sex and BMI based on an additive model.

<table>
<thead>
<tr>
<th>Study</th>
<th>SNP</th>
<th>Phenotype</th>
<th>Genotypes (genotype frequency)</th>
<th>β</th>
<th>s.e.m.</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>PPP-Botnia</td>
<td>rs606164</td>
<td>Insulinogenic index</td>
<td>GG (0.024)</td>
<td>19.08 (14.54)</td>
<td>CG (0.285)</td>
<td>16.42 (15.92)</td>
</tr>
<tr>
<td>(n=4201)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PPP-Botnia</td>
<td>rs1323070</td>
<td>Insulinogenic index</td>
<td>AA (0.432)</td>
<td>16.17 (16.13)</td>
<td>AG (0.441)</td>
<td>15.90 (15.81)</td>
</tr>
<tr>
<td>(n=4140)</td>
<td></td>
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<td></td>
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</tbody>
</table>

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variation may influence gene transcription. NDUFC2 encodes NADH dehydrogenase (ubiquinone) 1 subunit C2, which is located in complex I of the electron transport chain. Complex I is the largest component of the OXPHOS system and entry point of electrons from NADH into the electron transport chain, thereby playing a key role in regulating OXPHOS. NDUFC2 and its flanking genes, thyroid hormone responsive (THRS) and asparagine-linked glycosylation 8 (ALG8), appear to be conserved among chickens, humans, mice and rats. Since rs606164 are in LD with SNPs located in both THRS and ALG8, we cannot exclude that the effect on insulin secretion is mediated by these genes. However, based on the function of these genes, they are not likely to be involved in the regulation of insulin secretion, and we therefore suggest that the found association between rs606164 and insulinogenic index is mediated via NDUFC2.

The position of rs1323070 is ~24 kb downstream of COX7A2. COX7A2 encodes cytochrome c oxidase VIIa polypeptide 2, which is located in complex IV of the electron transport chain. Complex IV catalyses the mitochondrial electron transfers from cytochrome c to the reduction of oxygen to water. Although the location of rs1323070 is downstream of COX7A2 and not in LD with any SNP within this OXPHOS gene, it may affect the expression of COX7A2. It is also possible that rs1323070 influences a gene upstream of the SNP or a so far unknown regulatory region that mediates the effect on insulin secretion. Taken together, common polymorphisms in or near genes involved in OXPHOS may be of importance in insulin secretion and/or the pathogenesis of type 2 diabetes.

In conclusion, we have identified two polymorphisms associated with glucose-stimulated insulin secretion in vivo. These polymorphisms, rs606164 and rs1323070, are located adjacent to nuclear-encoded genes involved in OXPHOS. This is an exploratory follow-up study of a published GWAS, DGI, where we have selected SNPs nominal associated with insulin secretion for replication in an independent study. It remains to be seen whether the findings can be replicated in even larger studies and influence the risk of type 2 diabetes.

**Supplementary data**

This is linked to the online version of the paper at http://dx.doi.org/10.1530/EJE-10-0995.

**Declaration of interest**

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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**References**


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SNPs near OXPHOS genes and insulin secretion

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