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GENETICS OF TYPE 2 DIABETES AND THE METABOLIC SYNDROME

ACADEMIC DISSERTATION

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M.Sc.

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FACULTY OF MEDICINE
Lund University

To be presented, with the permission of the Medical Faculty of Lund University for public examination in
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Medicinskt Forsknings Centrum (MFC), Malmö University Hospital
entrance 59,
on September 21st, 2001 at 13.15.

Faculty Opponent
Professor Christian Ehnholm, National Institute of Health, Finland
GENETICS OF TYPE 2 DIABETES AND THE METABOLIC SYNDROME

AKADEMISK AVHANDLING

Mia Klannemark
Fil. Mag.

Institutionen för Medicin, Kirurgi och Ortopedi, Malmö
Avdelningen för Endokrinologi
Lunds Universitet

MEDICINSKA FAKULTETEN
Lunds Universitet

som med vederbörligt tillstånd av Medicinska Fakulteten vid Lunds
Universitet för avläggande av doktorsexamen i medicinska vetenskaper
kommer att offentligen försvaras i
Jubileumsaulan, Medicinskt Forskningscentrum
Universitetssjukhuset MAS, ingång 59

Fakultetsopponent
Professor Christian Ehnholm, National Institute of Health, Finland
Type 2 diabetes and the metabolic syndrome are highly prevalent disorders with severe complications such as cardiovascular disease. The aetiology of type 2 diabetes and the metabolic syndrome is not known, but the interaction between genetic factors and environmental triggers is important. The aim this thesis was to identify genetic factors that may increase susceptibility to these disorders by investigating candidate genes regulating lipolysis (hormone-sensitive lipase, HSL, lipoprotein lipase, LPL and phosphodiesterase 3B, PDE3B), thermogenesis (uncoupling protein 2, UCP2) and adipogenesis (peroxisome proliferator-activated receptor gamma, PPARG). Four of the genes were screened for mutations and identified variants were tested for association in large intra-familial and case-control association studies. Variability in the UCP2 gene was not associated with alterations in basal metabolic rate or with obesity. The gene encoding HSL was associated with type 2 diabetes in a case-control study, and the LIPE marker of the HSL gene showed distorted transmission to abdominally obese offspring. The PDE3B gene was associated with hyperinsulinaemia in genotype-discordant siblings. Haplotypes including several variants on chromosome 11 were unequally transmitted to offspring with abnormal glucose tolerance. The studies also provided evidence for an interaction between a variant in the LPL gene and insulin sensitivity. In a large, family-based multi-step study we could show that genetic variability in the gene encoding PPARG is associated with a reduced risk for diabetes, supported by the consistent results in a meta-analysis on the same variant. In conclusion, variability in genes regulating lipolysis and adipogenesis increase susceptibility to type 2 diabetes and the metabolic syndrome. Prospective studies will be helpful to establish the risk associated with the potential genetic risk factors presented in this thesis.

**Key words:** diabetes, metabolic syndrome, UCP2, HSL, LPL, PPARG, PDE3B
I want to know God’s thoughts.
The rest are details.

*Albert Einstein*
As far as the laws of mathematics refer to reality they are not certain, and as far as they are certain, they do not refer to reality.

Albert Einstein
Scientific papers included in this thesis


# Contents

## Abbreviations

1. Identification of the disease(s)  
   1.1 The metabolic syndrome  
   1.2 Diabetes mellitus  
   1.3 Dyslipidaemia  
   1.4 Obesity and abdominal obesity  
   1.5 Hypertension  
   1.6 Microalbuminuria  
   1.7 Treatment

2. Heritability of diabetes and the metabolic syndrome  
   2.1 How do we know if a disease has genetic components?  
   2.2 Complex genetic disease  
   2.3 Quantitative traits and polygenic disease  
   2.4 Thrifty genes  
   2.5 Thrifty phenotypes  
   2.6 Evidence that type 2 diabetes is inherited  
   2.7 Evidence that dyslipidaemia is inherited  
   2.8 Evidence that obesity is inherited  
   2.9 Is the metabolic syndrome inherited?  
   2.10 Are there one or several heritable traits of the metabolic syndrome?

3. Adipose tissue, lipolysis and energy expenditure  
   3.1 Adipogenesis  
   3.2 Adipose tissue and metabolism  
   3.3 Free fatty acids (FFAs)  
   3.4 Lipolysis  
   3.5 Energy expenditure and uncoupling proteins

4. Candidate genes that may contribute to type 2 diabetes and the metabolic syndrome  
   4.1 Uncoupling protein 2 (UCP2)  
   4.2 Hormone-sensitive lipase (HSL)  
   4.3 Lipoprotein lipase (LPL)
5. The aims of this thesis

6. Methodology

6.1 Study subjects
6.2 Phenotypic characterisation
6.3 Assays
6.4 Genotyping
6.4.1 PCR
6.4.2 Genotyping by PCR-RFLP
6.4.3 Genotyping by radioactive PCR
6.4.5 Genotyping by radioactive PCR-SBE
6.4.6 Genotyping by PCR-SBE with fluorescent detection
6.5 Mutation screening (SSCP) and sequencing
6.6 Determination of exon/intron boundaries of the UCP2 gene
6.7 Determination of the region upstream of the first coding exon of the UCP2 gene
6.8 Statistical analyses
6.8.1 Case-control studies
6.8.2 Transmission disequilibrium test (qualitative) (TDT)
6.8.3 Quantitative transmission disequilibrium test (QTDT)
6.8.4 Genotype-discordant sibling pair analysis
6.8.5 Discordant alleles test
6.8.6 Population attributable risk

7. Summary of studies I-V

7.1 Study I: No relationship between identified variants in the uncoupling protein 2 gene and energy expenditure
7.2 Study II: The putative role of the hormone-sensitive lipase gene in the pathogenesis of Type II diabetes mellitus and abdominal obesity
7.3 Study III: Interaction between the Asn291Ser variant of the LPL gene and insulin resistance on dyslipidaemia in high risk individuals for Type 2 diabetes mellitus
7.4 Study IV: The common PPARγ Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes
7.5 Study V: Association between a variant in the phosphodiesterase 3B gene and hyperinsulinemia in genotype-discordant sibling pairs
8. General discussion

9. Specific discussion
   9.1 Study I: Uncoupling protein 2 (UCP2)
   9.2 Study II: Hormone-sensitive lipase (HSL)
   9.3 Study III: Lipoprotein lipase (LPL)
   9.4 Study IV: Peroxisome proliferator-activated receptor gamma (PPARγ)
   9.5 Study V: Phosphodiesterase 3B (PDE3B)

10. Summary and conclusions

11. Populärvetenskaplig sammanfattning

12. Acknowledgements

13. References
### Abbreviations

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>%fat</td>
<td>percent body fat</td>
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<tr>
<td>ANOVA</td>
<td>analysis of variance</td>
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<tr>
<td>aP2</td>
<td>adipocyte lipid/ fatty acid binding protein</td>
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<td>APO</td>
<td>apolipoprotein</td>
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<td>ATP</td>
<td>adenosine triphosphate</td>
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<td>basal metabolic rate</td>
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<td>base pair</td>
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<td>cyclic adenosine monophosphate</td>
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<td>CEBP</td>
<td>CAAT enhancer binding protein</td>
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<tr>
<td>CI 95%</td>
<td>95% confidence interval</td>
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<td>cM</td>
<td>centiMorgan</td>
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<td>coefficient of variation</td>
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<td>cardiovascular disease</td>
</tr>
<tr>
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<td>deoxyribonucleic acid</td>
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<td>FCHL</td>
<td>familial combined hyperlipidaemia</td>
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<tr>
<td>FFA (=NEFA)</td>
<td>free fatty acids (non-esterified fatty acids)</td>
</tr>
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<td>FP</td>
<td>fluorescence polarisation</td>
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<tr>
<td>FRET</td>
<td>fluorescence resonance energy transfer</td>
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<td>GYS1</td>
<td>muscle glycogen synthase gene</td>
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<td>HDL</td>
<td>high density lipoprotein</td>
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<td>HOMA-IR</td>
<td>homeostasis model assessment insulin resistance index</td>
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<td>HSL</td>
<td>hormone-sensitive lipase</td>
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<td>IDDM (=T1DM)</td>
<td>insulin dependent diabetes mellitus (type 1 diabetes)</td>
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<tr>
<td>IFG</td>
<td>impaired fasting glucose</td>
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<tr>
<td>IGT</td>
<td>impaired glucose tolerance</td>
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<td>IRC</td>
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<td>insulin requiring for survival</td>
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<td>kb</td>
<td>kilo base pairs</td>
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<td>LADA</td>
<td>latent autoimmune diabetes in adults</td>
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<td>LDL</td>
<td>low density lipoprotein</td>
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<tr>
<td>LPL</td>
<td>lipoprotein lipase</td>
</tr>
<tr>
<td>Mb</td>
<td>mega base pairs</td>
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<td>MIDD</td>
<td>mitochondrial inherited diabetes and deafness</td>
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<td>MIN</td>
<td>mixed IDDM/NIDDM</td>
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<td>MODY</td>
<td>maturity onset diabetes of the young</td>
</tr>
<tr>
<td>NGT</td>
<td>normal glucose tolerance</td>
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<td>NIDDM (=T2DM)</td>
<td>non-insulin dependent diabetes mellitus (type 2 diabetes)</td>
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<tr>
<td>Acronym</td>
<td>Definition</td>
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<tr>
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<td>NIR</td>
<td>non-insulin requiring</td>
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<td>OGTt</td>
<td>oral glucose tolerance test</td>
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<td>OR</td>
<td>odds ratio</td>
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<td>OSD</td>
<td>observed sum of differences</td>
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<td>PCR</td>
<td>polymerase chain reaction</td>
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<td>phosphodiesterase 3B</td>
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<td>peroxisome proliferator-activated receptor γ</td>
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<td>QTDT</td>
<td>quantitative transmission disequilibrium test</td>
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<td>RFLP</td>
<td>restriction fragment length polymorphism</td>
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<td>SBE</td>
<td>single-base extension</td>
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<tr>
<td>SD</td>
<td>standard deviation</td>
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<td>SEM</td>
<td>standard error of the mean</td>
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<tr>
<td>SSCP</td>
<td>single-strand conformational polymorphism</td>
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<td>TDT</td>
<td>transmission disequilibrium test</td>
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<tr>
<td>TNFα</td>
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<td>Tzd</td>
<td>thiazolidinedione</td>
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<td>uncoupling protein 2</td>
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<tr>
<td>UCP3</td>
<td>uncoupling protein 3</td>
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<tr>
<td>WHO</td>
<td>world health organization</td>
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<tr>
<td>WHR</td>
<td>waist-to-hip ratio</td>
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<tr>
<td>VLDL</td>
<td>very low density lipoprotein</td>
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<tr>
<td>Nlr</td>
<td>non-insulin requiring</td>
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<tr>
<td>Ogtt</td>
<td>oral glucose tolerance test</td>
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<td>uncoupling protein 3</td>
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<tr>
<td>Who</td>
<td>world health organization</td>
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<tr>
<td>Whr</td>
<td>waist-to-hip ratio</td>
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<tr>
<td>Vldl</td>
<td>very low density lipoprotein</td>
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</table>
1. Identification of the disease(s)

1.1 The metabolic syndrome

The metabolic syndrome is a clustering of features associated with insulin resistance and risk factors for cardiovascular disease (CVD)\(^1\). The syndrome has been given many names such as the *insulin resistance syndrome*, *syndrome X* and the *dysmetabolic syndrome*\(^2-4\). The definition of the metabolic syndrome has been much discussed. In 1998 the World Health Organization (WHO) proposed a definition of the metabolic syndrome including diabetes, *impaired glucose tolerance* (IGT) and insulin resistance as invariable components and obesity, dyslipidaemia, hypertension and microalbuminuria as variable components (Figure 1)\(^1\). To have the metabolic syndrome the patient should have at least one of the invariable and two of the variable components. The prevalence of the syndrome increases with deterioration of glucose tolerance. In the Botnia study, 10% of subjects with normal glucose tolerance (NGT), 50% of subjects with IGT or impaired fasting glucose (IFG) and 80% of subjects with type 2 diabetes have the metabolic syndrome\(^5\). Subjects with IGT or IFG have a 3.6-fold increased risk for stroke and diabetic patients have a 2.2-fold increased risk for coronary heart disease if they have the metabolic syndrome\(^5\). The aetiology of the syndrome is not known. It has been suggested that *insulin resistance* is the common denominator and could be the cause of the other components\(^2,6\). The metabolic syndrome is per definition phenotypically heterogeneous. Whether it also has a heterogenous aetiology is not known. Many factors, including genetic factors, may increase or reduce the risk of developing the syndrome.

**Figure 1.** The metabolic syndrome according to the WHO definition from 1998\(^1\). AER, albumin excretion rate; BMI, body mass index; HDL, high-density lipoprotein cholesterol; WHR, waist-to-hip ratio.
1.2 Diabetes mellitus

Diabetes mellitus is a metabolic disorder defined by a disturbance in glucose metabolism leading to chronic hyperglycaemia. It is diagnosed by increased glucose levels in the fasting state or by a reduced glucose clearance after an oral glucose tolerance test (OGTT). Diabetes mellitus represents a spectrum of disorders with heterogenous aetiology but similar clinical signs (Figure 2). The worldwide prevalence of diabetes is about 4%, but varies between ethnic groups and degree of westernization. About 25% of diabetic subjects have diabetes of autoimmune aetiology (type 1 diabetes, and latent autoimmune diabetes in adults, LADA).

Autoimmune forms of diabetes develop due to a destruction of pancreatic β-cells by self-directed T-cells. The patient usually loses endogenous insulin production rapidly, manifested by ketoacidosis at onset, and the patient requires insulin treatment for survival (IRS) (Figures 3 and 4). Type 2 diabetes develops over a long time period, probably decades (Figure 3). The onset is insidious, and the patients may not require insulin therapy to control glycaemia during the first years after diagnosis. Type 2 diabetes is associated with the metabolic syndrome. In some families both type 1 and type 2 diabetes occur and the diabetic phenotype of these subjects is intermediary between the two major forms of diabetes. We have called this form of diabetes MIN (mixed IDDM/NIDDM). Autosomal dominant forms of diabetes are caused by insulin secretory defects (MODY) or mutations of the insulin receptor. Mitochondrial inherited diabetes and deafness (MIDD) is highly penetrant and caused by mutations of mitochondrial DNA.

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deficiency\textsuperscript{13,14}. Monogenic forms of diabetes can be caused by mutations of genes regulating insulin secretion and β-cell development\textsuperscript{15}.

\textbf{Figure 3.} Type 1 diabetes usually has a rather rapid onset whereas type 2 diabetes can develop over a long time-period, often preceded by stages like IFG or IGT.

\textbf{Figure 4.} Three subgroups of diabetes mellitus according to the need for insulin treatment\textsuperscript{1}. Type 1 diabetes usually develops before the age of 35 years and requires insulin treatment for survival (IRS). Type 2 diabetes can be insulin requiring for control (IRC) or non-insulin requiring (NIR).

\textbf{1.3 Dyslipidaemia}

Dyslipidaemia is defined by alterations in blood lipid levels. Lipids are transported in the blood in lipoprotein particles (Figure 5). The lipid levels can be very high in subjects affected by monogenic forms of dyslipidaemia\textsuperscript{16} like familial hypercholesterolaemia or familial hypertriglyceridaemic disorders. In the latter conditions the plasma triglyceride levels are commonly above 6 mmol/l in affected subjects, and can be around 50 mmol/l if chylomicron metabolism is altered. The clinical appearance of these severe lipid disorders include acute pancreatitis, acanthosis nigrans, xanthomas and high incidence of cardiovascular disease\textsuperscript{16}.
Figure 5. A schematic description of lipid and lipoprotein metabolism. Lipids are transported in the blood in lipoprotein particles and delivered to peripheral tissues via hydrolysis/esterification of triglycerides (lipoprotein lipase, LPL) and cholesterol (cholesterol ester transfer protein, CETP). Ingested fat is transported to the blood via the lymphatic system as chylomicrons. Remnant chylomicrons are metabolised by the liver. In between meals, the liver supplies peripheral tissues with triglycerides and cholesterol by secreting very-low-density lipoproteins (VLDL). VLDL increases in density when depleted of triglycerides, transforming into intermediate-density lipoproteins (IDL) and low-density lipoproteins (LDL). High-density lipoproteins (HDL) are produced in the liver to reverse cholesterol transport, a process requiring the enzyme lecithin-cholesterol acyl transferase (LCAT). Reverse cholesterol transport returns excess cholesterol from peripheral tissues for excretion as bile acids.
The prevalence of milder forms of dyslipidaemia varies between populations and generally increases with degree of westernization of the society. Even the milder forms of dyslipidaemia are associated with an enhanced risk for atherosclerosis\textsuperscript{17}. About 20-60\% of patients with type 2 diabetes have some form of dyslipidaemia, mostly elevated plasma levels of triglycerides and reduced plasma levels of HDL cholesterol\textsuperscript{18}. The excess plasma triglycerides reside in the VLDL subtraction and a large proportion of LDL is in the form of small and dense atherogenic particles\textsuperscript{18}.

### 1.4 Obesity and abdominal obesity

Obesity is a major health problem associated with increased mortality\textsuperscript{19}. Obesity is defined by an increase in body weight due to accumulation of excess body fat. Quantitative measures of obesity include the body mass index (BMI; height/weight\textsuperscript{2}), percent body fat (%fat) and the waist-to-hip ratio (WHR). Obesity (BMI above 30 kg/m\textsuperscript{2}) is very common, affecting 10-30\% of populations in Europe and the US\textsuperscript{20}. "Morbid obesity" (BMI above 40 kg/m\textsuperscript{2}) is less common but associated with severe medical complications. Abdominal obesity is defined by accumulation of fat in the abdominal region (WHR above 0.85 for women and 0.9 for men). Abdominal obesity is characterised by fat deposition in the viscera, and is strongly associated with insulin resistance\textsuperscript{21}. Abdominal obesity is more common among men\textsuperscript{22} and the prevalence increases in women as they pass the menopause, suggesting that sex hormones may influence body fat distribution. Obesity can be caused by factors that influence appetite or energy expenditure. Certain pharmacological agents, such as cortisol, can cause abdominal obesity as seen in Cushing’s syndrome. Adult-onset obesity is often localised in the central regions and associated with increased adipocyte size, "hypertrophic obesity"\textsuperscript{23}. Subjects with generalised, early-onset obesity often have an increased number of adipocytes, so called hyperplastic obesity.

### 1.5 Hypertension

Hypertension is defined as a chronic elevation of blood pressure, above 160 mmHg systolic and/or 90 mmHg diastolic pressure\textsuperscript{1}. Hypertension is considered a major risk factor for cardiovascular disease\textsuperscript{24,25}. The prevalence is 10-20\% in most populations\textsuperscript{26,27} and increases with age\textsuperscript{28}. Hypertension can be caused by factors that influence blood volume, vasodilation, peripheral arterial resistance and heart rate. Hypertension is influenced by salt intake, but sensitivity to salt varies between individuals\textsuperscript{29}.

### 1.6 Microalbuminuria

Microalbuminuria is the presence of 20-200 \( \mu \)g/min albumin in overnight urine\textsuperscript{1}. Microalbuminuria is an early sign of diabetic kidney disease\textsuperscript{30}, but also a predictor of cardiovascular disease\textsuperscript{31}. About 30-40\% of type 2 diabetic patients develop microalbuminuria after 25 years of diabetes duration\textsuperscript{32}. In diabetic subjects...
microalbuminuria is strongly associated with hypertension\(^3\). Only about 7% of non-diabetic hypertensive subjects develop microalbuminuria\(^4\). Hyperglycaemia per se might increase albumin excretion in the urine\(^5\).

### 1.7 Treatment

There are several options for the treatment of type 2 diabetes (sulphonylureas, metformin, thiazolidinediones (TZDs) and insulin), none of which has been able to change the inevitable deterioration of glucose tolerance characteristic of type 2 diabetes\(^6\). Therapeutic intervention can prevent microvascular complications if improved glycaemic control is achieved\(^7\). In contrast, most therapies have thus far had little or no effect on macrovascular complications\(^3\). This emphasises the need to treat not only hyperglycaemia in diabetic subjects, but also other risk factors like high blood pressure, obesity and dyslipidaemia. Diet and exercise are important instruments to control most features of the metabolic syndrome. Diet-and-exercise intervention over a four-year period halved the number of IGT subjects that progressed to type 2 diabetes\(^8\). Unfortunately, compliance is not always good and it may be difficult to maintain weight reduction.

Pharmaceutical compounds used for the treatment of obesity include drugs that suppress appetite (sibutramin) or fat-absorption (orlistat). In general, the effect of these agents is restricted to a weight reduction of about 10\(^\%\)\(^9\). Although such small weight reduction has a beneficial effect on insulin sensitivity\(^10\), it is not enough to reduce mortality in morbidly obese subjects. For these patients, surgery to reduce the size of the stomach is often considered (bariatric surgery). Once the excess weight has been lost many patients have reduced their energy expenditure\(^11\) and easily gain weight again (the so-called reduced obese state). WHO has proposed that obesity should be considered a chronic disease.

For the management of dyslipidaemia mainly statins and fibrates are used. Statins are HMG-CoA reductase inhibitors and reduce the levels of LDL-cholesterol and to some extent also plasma triglyceride levels\(^12\). Fibrates are particularly beneficial in patients with the metabolic syndrome, since they reduce the levels of plasma triglycerides, increase the levels of HDL-cholesterol and reduce the density of LPL-particles\(^12\). These agents have been shown to reduce coronary artery disease (CAD) or coronary events by 25-60\(^\%\)\(^2\). Treatment of hypertension include among others \(\beta\)-blockers, diuretics, calcium channel blockers and ACE inhibitors.

Understanding the mechanism(s) that cause the metabolic syndrome may help to develop better pharmacological agents targeted at the underlying pathogenic processes.
2. Heritability of diabetes and the metabolic syndrome

2.1 How do we know if a disease has genetic components?

The factors that influence a trait can be divided into familial genetic, familial non-genetic and non-familial (Figure 6). The relative contribution of these components varies from trait to trait, and in different environments.

![Figure 6. Both genetic and environmental factors contribute to complex genetic diseases. Environmental factors can be familial and non-familial.](image)

Two variables that describe the size of the familial genetic component can be calculated from family data: heritability ($h^2$) and the lambda ($\lambda$) value. Heritability is the variability of a trait that can be accounted for by heritable (genetic) factors. Heritability can be calculated from the difference of concordance rate among monozygotic and dizygotic twins. Since monozygotic twins share 100% genetic material and dizygotic twins share 50% genetic material, the concordance rate should be larger among monozygotic twins if the trait/disease has considerable genetic components. Twin studies may give variable results especially for late-onset diseases, and they are also very sensitive to selection bias. The $\lambda$ value (relative risk) gives an estimate of the risk of disease in subjects related to affected individuals relative to the risk in the general population. The $\lambda$ value cannot distinguish familial genetic from non-genetic components. Naturally, $\lambda$ will be low for common diseases, such as type 2 diabetes.

Segregation analyses investigate the mode by which a (genetic) disease is transmitted through families. Mendelian genetic disease can be dominant/ codominant or recessive, autosomal or X-/Y-linked and maternally transmitted. When the mode of inheritance cannot be determined this usually means that the disease is not inherited
Diseases (or traits) that can be caused by a combination of genetic and environmental factors are complex or multifactorial. Many of our most common diseases are complex, such as cancer, asthma, diabetes, obesity and even infectious diseases. These diseases are heritable, but what is inherited is not the disease itself but rather the susceptibility to it. Many complex diseases are polygenic, but there are also examples of monogenic complex diseases (conditional mutations). Phenylketonuria has a high penetrance—all subjects that carry the mutation will develop the clinical manifestations if subjected to the environmental trigger (phenylalanine). The environmental influence on a disease may vary with the degree to which the studied population has been exposed to environmental factors.

A person who develops a complex disease may carry several genetic factors that predispose to the disease, and the number of predisposing genes will most likely affect the severity as well as the age at onset of the disease. Individuals who develop the disease without carrying any of the genetic factors are called phenocopies. Presumably, phenocopies will be more common among subjects without any family history of the disease. Complex genetic diseases that can be precipitated by environmental factors alone have a high rate of phenocopies and are particularly difficult to study genetically.

All the traits of the metabolic syndrome have a continuous scale and are thus defined as quantitative. Quantitative genetic traits are generally believed to be polygenic, although monogenic traits can also be quantitative if the trait is influenced by environmental factors. The risk for cardiovascular disease increases as the associated traits become more pronounced, and defining when the disturbance becomes pathologic can be difficult.

Thrifty genes are genes that promote survival under a certain environmental stress. A classical example of a survival gene is the mutated form of the sickle-cell anaemia gene that in its heterozygous form protects against malaria. Another interesting example is the apolipoprotein (APO) E gene. The APO E4 allele is associated with
increased risk for Alzheimer’s disease and has a high frequency in Aborigines and low frequency in individuals from societies with a long-established agricultural economy\(^4^3\). Due to the risk of developing Alzheimer in old age, it has been suggested that the ancestral \(\varepsilon^4\) allele has been removed from populations that live longer.

**Figure 7.** The prevalence of diabetes increases with degree of westernization\(^4^4\). Diabetes is uncommon in the Chinese population, affecting less than 1% of the population. The frequency is higher in Chinese individuals born in China and living in Mauritius (15%). Aborigines (Australia, Nauru, Mexico) that have adopted the habits of a western society have much higher prevalence (>40%) than Caucasians (5-10%) and rural Aborigines (<1%).

The hypothesis that thrifty genes could be important for the pathogenesis of type 2 diabetes and the metabolic syndrome was first introduced in 1962\(^4^5\). During a long time of human (and mammalian) evolution we have been subjected to long periods of famine and unpredictable food supplies. In such environments, genetic selection would favour energy conserving genotypes. For example, storing energy as fat rather than glycogen would protect the individual against fatal consequences of starvation. An animal that presumably has been naturally selected for thrifty genes is the desert-based Israeli sand rat (Psammomus obesus). This rat is well adapted for its natural niche in the desert, probably with high survival during periods of food shortages. In a laboratory environment, however, it develops obesity, insulin resistance and diabetes (i.e. the metabolic syndrome)\(^4^6\). Other examples of how energy conserving alleles can be advantageous are seen in the ob and db mice heterozygous for mutations of the leptin and leptin receptor genes, respectively. Although of similar weight, these mice survive starvation better than their wildtype littermates\(^4^7\), a phenomenon that might be attributable to insulin resistance.

The thrifty genotype selection mechanism most likely also has been active in the evolution of human metabolism. The prevalence of most components of the metabolic syndrome is well known to vary between populations of different ethnic
background\textsuperscript{22,44,48}. After Australian aborigines adjusted to the habits of a western society, the prevalence of type 2 diabetes increased to 25\%\textsuperscript{49}. In China the prevalence of diabetes has been 0.5\% but currently the diabetes prevalence is escalating\textsuperscript{50}. Micronesians of Nauru and Pima Indians in Texas have the highest prevalence of type 2 diabetes in the world, affecting more than 40\% of the populations (Figure 7)\textsuperscript{44}. The highest prevalence of obesity has been reported in Western Samoa, with 60\% of the men and 80\% of the women affected\textsuperscript{51}. In populations with a high prevalence of diabetes and obesity, thrifty alleles may have accumulated due to genetic isolation.

2.5 Thrifty phenotypes

The development of type 2 diabetes, hypertension and other features related to the metabolic syndrome in adult life are associated with low birthweight\textsuperscript{52}. The reason for this could be that poor intrauterine nutrition permanently programs the body to a constant starvation-state, which would lead to the accumulation of excess energy. However, genetic predisposition can influence both birthweight and the development of diabetes: Mutations in the glucokinase gene lead to the development of diabetes (MODY2) in heterozygous individuals (autosomal dominant inheritance)\textsuperscript{53}. Carriers of MODY2 mutations have a mild insulin deficient/insulin sensitive form of diabetes and they seldom become obese. Glukokinase mutations have also been associated with low birthweight. Recently it was shown that subjects who carry glucokinase mutations are small at birth only if they inherit the mutation from their father\textsuperscript{54}. Carriers of glucokinase mutations can secrete insulin, but their β-cells have a higher glucose threshold for glucose-stimulated insulin secretion. If the mutation is transmitted from a diabetic mother the fetus will be subjected to high glucose levels (as glucose crosses the placenta) and the islets of the fetus will secrete normal insulin levels. This demonstrates that a mild insulin deficiency during growth may influence birthweight.

2.6 Evidence that type 2 diabetes is inherited

The risk of developing type 2 diabetes is approximately 3-4 times higher among first degree relatives of diabetic subjects compared to subjects without family history of diabetes (λ, value around 3.5)\textsuperscript{55}. Similar numbers have been calculated from offspring of diabetic subjects\textsuperscript{56}. If one parent has diabetes the risk that the offspring will develop the disease is about 40\%, and if both parents have diabetes the risk is approximately 70\%\textsuperscript{57,58}. This supports the hypothesis that there are familial factors that contribute to the disease and suggests that these factors to some extent are additive. Very high concordance rates of type 2 diabetes have been reported in monozygotic twins\textsuperscript{59,60}. These studies most likely have overestimated the concordance by ascertaining twins based upon affection status\textsuperscript{61}, and do not distinguish familial genetic from non-genetic components. One population-based twin study suggested concordance rates of 34\% among monozygotic and 16\% among
dizygotic twin pairs\textsuperscript{62}. Thus, approximately 40\% of the variability of the diabetic phenotype may be heritable (familial genetic). In one recent study, the heritability seemed to be higher for IGT and diabetes (0.60), than for diabetes alone (0.26)\textsuperscript{63}.

There are also some monogenic forms of diabetes with some similarities to classical type 2 diabetes but generally developing at earlier ages. Maturity onset diabetes of the young (MODY) represents insulin deficient/insulin sensitive forms of type 2 diabetes and make up about 5\% of all diabetic cases\textsuperscript{15,64}. MODY is caused by defects in the \(\beta\)-cell eventually leading to insulin deficiency. MODY1 is caused by mutations in the hepatocyte nuclear factor 4\(\alpha\) gene (chromosome 12q24.2), MODY2 by mutations in the glucokinase gene (chromosome 7p15-p13), MODY3 by mutations in the hepatocyte nuclear factor 1\(\alpha\) gene (chromosome 12q24.2), MODY4 by mutations in the insulin promoter factor 1 (chromosome 13q12.1) and MODY5 is associated with mutations in hepatocyte nuclear factor 1\(\beta\) gene (chromosome 17cen-q21.3). Diabetes can also develop as a consequence of mutations in the insulin receptor gene (chromosome 19p13.2)\textsuperscript{65} or in mitochondrial DNA (tRNA\textsubscript{Leu})\textsuperscript{66}, and familial forms of adipose tissue deficiency (partial and congenital lipodystrophy) are associated with diabetes\textsuperscript{67}.

2.7 Evidence that dyslipidaemia is inherited
Heritability estimates for plasma triglyceride and HDL cholesterol levels have ranged from 0.2-0.8\textsuperscript{68}. In a recent study including twins reared apart, genetic factors contributed to one third of the variability of plasma triglycerides and nearly half of the variability of HDL cholesterol levels\textsuperscript{69}. In particular, triglyceride levels seem to be highly influenced by individual-specific environmental factors. Severe lipid disorders are often due to mutations in genes regulating lipid metabolism, like familial hypercholesterolaemia (mutations in the LDL-receptor gene on chromosome 19p13.2), familial HDL deficiency (mutations in the gene encoding the ATP-binding cassette 1 on chromosome 9q22-q31) and type I hyperlipoproteinaemia (mutations in the \textit{LPL} and \textit{APOCII} genes on chromosomes 8p22 and 19q13.2)\textsuperscript{16}. Monogenic forms of dyslipidaemia can be extremely rare (\textit{APOCII} deficiency) to rare (familial combined hyperlipidaemia (FCHL)). FCHL is a relatively common form of familial dyslipidaemia, characterised by high incidence of cardiovascular disease representing 5-15\% of subjects with coronary artery disease\textsuperscript{20}. FCHL has been linked to several chromosomal regions\textsuperscript{71} including 1q21-q23\textsuperscript{71-73}, and may be mono- or oligogenic. The clinical appearance of FCHL typically varies between the members of an affected family (high triglyceride or high cholesterol levels or both)\textsuperscript{74,75}.

2.8 Evidence that obesity is inherited
Heritability estimates have varied between 0.2-0.9 for obesity and between 0.3-0.5 for abdominal obesity\textsuperscript{76-78}. Many of the available estimates include non-genetic familial factors, thus reflecting "familiality". In Pima Indians the familiality was 0.8
for body fat and waist circumference and 0.5 for BMI. Most studies agree on a heritability of BMI around 0.5, and the remaining variability of BMI seems to be largely attributed to shared environmental factors. Studies of twins have shown that the propensity to gain weight in response to overfeeding is largely heritable.

Monogenic obesity often develops in childhood and progresses with time. It can be caused by mutations in genes related to the regulation of appetite (the melanocortin receptor 4, pro-opiomelanocortin and prohormone convertase 1 genes on chromosomes 18q22, 2p21 and 5q15-q21) or metabolism (the leptin, leptin receptor and peroxisome proliferator-activated receptor γ genes on chromosomes 7q31.3, 1p31 and 3p25). Mutations in most of these genes require two mutated alleles to cause disease. However, 3-5% of subjects with BMI above 40 kg/m² have mutations in the melanocortin receptor 4 in these families obesity is inherited in a dominant fashion. Several chromosomal aberrations cause syndromes where obesity is one component, such as the fragile X, Prader-Willi/ Angelman, Bardet-Biedl and Turner syndromes. Familial partial lipodystrophy (adipose tissue deficiency) is an autosomal dominant disorder of fat redistribution that develops after puberty and is caused by mutations in the lamin A/C gene (chromosome 1q21.2). The body fat is redistributed from the periphery to central regions of the upper body, such as the abdomen, face and neck. There are also forms of generalised lipodystrophy, for example the Berardinelli-Seip syndrome (BSCL), which is congenital and seems to be a heterogenous autosomal recessive disorder caused by mutations in either BSCL1 (chromosome 9q34) or BSCL2 (chromosome 1q13).

2.9 Is the metabolic syndrome inherited?

All the components of the metabolic syndrome seem to have a complex polygenic background. Monogenic forms of each feature alone show that these disorders can be caused by single-gene mutations. In the general population it is likely that the risk alleles will be common and that protective alleles as well as risk alleles may be operating in the same individual. Although the features of the metabolic syndrome are common in most parts of the world, the prevalence varies a lot between rural and westernized populations, suggesting that genetic background and habitual factors play an important role.

Reports in the literature have suggested that 10 to 90% of the variability of metabolic cardiovascular risk factors is genetically determined. This emphasises the instability of heritability estimates. Inconsistent reports can be explained by differences in methodology, selection bias and data acquisition, and age of the studied population. All features of the metabolic syndrome are associated with insulin resistance, which could be a common denominator. Most studies have shown that around 50% of the variability of insulin resistance may be genetically determined, and that the remaining variability is explained by individual-specific factors. The familiality of insulin resistance is also illustrated by a higher prevalence among first-degree relatives of diabetic subjects (45%) compared to subjects with no family history of
diabetes (20%)\textsuperscript{12}. Hypertension and microalbuminuria are also highly heritable. It has been estimated that 10-80\% of the variability of blood pressure is attributable to genetic factors. The heritability of systolic blood pressure may be highly age-dependent since the concordance is much higher in younger twins\textsuperscript{82}. Intrauterine factors could also be important for the metabolic syndrome. Such factors may in particular be important for hypertension, as blood pressure variability seems to be partly explained by environmental factors shared by twins reared apart\textsuperscript{78}. Most diabetic subjects with microalbuminuria also have hypertension, which makes it difficult to distinguish between factors that contribute to these traits separately. About 30\% of the variability of albumin excretion seems to be heritable\textsuperscript{83}, but whether this is due to concomitant hypertension needs to be clarified. Several studies have shown that the heritability of coronary heart disease (CHD) exceeds 0.5\textsuperscript{78}. It is important to remember that also behavioural risk-factors for CVD can be genetically related. Heritability estimates of smoking for example have suggested that a substantial proportion is genetic (28-84\%)\textsuperscript{78}. The metabolic syndrome may not always be inherited, but it seems heritable.

### 2.10 Are there one or several heritable traits of the metabolic syndrome?

The metabolic syndrome clusters predominantly in families with diabetes. About 80\% of type 2 diabetic subjects have the metabolic syndrome\textsuperscript{3} whereas only 30\% of obese individuals are insulin resistant. First degree relatives of diabetic subjects often develop the metabolic syndrome already before the onset of diabetes\textsuperscript{84}, emphasising that hyperglycaemia develops as a consequence of the underlying metabolic defects. First-degree relatives of subjects with type 2 diabetes have increased abdominal deposition of fat, and are more insulin resistant than subjects without a family history of type 2 diabetes\textsuperscript{12}. In these subjects, abdominal obesity usually precedes insulin resistance and the two variables are highly correlated. This does not mean that insulin resistance is caused by abdominal obesity; syndromes of severe insulin resistance are not always associated with obesity.

The metabolic syndrome may have a single central aetiologic component or it may be caused by different factors that increase the risk for CVD. Few studies have been performed to elucidate this question. In one study, twins reared either together or apart, BMI and insulin resistance were largely co-inherited\textsuperscript{69}. Systolic blood pressure, plasma triglycerides and HDL cholesterol levels were to some extent influenced by the same genetic component, but also by independent genetic factors. Taken together this suggests that a single factor could initiate the syndrome by influencing fat accumulation or insulin sensitivity. Additional environmental factors and genetic factors influencing lipaemia and blood pressure may aggravate the associated symptoms.
3. Adipose tissue, lipolysis and energy expenditure

3.1 Adipogenesis

Differentiation of adipocytes into functional insulin sensitive cells of fat storage is called adipogenesis. Glucocorticoids and growth hormone promote adipogenesis in pre-adipocytes. Certain internal factors are needed to initiate the transcriptional cascade that makes the cell to develop into an adipocyte. CCAAT/enhancer binding proteins (C/EBPα and C/EBPδ) and peroxisome proliferator-activated receptor gamma (PPARγ) are transcription factors that play important roles in the regulation of adipocyte differentiation. Adult-onset obesity is associated with increased fat cell size, and large fat cells seem to be less insulin sensitive than smaller cells. Whether this is a cause or a consequence of obesity is not known. Defective deposition of fat in adipose tissue seems to promote storage of fat in other organs, such as the liver, skeletal muscle and pancreas, and could be an important factor contributing to insulin resistance.

3.2 Adipose tissue and metabolism

The adipose tissue is an endocrine organ secreting several hormones/ cytokines into the blood stream. Factors secreted from adipose tissue may convey signals to the brain, the β-cells and skeletal muscle to adapt to changes in fat stores by modulating feeding, insulin secretion and insulin sensitivity. The discovery of leptin has demonstrated a new role for adipose tissue in the regulation of appetite and energy expenditure by signalling the body’s state of adiposity to the brain. Resistin and adiponectin are considered to modulate insulin sensitivity in mice, although the role of resistin in human metabolism has been questioned. The cytokine tumour necrosis factor alpha (TNFα) inhibits insulin signalling in adipose tissue, and can thereby stimulate lipolysis.

Disturbed adipose tissue development and metabolism may lead to insulin resistance, which may precipitate diabetes if insulin secretory capacity fails to compensate. Evidence to support this comes from studies of lipodystrophies associated with diabetes. The A-ZIP/F-1 mice lacks subcutaneous adipose tissue and is characterised by fat deposits in the liver, muscle and β-cells, as well as by insulin resistance and hyperglycaemia. Insulin resistance and hyperglycaemia can be reverted by implantation of adipose tissue. Mice lacking the glucose-transporter 4 (GLUT4) in adipose tissue have normal adipocyte mass but develop insulin resistance in the liver and skeletal muscle. This suggests that insulin sensitivity of the adipocyte may be important for the maintenance of whole-body insulin sensitivity.

An increased amount of adipose tissue in the visceral region is associated with insulin resistance, diabetes and CVD. The reason for this is not known, but visceral fat is metabolically highly active, with a large output of FFA. FFA from visceral fat is metabolically highly active, with a large output of FFA.
FFA levels are increased in diabetic and obese individuals, and associated with an increased risk for type 2 diabetes and cardiovascular disease. There is evidence to suggest that increased serum FFA could be a familial trait predisposing to CVD. For example, the prevalence of CVD in the parental generation is increased in subjects with elevated serum levels of FFA. FFA per se could have deleterious effects on insulin sensitivity and insulin secretion. FFAs compete with glucose metabolism in skeletal muscle, leading to insulin resistance and reduced glycogen synthesis. In fact, forcing FFA to the skeletal muscle by overexpressing the LPL gene in muscle of transgenic mice leads to insulin resistance. Intramuscular triglyceride levels are increased in insulin resistant non-diabetic individuals and correlate with the rate of insulin stimulated glucose utilisation. Long-term exposure of the β-cell to high serum FFA levels reduces insulin secretion. Recent studies have shown that depletion of such excess triglycerides from pancreas, liver and skeletal muscle using TZDs results in improved insulin sensitivity. Intracellular breakdown of triglycerides could in some tissues provide substrates for intracellular signalling molecules such as diacylglycerol and phospholipids.

3.4 Lipolysis

Fat storage is regulated by the hydrolysis of triglycerides to FFAs, a process called lipolysis. The rate-limiting step of intracellular lipolysis is catalyzed by hormone-sensitive lipase (HSL). The main function of HSL in normal physiology is to release stored fat during starvation or endurance training, providing energy as FFA to the heart and skeletal muscle. Catecholamines and glucagon stimulate and insulin inhibits intracellular lipolysis. After a meal, lipolysis of triglycerides stored in chylomicrons or VLDL particles produces FFA that can be transported into the cell for storage. This step is catalyzed by LPL, which is produced by adipose tissue and skeletal muscle and adheres onto the endothelial cell wall. For efficient transfer of fat from plasma into tissues, insulin activates LPL and inactivates intracellular lipolysis. The anti-lipolytic effect of insulin is mediated via the insulin receptor leading to the activation of phosphodiesterases (PDEs), predominantly PDE3B. PDE3B hydrolyses the activator of HSL, cAMP, and thereby reduces serum FFA levels by 80% after a normal meal. HSL mRNA and protein levels are decreased in obese subjects. Subjects with polycystic ovary syndrome (PCOS) or FCHL as well as obese subjects and their first-degree relatives show reduced response to catecholamine-induced lipolysis. The OLETF (Otsuka Long-Evans Tokushima Fatty) rat represents another model of the metabolic syndrome with increased visceral fat accumulation and a high incidence of atherosclerosis.

3.3 Free fatty acids (FFAs)

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lipolysis. Also, in many studies the suppression of FFA in response to insulin was impaired in diabetic\textsuperscript{120-122} and obese prediabetic\textsuperscript{123,123} subjects and in patients with FCHL\textsuperscript{124} subjects. The sensitivity to the anti-lipolytic action of insulin was improved with TZD treatment\textsuperscript{125}.

Lipolysis is a powerful regulator of fat redistribution. A change in lipolytic activity in tissues could redirect fat from one region to another. During pregnancy the activity of LPL is increased and the activity of HSL is decreased in mammary glands resulting in increased accumulation of fat\textsuperscript{126}. If abdominal depots are more sensitive to insulin and more resistant to catecholamines, relative to subcutaneous adipose tissue, this will redirect subcutaneous fat to the abdominal region. This could explain the predisposition to abdominal obesity observed in subjects with type 2 diabetes, in whom visceral fat seems to be more sensitive to insulin than peripheral subcutaneous fat\textsuperscript{127}. Disturbed regulation of lipolysis can also lead to alterations in blood lipid levels. Increased lipolytic activity in adipose tissue could increase serum FFA levels, and reduced LPL activity in the sera could induce post-prandial hyperlipidaemia. Lipolysis clearly can be of importance for the maintenance of body fat stores. Reduced lipolytic rate increased adipose tissue mass in the adipocyte lipid/ fatty acid binding protein (aP2) knockout and the monosodium glutamate (MSG) mice.
Neonatal administration of monosodium glutamate destroys the arcuate nuclei in the hypothalamus, and these mice develop increased adiposity despite of normal eating behaviour. Interestingly, the aP2 knockout mouse has disturbed insulin secretion, supporting the existence of an adipoinsular axis. The perilipin isoform knockout mice have constitutively activated lipolysis, small adipocytes, reduced adipose mass, increased lean body mass and energy expenditure, and are resistant to the development of obesity when fed a high-fat diet.

3.5 Energy expenditure and uncoupling proteins

The amount of fat stored after ingestion of food varies between individuals. There are mainly two mechanisms responsible for this thermogenesis and energy expenditure. Basal energy expenditure is the energy spent for the maintenance of the basal cellular metabolism, and is measured at isothermal conditions at rest. Energy expenditure is influenced by environmental factors and increases in response to certain dietary factors and a high level of physical activity. Obesity is associated with low energy expenditure, and low energy expenditure predicts future weight gain. Brown adipose tissue (BAT) is rich in mitochondria and actively uncouples the respiratory chain from ATP synthesis. Oxidation of nutrients in the respiratory chain and the synthesis of ATP from ADP take place in the inner mitochondrial membrane. These processes are coupled and electron transport in the respiratory chain is inhibited in lack of ADP. During the electron transport, protons are transported across the inner membrane, building up a proton gradient that drives the ATP synthease. ATP synthesis can be uncoupled from the respiratory chain if the proton gradient is discharged, and instead of storing the energy as ATP it can be released as heat. In fact, despite its unacceptable side-effects, the chemical uncoupler dinitrophenol was used as a weight-lowering agent in the 1930's. The biological uncoupler thermogenin or uncoupling protein (UCP1 or simply UCP) was discovered in the late 1970's and is located in brown adipose tissue. Human babies have brown adipose tissue between the scapulae to produce heat during their first year of life, whereas adult individuals only have very small amounts of brown adipose tissue. The discovery of uncoupling proteins located in tissues that are more abundant in the human body (UCP2, UCP3 and UCP4) reinforced the idea that the uncoupling mechanism could be important for the regulation of thermogenesis and energy expenditure in human adults. The amino acid homology between UCP2/UCP3 and UCP1 is about 55%. In spite of this homology, an uncoupling function of UCP2 and UCP3 has not been clearly established. Although overexpression of UCP2 or UCP3 in yeast resulted in depolarisation of the mitochondrial membrane, uncoupling activity was not increased.

Data from animal models suggest that ablation of brown adipose tissue induces hyperphagia and obesity. Although mice without the UCP1 gene are unable to increase thermogenesis in response to cold, these mice have normal energy expenditure and uncoupling proteins. The amount of fat stored after ingestion of food varies between individuals. There are mainly two mechanisms responsible for this thermogenesis and energy expenditure. Basal energy expenditure is the energy spent for the maintenance of the basal cellular metabolism, and is measured at isothermal conditions at rest. Energy expenditure is influenced by environmental factors and increases in response to certain dietary factors and a high level of physical activity. Obesity is associated with low energy expenditure, and low energy expenditure predicts future weight gain. Brown adipose tissue (BAT) is rich in mitochondria and actively uncouples the respiratory chain from ATP synthesis. Oxidation of nutrients in the respiratory chain and the synthesis of ATP from ADP take place in the inner mitochondrial membrane. These processes are coupled and electron transport in the respiratory chain is inhibited in lack of ADP. During the electron transport, protons are transported across the inner membrane, building up a proton gradient that drives the ATP synthease. ATP synthesis can be uncoupled from the respiratory chain if the proton gradient is discharged, and instead of storing the energy as ATP it can be released as heat. In fact, despite its unacceptable side-effects, the chemical uncoupler dinitrophenol was used as a weight-lowering agent in the 1930's. The biological uncoupler thermogenin or uncoupling protein (UCP1 or simply UCP) was discovered in the late 1970's and is located in brown adipose tissue. Human babies have brown adipose tissue between the scapulae to produce heat during their first year of life, whereas adult individuals only have very small amounts of brown adipose tissue. The discovery of uncoupling proteins located in tissues that are more abundant in the human body (UCP2, UCP3 and UCP4) reinforced the idea that the uncoupling mechanism could be important for the regulation of thermogenesis and energy expenditure in human adults. The amino acid homology between UCP2/UCP3 and UCP1 is about 55%. In spite of this homology, an uncoupling function of UCP2 and UCP3 has not been clearly established. Although overexpression of UCP2 or UCP3 in yeast resulted in depolarisation of the mitochondrial membrane, uncoupling activity was not increased.

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weight\textsuperscript{142}. Adipose tissue and skeletal muscle are abundant in mice and men, and one could expect that altered uncoupling activity in these tissues would influence energy expenditure and/or thermogenesis. This is supported by resistance to weight-gain on a high-fat diet in mice with ectopic expression of UCP1 in white adipose tissue (WAT)\textsuperscript{143} or skeletal muscle\textsuperscript{144}. UCP2 is expressed in many tissues, most abundantly in white adipose tissue\textsuperscript{136,137}, whereas UCP3 is expressed in skeletal muscle\textsuperscript{139}. Therefore, one could expect that altered UCP2 or UCP3 activity would influence energy expenditure and/or obesity in human subjects.
Several chromosomal regions have been suggested to contain genes that predispose to type 2 diabetes or quantitative measures associated with obesity. Adiposity has been linked to chromosomes 2p (fat mass or leptin levels), 20q (%fat) and 11q21-q22 (%fat), and basal metabolic rate has been linked to chromosome 11q13. Type 2 diabetes has been linked to chromosomes 1q, 2q (NIDDM1), 12q (NIDDM2) and 20q, and recent data from the Botnia study reported suggestive linkage to chromosomes 9q (type 2 diabetes) and 18p (obese type 2 diabetes). The calpain 10 gene was the first example of positional cloning of a gene that might contribute to type 2 diabetes. The calpain 10 (CAPN10) gene is located in the NIDDM1 region (chromosome 2q) and a haplotype variant of this gene seems to predispose to type 2 diabetes in several but not all populations. In the Botnia population, subjects carrying the SNP43 11 or 12 genotypes were more insulin resistant than their gender-matched genotype-discordant siblings, and both diabetic and non-diabetic carriers of this allele had elevated FFA levels, compared to non-carriers (Marju Orho-Melander, unpublished).

Several genes involved in the metabolism of FFA seem to contribute to susceptibility to features associated with type 2 diabetes, the metabolic syndrome and CVD, including the genes encoding the β-adrenergic receptors (ADRB1-3, chromosomes 10p24-q26, 5q32-q34 and 8p12-p11.2, respectively) and the fatty acid binding protein 2 (FABP2, chromosome 4q28-q31). Recently, a genome-wide scan of quantitative traits associated with the metabolic syndrome was performed, suggesting that several of these traits link to chromosomes 3q27 and 17p12. Preliminary data of a gene located in the 3q27 region, adiponectin, support a role for adiponectin in the modulation of insulin resistance. In this thesis we have concentrated on five candidate genes that are important for the regulation of energy expenditure, lipolysis and adipose tissue development.

### 4. Candidate genes that may contribute to type 2 diabetes and the metabolic syndrome

Mutations of nearly 1000 genes are known to cause monogenic disease or clearly increase the susceptibility for complex traits. Recent data show that almost half of all disease genes encode enzymes or enzyme co-activators. Mutations in enzyme and enzyme co-activator genes were particularly over-represented in diseases developing during the first year of life and in diseases emerging after the age of 50. Diseases caused by these mutations were often transmitted recessively. Mutations of transcription factors often caused disease that developed in utero, and these diseases were often transmitted in a dominant fashion. It is thus highly likely that mutations increasing the susceptibility to type 2 diabetes and the metabolic syndrome may be found in enzymes regulating glucose and lipid metabolism, and that the phenotype may in some cases be more obvious in homozygous carriers.

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Several genes involved in the metabolism of FFA seem to contribute to susceptibility to features associated with type 2 diabetes, the metabolic syndrome and CVD, including the genes encoding the β-adrenergic receptors (ADRB1-3, chromosomes 10q24-q26, 5q32-q34 and 8p12-p11.2, respectively) and the fatty acid binding protein 2 (FABP2, chromosome 4q28-q31). Recently, a genome-wide scan of quantitative traits associated with the metabolic syndrome was performed, suggesting that several of these traits link to chromosomes 3q27 and 17p12. Preliminary data of a gene located in the 3q27 region, adiponectin, support a role for adiponectin in the modulation of insulin resistance. In this thesis we have concentrated on five candidate genes that are important for the regulation of energy expenditure, lipolysis and adipose tissue development.
4.1 Uncoupling protein 2 (UCP2)

UCP2 was discovered in 1997\textsuperscript{136,137} and has since then been intensely studied with over 300 publications in PubMed. The \textit{UCP2} gene is encoded by 6 coding and 2 non-coding exons, spanning a region of 8.6 kb on chromosome 11q13 (accession number NT_009296 at \url{www.ncbi.nlm.nih.gov}) (Figure 18, results, page 51). The mRNA is 2.1 kb and the protein consists of 309 aminoacids (accession number XM_035028). The UCP2 and UCP3 proteins have 71\% homology, and UCP2 is 55\% homologous with UCP1\textsuperscript{139}. Obesity is associated with lower UCP2 mRNA levels in visceral fat, but no differences in UCP2 mRNA levels have been seen neither in subcutaneous fat nor in skeletal muscle between lean and obese subjects\textsuperscript{140}. UCP2 mRNA levels increase in response to fasting\textsuperscript{150-151} a finding which challenges the view that UCP2 would be a positive regulator of energy waste. In diabetic subjects the upregulation of UCP2 expression in response to fasting seems to be impaired\textsuperscript{151}. However, care should be taken in the interpretation of UCP2 mRNA levels since it has been shown that UCP2 is also regulated at translational steps\textsuperscript{152}.

4.2 Hormone-sensitive lipase (HSL)

HSL is a major regulator of lipolysis in many tissues, catalysing the hydrolysis of mono-, di- and triacylglycerols and cholesterol esters to FFA, glycerol and cholesterol\textsuperscript{109}. Adipose tissue lipolysis mainly provides substrates for lipid oxidation in other tissues and organs and is activated by molecules stimulating the cAMP/protein kinase A (PKA) complex such as adrenaline, adrenocorticotrophic hormone (ACTH) and glucagon.

The \textit{HSL} gene is encoded by 9 exons\textsuperscript{153}, spanning a region of 26 kb on chromosome 19q13.1-q13.2 (accession number NT_011128) (Figure 19, results, page 52). The mRNA is 3.8 kb and the protein consists of 1076 aminoacids (accession number XM_008882). The regulatory region upstream the \textit{HSL} gene seems complex, including at least five alternative first exons and two separate promoters differentially activated in various tissues\textsuperscript{154}. This implies that transcriptional regulation of the gene may be important for tissue-specific expression. The \textit{acute regulation} of HSL involves phosphorylation mediated by the cAMP/PKA complex\textsuperscript{155}, and this phosphorylation seems to increase the propensity of HSL to interact with other proteins\textsuperscript{156}. It has been suggested that HSL interacts with a number of proteins, including perilipin\textsuperscript{157}, aP2\textsuperscript{158} and lipotransin\textsuperscript{159}. HSL needs to be translocated to the lipid droplet for efficient lipolytic activation\textsuperscript{157,160}, and this translocation could be dependent on protein-protein interactions. Perilipin seems to protect the triglyceride pool from lipolytic breakdown, as judged from adipose tissue of perilipin deficient mice which has constitutively activated HSL and lipolysis\textsuperscript{130}. It has been proposed that the interaction of HSL with aP2 prevents substrate-inhibition and that aP2 would rapidly bind to released FFAs, dissociate from HSL and transport FFA to the plasma membrane\textsuperscript{158}. This hypothesis is supported by aP2 deficient mice which display accumulation of intracellular FFA in adipocytes\textsuperscript{129}. The interaction of HSL with
lipotransin has only been detected in the presence of insulin and could provide a mechanism preventing the translocation of HSL to the lipid droplet159. Furthermore, there is evidence that HSL is functionally active as a homodimer in vivo, and that dimerization increases HSL activity161. In one mouse strain the lack of HSL is associated with increased abdominal fat stores162. However, knocking out the HSL gene in mice does not seem to influence total body adiposity162,163. This indicates a redundancy of HSL activity in adipose and perhaps other relevant tissues, suggesting that other lipolytic enzymes could be active in the adipocyte and substitute HSL in its absence. Under basal conditions, the rate of lipolysis does not entirely correlate with HSL activity in human subjects164, indicating that other lipolytic enzymes might be expressed and active. However, β-adrenergic stimulation of adipose tissue lipolysis is highly dependent upon HSL activity165 and the HSL knockout mice show a markedly reduced β-adrenergic response162,163. In addition, it is not known if substitution of HSL activity by other lipolytic enzymes will take place in the presence of a defective HSL protein. Increased HSL activity in skeletal muscle could contribute to insulin resistance by modulating intracellular FFA metabolism that compete with glucose metabolism. HSL is activated by adrenaline and muscle contractions in skeletal muscle166,167. In male reproductive organs HSL cholesterol esterase activity has proven crucial for sperm production, and male mice deficient of HSL are infertile163. In the β-cell, lipolytic activity could modulate glucose-stimulated insulin secretion (GSIS)168. In fact, transgenic mice overexpressing HSL in β-cells develop glucose intolerance when challenged with a high-fat diet (Maria Sörhede-Winzell, EASD presentation 308, Jerusalem 2000). In the β-cell lipolysis may also represent an alternative source of energy independent of glucose. The effect of glucagon-like peptide-1 (GLP1) on glucose-stimulated insulin secretion and potentially on the activation of HSL169 may play an important role in insulin secretion.

4.3 Lipoprotein lipase (LPL)

LPL belongs to another family of lipases including the pancreatic and the hepatic lipase. These lipases have structural similarities, are secreted and adhere to heparan sulphate proteoglycans on the endothelial wall. Their function is to release FFA from circulating lipoproteins, and increase the uptake of FFA in the tissue where they are expressed. Upon heparin treatment they are released into the blood stream. LPL is the primary enzyme responsible for the conversion of lipoprotein triglycerides into FFA. Maximal activity of LPL requires the presence of its co-activator, APOCII, situated on triglyceride-rich lipoproteins. In contrast to HSL which is inhibited by insulin, the activity of LPL is enhanced by insulin. The LPL gene is encoded by 10 exons spanning a region of 28 kb on chromosome 8p22 (accession number NT_008271). The mRNA is 3.5 kb and the protein consists of 475 aminocids (accession number XM_044682). LPL is most active as a homodimer170. Over 80 variants and mutations have been identified in the LPL gene,
many of which have a substantial influence on the phenotype of the carrier. Type I hyperlipoproteinaemia is an autosomal recessive disorder caused by mutations in the LPL gene. Subjects affected by this disorder are particularly sensitive to high-fat diets. Even if LPL deficiency is not lethal in man, LPL knockout mice die within their first day of life. When the mice start to suckle they develop severe hyperlipoproteinaemia. Even if LPL deficiency is not lethal in man, LPL hyperlipoproteinaemia is an autosomal recessive disorder caused by mutations in the LPL gene. Subjects affected by this disorder are particularly sensitive to high-fat diets. Even if LPL deficiency is not lethal in man, LPL knockout mice die within their first day of life. When the mice start to suckle they develop severe hyperlipoproteinaemia resulting in cyanosis (chylomicrons obstruct the arterioles of the lung). Haploinsufficiency of the LPL gene has some influence on lipaemia in human subjects. Several variants of the LPL gene have been identified in the general population, including four coding (Asp9Asn, Gly188Glu, Asn291Ser, Ser447X) and two non-coding variants that potentially could interfere with regulatory elements (T-93G and a HaeIII polymorphism in intron 8). These variants have been associated with dyslipidaemia and increased cardiovascular risk, and haplotype analysis suggests that several of them independently influence the lipid profile.

It has been proposed that LPL could contribute to obesity as the LPL gene is upregulated in adipose tissue of obese subjects. This may rather reflect a consequence than a cause of obesity for the following reasons. Firstly, human subjects lacking LPL and mice haploinsufficient for LPL are neither lean nor obese. Secondly, mice overexpressing LPL in adipose tissue are not obese due to upregulation lipolysis (HSL activity). Interestingly, overexpression of LPL in skeletal muscle results in whole-body insulin resistance, and sometimes myopathy, suggesting that an increased intramuscular FFA metabolism may have harmful effects on muscle glucose metabolism.

4.4 Peroxisome proliferator-activated receptor gamma (PPARγ)

PPARγ is a transcription factor of the orphan nuclear receptor family, which means that the natural ligand is not known. PPARγ was cloned investigating proteins that interact with the 5′ flanking region of the aP2 gene. Ectopic expression of PPARγ in fibroblasts promote adipogenesis. There are at least three PPARs, PPARα (or simply PPAR), PPARγ and PPARδ. PPARα is expressed in the liver and skeletal muscle and controls the regulation of genes involved in fatty acid oxidation. The beneficial influence of fibrates on lipid metabolism is from the activation of PPARα. The function of PPARδ is less defined. PPARγ heterodimerises with another transcription factor, the retinoid X receptor (RXR). Long-chain FFA and prostaglandins have been proposed as naturally activating PPARγ ligands. TZDs are synthetic activating ligands for the PPARγ/RXR heterodimer and mediate at least some of the pleiotrophic effects that TZDs have on insulin action, including skeletal muscle glucose uptake.

The PPARγ gene is encoded by 7 exons, including the PPARγ2-specific exon B (Figure 21, results, page 54). The gene spans a region of 83 kb on chromosome 3p25 (accession number NT_005718). The gene has two major transcription initiation sites, corresponding to two common isoforms of the mRNA. The PPARγ1 mRNA...
is 1.6 kb and the protein consists of 477 amino acids (accession number XM_051559), and the PPARγ2 protein is 28 amino acids longer (encoded by exon B, Figure 21, results, page 54).

Knockout of the PPARγ gene in mice is lethal\(^{183}\). By generating chimeric PPARγ homozygous knock-out mice it was established that the gene is required for fat cell development, since no cells lacking PPARγ could be identified in the adipose tissue of these animals\(^{184}\). In spite of this, mice heterozygous for the PPARγ gene were of normal weight and had normal adipose tissue development\(^{185}\). The mice were more insulin sensitive than their wild-type littermates.

PPARγ is predominantly expressed in adipose tissue (mainly PPARγ2), although the PPARγ1 isofrom has been identified in skeletal muscle at 10% of the levels in adipose tissue\(^{186}\). PPARγ mRNA levels have been reported upregulated or unchanged in skeletal muscle of type 2 diabetic patients and in visceral adipose tissue and skeletal muscle of obese individuals\(^{186,187}\) compared to healthy control subjects. PPARγ expression in adipose tissue is downregulated in response to a very-low calorie diet in vivo\(^{187}\). TZD treatment upregulates PPARγ1 mRNA and protein expression in skeletal muscle in both diabetic and non-diabetic subjects\(^{188}\) but the glucose- and insulin-lowering influence of TZDs in mice seems to be dependent upon adipose tissue\(^{189}\).

### 4.5 Phosphodiesterase 3B (PDE3B)

Phosphodiesterases hydrolyse cAMP, thus inactivating an important intracellular second messenger. At least eleven families of structurally related phosphodiesterases have been identified\(^{190}\). The phosphodiesterase isoenzymes differ in their affinity for cAMP, cellular location, mechanisms of regulation and tissue expression pattern. In most cell types several phosphodiesterases are co-expressed, producing a highly sophisticated regulation of cAMP levels. PDE3B is a membrane-bound protein and probably located in the endoplasmic reticulum. PDE3B is mainly expressed in insulin-sensitive cells like adipocytes, hepatocytes and pancreatic β-cells\(^{111}\). The signalling pathway by which insulin regulates PDE3B activity is only partially understood. In the adipocyte, PDE3B activation seems to be dependent on phosphoinositol-3 kinase and protein kinase B (Akt2)\(^{191}\). It has a high affinity for cAMP (active at low cAMP concentrations) and can be inhibited by high levels of cGMP.

The PDE3B gene is encoded by 16 exons\(^{192,193}\) covering 220 kb on chromosome 11p15.1 (accession number NT_009062 ) (Figure 23, results, page 56). The mRNA is 3.3 kb and the protein consists of 1112 aminoacids (accession number NM_000922). The lipolytic effect of TNFα involves the downregulation of PDE3B\(^{194}\). In the adipocyte, PDE3B accounts for 90% of the cells total phosphodiesterase activity and mediates the antilipolytic action of insulin\(^{112,195}\). In the hepatocyte, insulin inhibits glycogenolysis by activating PDE3B\(^{196,197}\). Studies have shown that activation of PDE3 in the β-cell can inhibit insulin secretion stimulated by increased cAMP levels.
Potentiation of insulin secretion at high glucose levels by an increase in intracellular cAMP levels might represent a mechanism by which the β-cell adapts to an increased insulin demand. Insulin stimulates insulin growth factor-1 (IGF-1) in the liver and IGF-1 is known to inhibit insulin secretion. Both IGF-1 stimulate PDE3B and it has been suggested that PDE3B may mediate negative feedback on insulin secretion.
The overall aim of this thesis was to identify genetic variation that increase the susceptibility to type 2 diabetes and the metabolic syndrome by investigating candidate genes in adipose tissue and lipid metabolism.

The specific aims were:

I) To identify mutations and variations in the coding region of the uncoupling protein 2 gene in obese patients with reduced energy expenditure, and to investigate if a common variant in this gene is associated with alterations in energy expenditure.

II) To identify mutations and variations in the coding region of the hormone sensitive lipase gene in diabetic patients with hypertriglyceridaemia, and to investigate if a microsatellite marker in the gene is associated with diabetes and/or abdominal obesity.

III) To investigate if a common variant in the lipoprotein lipase gene, Asn291Ser, is associated with dyslipidaemia in prediabetic and diabetic subjects, and to see if the association between Asn291Ser and dyslipidaemia in normoglycaemic subjects is altered by the presence of insulin resistance or obesity.

IV) To study if sixteen previously published associations between genetic variations and type 2 diabetes or prediabetic phenotypes can be replicated using a multi-step family-based approach. To identify mutations and variations in the coding region of the peroxisome proliferator-activated receptor gamma gene in diabetic patients.

V) To identify mutations and variations in the coding region of the phosphodiesterase 3B gene in diabetic patients, and to investigate if a common variant in the gene is associated with diabetes and/or prediabetic phenotypes.

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IV) To study if sixteen previously published associations between genetic variations and type 2 diabetes or prediabetic phenotypes can be replicated using a multi-step family-based approach. To identify mutations and variations in the coding region of the peroxisome proliferator-activated receptor gamma gene in diabetic patients.

V) To identify mutations and variations in the coding region of the phosphodiesterase 3B gene in diabetic patients, and to investigate if a common variant in the gene is associated with diabetes and/or prediabetic phenotypes.
6. Methodology

6.1 Study subjects

The study subjects were selected from Finland and Southern Sweden (Figure 9). Phenotypic characteristics of the study subjects are presented in Tables 1-5. All subjects have given informed consent, and the local ethic committees have approved of the study. Diagnosis of diabetes, IGT and IFG was based upon criteria established by the WHO or by a previous diagnosis of diabetes and treatment with oral agents and/or insulin. WHO criteria from 1985 were used in studies 1, 2 and 3 and WHO criteria from 1998 in studies 4 and 5. All subjects studied in this thesis are part of the Botnia study which started in 1990 in the Botnia region of western Finland and later extended to other parts of Finland and southern Sweden. To date, the Botnia study includes 1389 families with 9315 subjects, 3379 of whom have type 2 diabetes and 924 that are healthy control spouses. In particular the families from the Botnia region represent a genetically homogenous and young population, which is ideal for studies of complex genetic diseases.

Figure 9. The study subjects were selected from Sweden and Finland, including the Botnia region in western Finland.
Table 1. Phenotypic characteristics of the subjects in study I.

<table>
<thead>
<tr>
<th></th>
<th>Metabolic syndrome subjects</th>
<th>Control subjects</th>
<th>Mutation screened subjects</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (men/women)</td>
<td>55 (28/27)</td>
<td>46</td>
<td>30</td>
</tr>
<tr>
<td>Age (years)</td>
<td>61±13</td>
<td>64±11</td>
<td>58±13</td>
</tr>
<tr>
<td>Number (%) of MSDR cases§</td>
<td>52 (95)</td>
<td>5 (11)</td>
<td>25 (83)</td>
</tr>
<tr>
<td>Number (%) of diabetic cases†</td>
<td>42 (76)</td>
<td>-</td>
<td>21 (70)</td>
</tr>
<tr>
<td>Age at onset of diabetes</td>
<td>57±12</td>
<td>-</td>
<td>57±10</td>
</tr>
<tr>
<td>HbA1c (%)</td>
<td>7.6</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Free fatty acids (µM)</td>
<td>858±273</td>
<td>713±14</td>
<td>738±264</td>
</tr>
<tr>
<td>HOMA-IR index*</td>
<td>22.9±17.7</td>
<td>7.2±6.6</td>
<td>16.3±10.0</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>32±5</td>
<td>23±3</td>
<td>31±4</td>
</tr>
</tbody>
</table>

Data are numbers or mean ± standard deviation (SD). MSDR is the metabolic syndrome according to the proposal by the World Health Organization (WHO) in 1998. §Type 2 diabetes mellitus according the WHO consultation in 1985. *HOMA-IR index is reported only for subjects not treated with insulin.

Table 2. Phenotypic characteristics of the subjects in study II.

<table>
<thead>
<tr>
<th></th>
<th>Type 2 diabetic subjects</th>
<th>Control subjects</th>
<th>TDT offspring subjects</th>
<th>Mutation screened subjects</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (men/women)</td>
<td>235 (115/120)</td>
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<td>42 (23/19)</td>
<td>89 (53/36)</td>
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<tr>
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<td>10 (7)</td>
<td>10 (24)</td>
<td>80 (90)</td>
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<tr>
<td>Number (%) of diabetic cases†</td>
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<td>-</td>
<td>-</td>
<td>62 (70)</td>
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<tr>
<td>Age at onset of diabetes</td>
<td>54±9</td>
<td>-</td>
<td>-</td>
<td>52±11</td>
</tr>
<tr>
<td>HbA1c (%)</td>
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<td>5.3±0.5</td>
<td>5.5±0.6</td>
<td>7.4±2.1</td>
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<tr>
<td>Free fatty acids (µM)</td>
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<td>711±218</td>
<td>717±259</td>
<td>1152±464</td>
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<tr>
<td>HOMA-IR index*</td>
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<td>9.6±10.7</td>
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<tr>
<td>BMI (kg/m²)</td>
<td>27±5</td>
<td>25±3</td>
<td>27±5</td>
<td>30±4</td>
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Table 2. Phenotypic characteristics of the subjects in study II.

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<tr>
<th></th>
<th>Type 2 diabetic subjects</th>
<th>Control subjects</th>
<th>TDT offspring subjects</th>
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<tr>
<td>n (men/women)</td>
<td>235 (115/120)</td>
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<td>Age (years)</td>
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<td>60±12</td>
<td>37±9</td>
<td>56±14</td>
</tr>
<tr>
<td>Number (%) of MSDR cases§</td>
<td>127 (54)</td>
<td>10 (7)</td>
<td>10 (24)</td>
<td>80 (90)</td>
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<tr>
<td>Number (%) of diabetic cases†</td>
<td>235 (100)</td>
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<td>HbA1c (%)</td>
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<td>717±259</td>
<td>1152±464</td>
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<td>HOMA-IR index*</td>
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<td>2.2±1.4</td>
<td>9.6±10.7</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>27±5</td>
<td>25±3</td>
<td>27±5</td>
<td>30±4</td>
</tr>
</tbody>
</table>

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before and during the IVGTT. The euglycaemic clamp was performed with an intravenous bolus-injection of glucose (0.3 g 20% glucose /kg body weight) and venous blood sampling every 2 minutes for the first 10 minutes and then every 5 minutes for 50 minutes. Energy expenditure was measured two to three times with 5 minutes rest between each reading. Venous blood was sampled for extraction of DNA and for measurement of HbA1c and lipids, and albumin excretion rate was measured from timed overnight urine. The subjects were asked about their medical treatment, family-history of diabetes and related disease. Age at onset of diabetes and diabetic complications were checked from medical records. Most subjects (except those that have very severe diabetes, fasting glycaemia >10 mmol/l) underwent an OGTT. The OGTT was performed by the ingestion of 75 g glucose dissolved in water and venous blood sampling at –10, 0, 30, 60 and 120 minutes to measure glucose, insulin and c-peptide concentrations. Insulin resistance was estimated with the homeostasis model assessment (HOMA-IR) index and calculated as fasting insulin times fasting plasma glucose divided by 22.5. Some subjects (Study I) underwent the so-called Botnia clamp, which is an intravenous glucose tolerance test (IVGTT) directly followed by an euglycaemic clamp. The IVGTT was performed with an intravenous bolus-injection of glucose (0.3 g 20% glucose /kg body weight) and venous blood sampling every 2 minutes for the first 10 minutes and then every 5 minutes for 50 minutes. Energy expenditure was measured before and during the IVGTT. The euglycaemic clamp was performed with an Insulin sensitivity index was calculated as fasting insulin times fasting plasma glucose divided by 22.5. Some subjects (Study I) underwent the so-called Botnia clamp, which is an intravenous glucose tolerance test (IVGTT) directly followed by an euglycaemic clamp. The IVGTT was performed with an intravenous bolus-injection of glucose (0.3 g 20% glucose /kg body weight) and venous blood sampling every 2 minutes for the first 10 minutes and then every 5 minutes for 50 minutes. Energy expenditure was measured before and during the IVGTT. The euglycaemic clamp was performed with an

### Table 3. Phenotypic charateristics of the subjects in study III.

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<tr>
<th>Type 2 diabetic subjects</th>
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<td>278</td>
</tr>
<tr>
<td>(99/93)</td>
<td>(152/126)</td>
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<tr>
<td>Age (years)</td>
<td>63±12</td>
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<td>60 and 120 minutes</td>
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<tr>
<td>HbA1c (%)</td>
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<td>Free fatty acids (µM)</td>
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<td>723±211</td>
</tr>
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<td>HOMA-IR index</td>
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<tr>
<td>BMI (kg/m²)</td>
<td>28±5</td>
<td>27±3</td>
</tr>
</tbody>
</table>

Data are numbers or mean ± standard deviation (SD). MSDR is the metabolic syndrome according to the proposal by the World Health Organization (WHO) in 1998. *Type 2 diabetes mellitus according the WHO consultation in 1998. *HOMA-IR index is reported only for subjects not treated with insulin.

### 6.2 Phenotypic characterisation

The subjects included in the Botnia study have been extensively phenotyped. All subjects have undergone at least one health check to which they arrived fasting. The subjects were weighed and waist circumference, hip circumference and height were measured. Fat mass was assessed with the Futrex infrared and bioelectrical impedance methods (BIA 101, RJL systems, Detroit, MI). Blood pressure (sitting) was measured two to three times with 5 minutes rest between each reading. Venous blood was sampled for extraction of DNA and for measurement of HbA1c and lipids, and albumin excretion rate was measured from timed overnight urine. The subjects were asked about their medical treatment, family-history of diabetes and related disease. Age at onset of diabetes and diabetic complications were checked from medical records. Most subjects (except those that have very severe diabetes, fasting glycaemia >10 mmol/l) underwent an OGTT. The OGTT was performed by the ingestion of 75 g glucose dissolved in water and venous blood sampling at –10, 0, 30, 60 and 120 minutes to measure glucose, insulin and c-peptide concentrations. Insulin resistance was estimated with the homeostasis model assessment (HOMA-IR) index and calculated as fasting insulin times fasting plasma glucose divided by 22.5. Some subjects (Study I) underwent the so-called Botnia clamp, which is an intravenous glucose tolerance test (IVGTT) directly followed by an euglycaemic clamp. The IVGTT was performed with an intravenous bolus-injection of glucose (0.3 g 20% glucose /kg body weight) and venous blood sampling every 2 minutes for the first 10 minutes and then every 5 minutes for 50 minutes. Energy expenditure was measured before and during the IVGTT. The euglycaemic clamp was performed with an
intravenous infusion of insulin and simultaneous infusion of glucose to maintain glucose levels at 5.5 mmol/l for 2 hours, and mean glucose infusion rate between 60-120 minutes was used to estimate insulin sensitivity (the M-value). During the clamp glucose levels were measured every 5 minutes and clamped at 5.5 mmol/l.

Table 4A. Phenotypic characteristics of TDT offspring and subjects screened for mutations in study IV.

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<th>Mutation screened subjects</th>
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<tr>
<td>T2DM/IFG/IGT&lt;sup&gt;a&lt;/sup&gt;</td>
<td>Non-diabetic</td>
</tr>
<tr>
<td>n (men/women)</td>
<td>333</td>
</tr>
<tr>
<td>Age (years)</td>
<td>39±9</td>
</tr>
<tr>
<td>Number (%) of MSDR cases&lt;sup&gt;g&lt;/sup&gt;</td>
<td>149 (45)</td>
</tr>
<tr>
<td>Number (%) of diabetic cases&lt;sup&gt;f&lt;/sup&gt;</td>
<td>126 (38)</td>
</tr>
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<td>Age at onset of diabetes</td>
<td>38±12</td>
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<tr>
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<td>Free fatty acids (µM)</td>
<td>742±280</td>
</tr>
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<td>5.0±7.1</td>
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<tr>
<td>BMI (kg/m&lt;sup&gt;2&lt;/sup&gt;)</td>
<td>27±5</td>
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Data are numbers or mean ± standard deviation (SD). MSDR is the metabolic syndrome according to the proposal by the World Health Organization (WHO) in 1998.<sup>g</sup> Type 2 diabetes mellitus according the WHO consultation in 1998 and including subjects that have plasma glucose levels above 9.605 mmol/l 2 hours after an oral glucose tolerance test. *HOMA-IR index is reported only for subjects not treated with insulin. The offspring have type 2 diabetes (T2DM), impaired fasting glucose (IFG) or impaired glucose tolerance (IGT).<sup>b</sup> The 90 subjects are from 68 nuclear families.

### 6.3 Assays

Fasting blood glucose was measured with a glucose oxidase method using a Beckman Glucose Analyser II (Beckman Instruments, Fullerton, CA) (coefficient of variation (CV) <1%). Serum insulin (interassay CV 5%; Pharmacia, Uppsala, Sweden), C-peptide (interassay CV 9%) and leptin (interassay CV 4.5%) concentrations were measured with radioimmunoassay. Glycated haemoglobin (HbA1c) was analysed using high-pressure liquid chromatography (HPLC). Fasting plasma triglycerides (CV 2.2%), total cholesterol (CV 2.1%) and cholesterol in the precipitated HDL subfraction (CV 4.6%) were measured on a Cobas Mira analyser (Hoffman LaRoche, Basle, Switzerland). Apolipoprotein A-I (CV 3.5%) and A-II (CV 3.7%) were measured by turbidimetric methods using commercially available kits (Boehringer Mannheim), and apolipoprotein B (CV 4.4%) concentrations were measured by an immunochemical assay (Orion Diagnostica, Espoo, Finland). Serum FFA was measured with an enzymatic assay and intravenous infusion of insulin and simultaneous infusion of glucose to maintain glucose levels at 5.5 mmol/l for 2 hours, and mean glucose infusion rate between 60-120 minutes was used to estimate insulin sensitivity (the M-value). During the clamp glucose levels were measured every 5 minutes and clamped at 5.5 mmol/l.

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spectrophotometric detection (ACS-ACOD-kit, Wako Chemicals, Neuss, Germany) (CV 1.6%). Basal and isoprenaline-stimulated lipolytic activity in subcutaneous adipose tissue was assessed using glycerol corrected for cell number as a lipolytic index\(^{17}\). Genomic DNA was extracted from peripheral blood lymphocytes using standard methods\(^{201}\). Briefly, white blood cells were separated from blood by centrifugation in high sucrose. The cells were lysed with protease K and sodium dodecyl sulphate (SDS). Proteins were salt-precipitated and separated together with other cell debris by centrifugation. Genomic and mitochondrial DNA from the supernatant was precipitated with isopropanol, washed with ethanol and stored at -20°C in 0.5-3 µg/µl.

Table 4B. Phenotypic characteristics of the sibling pairs and case-control subjects in study IV.

<table>
<thead>
<tr>
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<th>Sibling pairs(^{a})</th>
<th>Case-control study</th>
</tr>
</thead>
<tbody>
<tr>
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<td>Type 2 diabetic</td>
<td>Non-diabetic</td>
</tr>
<tr>
<td></td>
<td>siblings</td>
<td>subjects</td>
</tr>
<tr>
<td>n (men/women)</td>
<td>612</td>
<td>518</td>
</tr>
<tr>
<td>(283/329)</td>
<td>(216/302)</td>
<td>(252/229)</td>
</tr>
<tr>
<td>Age (years)</td>
<td>65±10</td>
<td>62±10</td>
</tr>
<tr>
<td>Number (%) of MSDR cases(^{b})</td>
<td>435 (71)</td>
<td>68 (13)</td>
</tr>
<tr>
<td>Number (%) of diabetic cases(^{b})</td>
<td>612 (100)</td>
<td>-</td>
</tr>
<tr>
<td>Age at onset of diabetes</td>
<td>57±11</td>
<td>-</td>
</tr>
<tr>
<td>HbA1c (%)</td>
<td>7.3±1.8</td>
<td>5.4±0.6</td>
</tr>
<tr>
<td>Free fatty acids (µM)</td>
<td>889±394</td>
<td>705±216</td>
</tr>
<tr>
<td>HOMA-IR index*</td>
<td>6.4±7.1</td>
<td>2.6±2.7</td>
</tr>
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<td>BMI (kg/m(^2))</td>
<td>29±5</td>
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6.4 Genotyping

Genotyping was performed with DNA amplification using polymerase chain reaction (PCR). 5-10% of the samples from all cohorts were randomly tested for reproducibility, and genotyping was repeated from stock DNA. Allelic and genotypic frequencies were tested for Hardy-Weinberg equilibrium with \(\chi^2\)-test: if the frequency of allele 1 is p and allele 2 is q then the number of heterozygotes should be 2pq, and of homozygotes p\(^2\) (allele1) and q\(^2\) (allele 2).

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6.4.1 PCR

The PCR reactions were performed with initial denaturation (96 °C for 3 min) followed by 30 or 35 cycles of denaturation (96 °C for 30 s), annealing (30 s) and extension (72 °C for 30 s), followed by final extension (72 °C for 10 min). Annealing temperature was generally set two degrees below the Tm (Tm=[2x n(A+T)]+[4x n(G+C)]) of the primer with the lowest melting temperature. The reactions were performed in a total volume of 20 µl in an ammonium sulphate buffer (16 mmol/l (NH₄)₂SO₄, 67 mmol/l Tris (pH 8.8), 0.01% Tween 20) or Tris-buffer for Taq polymerase from Perkin-Elmer, Foster City, CA or Pharmacia, Uppsala, Sweden (10 mM Tris-HCl, pH 8.3; 50 mM KCl; 0.1% w/v gelatine). The reactions were performed with 0.13 mmol/l dNTP, 1.5 mmol/l MgCl₂, 0.2 µmol/l of both primers and 0.5 U Taq polymerase using 25 ng genomic DNA as template. Either 3% dimethylsulphoxide (DMSO), 1.5% formamide or 5% glycerol were used to increase PCR-sensitivity.

6.4.2 Genotyping by PCR-RFLP

The UCP2 Ala55Val polymorphism was genotyped by PCR-amplification with a mismatch primer followed by HincII digestion. The mismatch created a HincII site in sequences coding for a valine (GTC) and allowed electrophoretical separation of valine allele (216 and 25 bp) and alanine allele (241 bp) on agarose gels.
All HSL gene single nucleotide variants were amplified with PCR and cut with restriction enzymes (PCR-RFLP): The C2268T variant (exon 9) was cut with *BcnI* and the G41T variant (exon B) was cut with *DpnII*.

The *PDE3B* G1389A variant (exon 4) was PCR-amplified and the PCR product was cut with *HaeIII*, which cuts the G allele into two fragments of 165 and 88 bp (Figure 10). The *ABCC8 (SUR1)* G3819A variant (exon 9; also referred to as exon 31 in the literature) was PCR-amplified with a mismatch primer and the PCR-products were digested with *NlaIV* digestion. The mismatch creates a *NlaIV* site in sequences coding for G and the G alleles were cut into two fragments of 125 and 25 bp.

### 6.4.3 Genotyping by radioactive PCR

The *LIPE* marker is a (CA)$_n$ dinucleotide repeat, located in intron 7 of the *HSL* gene$^{202}$. It was genotyped with radioactive PCR using $\gamma$–ATP end-labelled primer (Figure 11). PCR was performed in a total volume of 15 µl. The amplified products were separated on a denaturing polyacrylamide gel.

### Figure 10. Genotyping the G1389A variant of the PDE3B gene by PCR-RFLP.

The figure illustrates genotyping of five samples (1-5). Lanes 1 and 4 represent individuals homozygous for the G allele, lanes 2 and 3 heterozygous individuals and lane 5 an individual that is homozygous for A.

### Figure 11. The LIPE microsatellite marker was genotyped with radioactively labelled primer and the alleles separated by size on a polyacrylamide gel. The Figure shows the genotypes of six samples (1-6) with the following genotypes: 1/1, 2/2, 2/10, 3/7, 1/2, and 2/10.
6.4.5 Genotyping by radioactive PCR-SBE

The *LPL* Asn291Ser variant was genotyped with an allele-specific mini-sequencing method (single-base extension, SBE), using a biotinylated downstream primer for PCR-amplification\textsuperscript{203}. The biotinylated PCR-fragment was linked to a streptavidin-coated well, incubated with detection primer and [\(^{3}H\)]dGTP, and a liquid scintillation counter was used to detect allelic variants with an A at the second position of codon 291.

6.4.6 Genotyping by PCR-SBE with fluorescent detection

In *study IV*, genotyping was performed with SBE using fluorescence polarization (SBE-FP) or fluorescence resonance energy transfer (SBE-FRET)\textsuperscript{204,205}. After PCR, shrimp alkaline phosphatase and exonuclease were added to degenerate excess dNTP and primers. Thereafter the variable nucleotide was PCR-amplified with a fluorescently labelled base. The genotypes were analyzed with an Analyst Fluorescence Plate-reader (Figure 12).

![Figure 12](scatterplot.png)

*Figure 12*. Scatterplot of genotypes determined with the SBE-FP method. The samples were irradiated with plane-polarized light. The light emitted from the fluorescent markers is of different wavelengths and the spread of the emitted light(s) determines the genotype. The light is more scattered from the fluorescently labelled nucleotides that have not been incorporated onto the SBE-primer. The output signals were plotted in a scatterplot and genotypes that lie within a certain distance from known control samples were determined.

For the SBE-FRET method the variable nucleotide was PCR-amplified with a fluorescently labelled base in an ABI 7700. The differences in fluorescence (read during the extension phase) between cycle 6 and cycle 1...
were calculated for ROX and TAMRA after matrix correction for spectral overlap and these differences were used to assign genotypes (Figure 13). In both methods, genotypes were assigned by clustering the data from 96 to 960 individuals and assignments were reviewed by at least two individuals.

![Figure 13](image)

**Figure 13.** Each PCR-cycle was monitored in a Taqman and after each cycle the fluorescent markers were irradiated with plane-polarized light. The light emitted from the fluorescent markers is of different wavelengths and the spread of the emitted light(s) determines the genotype.

6.5 Mutation screening (SSCP) and sequencing

For the mutation screening we used the single-strand conformational polymorphism (SSCP) technique. PCR was performed with 0.5 µCi α-32P-dCTP using intronic primers for amplification of coding and non-coding exons (Figure 14). A minimum distance of 25 bp between the intronic primer and the exon border was used when possible to allow detection of variants that could alter splicing. PCR products were separated on non-denaturing polyacrylamide gels in two conditions. When differences in band pattern were observed, PCR-products were sequenced bidirectionally. Heterozygous variants were confirmed by PCR-RFLP. Using this SSCP procedure, the estimated degree of mutation detection is around 95% in our laboratory (data from studies on monogenic disorders).

![Figure 14](image)

**Figure 14.** The mutation of the HSL exon B (nucleotide 41) as detected by SSCP. The picture shows the single-strand conformations of HSL exon B amplified by PCR with radioactively labelled nucleotides. Sample 2 has an alternative conformation (indicated by the arrow), which is due to a rare T allele at position 41.
6.6 Determination of exon/intron boundaries of the UCP2 gene
Using information about the exon/intron boundaries of the human UCP1 gene, introns of the human UCP2 gene were positioned while assuming conserved exon/intron structure between the genes. Exonic primers were constructed on both sides of each intron, and the introns were amplified by PCR and sequenced bidirectionally. Exon/intron borders were positioned by applying the GT/AG rule.

6.7 Determination of the region upstream of the first coding exon of the UCP2 gene
Genomic DNA was cut at nucleotide 77 of the second coding exon of UCP2 and at an unknown position upstream the coding region using NcoI. The fragmented genomic DNA was religated, generating circularised fragments of exon 1 extended with an unknown segment upstream of the gene. A 2.3 kb long circular fragment containing approximately 2 kb upstream of the first coding exon was generated. Two rounds of PCR were then performed using nested primers, and 295 bp of the region upstream of the first coding exon was determined by sequencing.

6.8 Statistical analyses
Statistical analyses were performed using the BMDP New System for Windows statistical package (Biomedical Data Processing, Los Angeles, CA). Descriptive clinical data were compared with the Student’s t-test (mean ± standard deviation (SD)). Differences in clinical characteristics of different genotype carriers were tested by Student’s t-test or Mann-Whitney non-parametric test (mean ± standard error of the mean (SEM) or median (interquartile range)). Bonferroni correction for multiple comparisons was used and reported when specified, although the corrected p-value can be considered too conservative when variables are not independent. Genetic interaction with physiological parameters was calculated by two-way analysis of variance (ANOVA). P-values of <0.05 were considered statistically significant.

6.8.1 Case-control studies
The case-control design is illustrated in Figure 15. The significance of differences in allele frequencies and allele frequency distributions were tested with Pearson χ²-analysis, and Fisher’s exact test (two-tailed) when expected numbers were too low (<5) to ensure the validity of the χ². In study 2 alleles with expected frequencies of less than 5.0 were pooled to assure the validity of the χ²-test. Comparative risk was estimated with the odds ratio (OR) and 95% confidence intervals (CI95%) were calculated.
6.8.2 Transmission disequilibrium test (qualitative) (TDT)

The transmission disequilibrium test is illustrated in Figure 16. In study II, the extended TDT (ETDT) analysis was performed to follow transmission of multiple alleles. The ETDT-program (version 1.4), which logistically regresses counts of transmitted and non-transmitted alleles in an allele-wise or genotype-wise model207 was used. Results are given as $\chi^2$-values and non-significant comparisons between the results from the two models indicate that the material is well fitted for the analysis. In study IV, TDT was performed using $\chi^2$ tests. In study V, TDT was performed using Genehunter 2.1208 implementing the TDT2 function to analyse haplotype data.

6.8.3 Quantitative transmission disequilibrium test (QTDT)

The quantitative transmission disequilibrium test (QTDT) was analysed using the variance components model with age, gender and BMI as covariates. In study IV the TDTQ5209 and in study V the Abecasis model210 (www.well.ox.ac.uk/asthma/QTDT) were used.

6.8.4 Genotype-discordant sibling pair analysis

Analyses comparing siblings are illustrated in Figure 17. Phenotypic differences between genotype discordant sibling pairs were compared using a simulation-based permutation test. The observed sum of differences (OSD) is the sum of differences

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Figure 15. A schematic representation of the case-control design. Unrelated subjects matched (pair- or group-wise) for age and ethnic origin but discordant for the disease are compared for allele frequencies.

Figure 16. A schematic representation of the TDT analysis. The parental affection status is not necessary for the analysis and parental transmissions are informative only from heterozygote parents. In this example, both parents transmitted the 1-allele. If 1-alleles are significantly over-transmitted to affected offspring in a large sample of parent-offspring trios this suggests that the 1-allele is associated with the disease.
between sibling pairs ($\Sigma(sibling1 - sibling2)$. The OSD is compared to the total distribution of $10^6$ permutations of the data set to determine the level of significance.

$\Sigma(sibling1 - sibling2)$.

**Figure 17. Analyses comparing siblings.** The sibling pairs can be matched for affection status, both either being non-affected (a) or affected (b). Siblings discordant for a specific genotype can be compared with regards to their phenotype. Siblings discordant for the phenotype (one affected and one non-affected) (c) can be compared for allele frequency (discordant alleles test, DAT).

6.8.5 Discordant alleles test

The discordant alleles test (DAT) is a pair-wise test comparing the frequency of alleles in phenotypically discordant siblings using a $\chi^2$ test (Figure 17).

6.8.6 Population attributable risk

Population attributable risk (PAR) was calculated assuming a multiplicative model (PAR = $X-1)/X$, where $X = (1-f)^2 + 2f(1-f) \gamma + f^2 \gamma^2$). PAR is largely determined by the frequency of the risk allele ($f$), and the estimated genotype relative risk (GRR, $\gamma$).

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7. Summary of studies I-V

7.1 Study I: No relationship between identified variants in the uncoupling protein 2 gene and energy expenditure

The aim of this study was to explore if genetic variability of the UCP2 gene contributes to reduced energy expenditure in lean and obese subjects, and whether it increases the susceptibility to develop obesity. To accomplish this we included subjects with information on basal metabolic rate (BMR). To screen the gene for mutations we first identified the exon/intron boundaries by sequencing. The human UCP2 gene was similar to the UCP1 gene in its exon/intron structure, with six exons covering 5 kb genomic sequence (Figure 18). The coding regions of the gene were screened for mutations in 30 obese subjects with low BMR, revealing a common polymorphism in exon 2, changing alanine to valine in codon 55 (Figure 18). The Ala55Val variant was not associated with BMR in 51 healthy controls from Finland or in 55 patients with the metabolic syndrome from Sweden. Neither was there any difference in allele or genotype frequency distribution between patients with the metabolic syndrome and 46 healthy controls from Sweden. The results suggest that mutations in the coding regions of the UCP2 gene do not affect BMR and do not contribute to increased susceptibility to obesity or the metabolic syndrome.

Figure 18. The UCP2 gene consists of 6 coding exons and 2 non-coding exons. The Ala55Val variant is located in exon 2.

7.2 Study II: The putative role of the hormone-sensitive lipase gene in the pathogenesis of Type II diabetes mellitus and abdominal obesity

The aim of this study was to investigate if genetic variability of the HSL gene contribute to abdominal obesity and type 2 diabetes. The subjects were selected based upon presence or absence of abdominal obesity and low HDL cholesterol levels for association studies and mutation screening of the HSL gene. We used the LIPE microsatellite marker in intron 7 of the gene (Figure 19) to investigate association between the gene and type 2 diabetes. The allele frequency distribution of the LIPE marker was different between 235 diabetic subjects and 146 healthy control...
subjects (p=0.002), suggesting that the LIPE marker was associated with type 2 diabetes. In a transmission disequilibrium test the transmission of LIPE marker alleles to 42 abdominally obese subjects with first degree family history of diabetes was distorted (p<0.05). There was no significant difference in allele frequency distribution of LIPE among non-diabetic subjects with high and low lipolytic rate in subcutaneous adipose tissue (p=0.07).

Figure 19. The HSL gene consists of 9 coding exons and two upstream exons. The LIPE marker is located in intron 7. Two silent variants were identified, one in exon B and another one in exon 9.

Figure 20. A family with a silent mutation in HSL exon B. Open symbols represent normoglycaemic subjects and filled symbols type 2 diabetic cases.
Mutation screening of abdominally obese subjects with the metabolic syndrome and subjects with high plasma triglycerides revealed two novel silent variants. In exon 9, a relatively common C→T change in codon 756 (alanine→alanine, nucleotide 2268) was detected. The variant did not co-segregate with diabetes or obesity, and allele and genotype frequencies did not differ between patients with the metabolic syndrome and healthy controls. In the non-coding exon B, a G→T change in nucleotide 41 was detected in one subject. As illustrated in Figure 20, the variant did not co-segregate with diabetes or obesity. No other carriers of the variant were detected among patients with the metabolic syndrome or healthy controls.

7.3 Study III: Interaction between the Asn291Ser variant of the LPL gene and insulin resistance on dyslipidaemia in high risk individuals for Type 2 diabetes mellitus

In this study we examined whether the Asn291Ser variant in the LPL gene was associated with dyslipidaemia in insulin resistant and type 2 diabetic subjects using a case-control design including 192 diabetic subjects, 278 non-diabetic subjects with first-degree family history of diabetes and 226 healthy control subjects with no known family history of diabetes. There was no difference in allele or genotype frequencies between diabetic subjects, first-degree relatives of diabetic subjects and controls. The serine allele was more common among normoglycaemic subjects with high plasma triglyceride levels than among subjects with normal triglyceride levels (p<0.05). Normoglycaemic serine carriers had three times greater risk of hypertriglyceridaemia than non-carriers (p<0.001). Of the normoglycaemic serine carriers, 46% had plasma triglyceride levels in the top quartile. There was a significant interaction between the Asn291Ser variant and insulin resistance, so that insulin resistant serine carriers developed more severe hypertriglyceridaemia than insulin sensitive carriers (p=0.05). In the diabetic subjects serine carriers were evenly distributed between all quartiles and they had no increased risk for hypertriglyceridaemia, even if they were insulin resistant.

7.4 Study IV: The common PPARγ Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes

The aim of this study was to investigate whether earlier reported associations could be replicated in Scandinavian subjects using a family-based approach. For this purpose we studied the role of 16 variants in 14 genes, that previously had been associated with type 2 diabetes, in Scandinavian parent-offspring trios. All offspring had type 2 diabetes, IGT or IFG. Variants that were associated with the trait in the trios were further tested in three independent replication sets: two samples of cases and controls from Scandinavia and French Canada and in Scandinavian sibling pairs discordant for diabetes. Variants that were associated with diabetes in these sets of patients were tested for association with quantitative variables in a set of parent-offspring trios with abdominally obese or lean normal glucose tolerant offspring. In
addition, we tried to identify new variants in the coding region of the \textit{PPAR\textgamma} gene in diabetic subjects belonging to families with some evidence of linkage to chromosome 3p25 in a previous genome-wide scan.

Three of the 16 tested gene variants were rare or absent and could not be tested in this material of subjects (Gly40Ser of the glucagon receptor gene, Val985Met of the insulin receptor gene and Ser20Gly of the islet amyloid polypeptide gene). Of the remaining thirteen variants, only two were associated with diabetes, Pro12Ala of the \textit{PPAR\textgamma} and a silent C/T variant in exon 22 of the sulphonylurea receptor gene (\textit{ABCC8}). Of the 12Pro alleles in the \textit{PPAR\textgamma} gene, 104 were transmitted and 81 were not transmitted from heterozygous parents (p=0.045, one-sided). Of the T alleles of the \textit{ABCC8} gene 26 were transmitted and 12 were not transmitted from heterozygous parents (p=0.012, one-sided). This indicates a significant over-transmission of these alleles to offspring with abnormal glucose tolerance. Only the association with the \textit{PPAR\textgamma} variant was confirmed in the replication sets. The \textit{PPAR\textgamma} 12Pro allele was also more frequent in diabetic subjects compared with their non-diabetic siblings (discordant alleles test (DAT); of the diabetic siblings 37 had alanine alleles and of the non-diabetic siblings 50 had alanine alleles, p=0.016, one-sided). The \textit{PPAR\textgamma} 12Pro allele was more frequent in Scandinavian (85% vs. 83%, p=0.11, one-sided) and French Canadian (91% vs. 87%, p=0.10, one-sided) diabetic patients compared to control subjects. Although all replication studies were not statistically significant by themselves, the data was significant after pooling (p=0.012). In the replication data of the \textit{ABCC8} variant, the T allele was slightly less frequent in Scandinavian diabetic siblings compared to non-diabetic siblings (3.5% vs. 4.9%, p=0.06, one-sided). This was in contrast with the overtransmission of the T allele in the TDT data and the \textit{ABCC8} variant was not studied further. The quantitative transmission disequilibrium test (QTDT) did not show any quantitative correlations with insulin sensitivity (HOMA-IR index), BMI or percent body fat between parental and offspring generations and the transmission of 12Pro or 12Ala alleles. Meta-analysis of all published reports on this variant in relation to diabetes showed that the frequency of the 12Ala allele was consistently less frequent in diabetic than control subjects (p=0.00007), although the individual study groups were mostly too small to provide statistically significant results.
show a statistical difference. The risk associated with the 12Ala allele was 0.8 (CI95%=0.7-0.9) in the pooled data, indicating that the 12Ala allele protects against development of type 2 diabetes. Since the risk allele (12Pro) is common, the risk attributed to the 12Pro allele in the general population was estimated to be approximately 25% (genotype relative risk 1.25 and allele frequency about 85%). Mutation screening of 90 diabetic subjects from 68 families identified one novel variant in one subject, changing a leucine to an isoleucine at codon 178 (Figure 21), but the variant did not co-segregate with diabetes or obesity (Figure 22).

### Figure 22. A family with the Leu178Ile mutation in exon 3 of the PPARγ gene. Open symbols represent normoglycaemic subjects, filled symbols type 2 diabetic patients and two-coloured symbols subjects with impaired glucose tolerance.

#### Table 22

<table>
<thead>
<tr>
<th>Study</th>
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<th>Rare Variant in Exon 3</th>
<th>Common Polymorphism in Exon 4</th>
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<td>N/A</td>
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<td>V</td>
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7.5 Study V: Association between a variant in the phosphodiesterase 3B gene and hyperinsulinemia in genotype-discordant sibling pairs

The aim of this study was to investigate if genetic alterations in the coding region of the PDE3B gene contribute to adiposity, insulin response or insulin sensitivity and increase the risk to develop type 2 diabetes and/ or impaired glucose tolerance. The coding region of the gene was screened for mutations in 40 subjects, including 20 subjects with type 2 diabetes and 10 sibling pairs discordant for the PDE3B G1389A variant. One novel variant was identified in intron 6 of one diabetic subject (Figure 23). A silent common polymorphism in exon 4, changing a nucleotide in position 1389 from guanine to adenine, was studied further using a genotype-discordant sibling pair design.

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The G1389A variant was investigated in relation to quantitative variables using a genotype-discordant sibling pair design. Siblings matched with at least one other sibling for gender and diabetic status were genotyped. This identified 266 sibling pairs discordant for the variant. Siblings discordant for the variant had similar fasting glucose and lipid levels and similar body composition. Siblings homozygous for the A allele had lower insulin levels 2 hours after OGTT compared to siblings carrying one or two G-alleles (p=0.0015). Sibling pairs discordant for PDE3B G1389A but matched for a variant in the sulphonylurea receptor gene (ABCC8) that previously has been associated with hyperinsulinaemia (G3819A), differed in 2-hour insulin levels (p=0.048). The association appeared stronger in sibling pairs discordant for both PDE3B/G1389A and ABCC8/G3819A (p=0.000035). The transmission of G1389A to offspring with IGT or IFG was tested in 108 parent-offspring trios. Two-hour insulin levels did not differ between carriers of A and G alleles in a quantitative TDT analysis. However, haplotype TDT including several variants in the region (Figure 24) showed that 1389A haplotypes were over-transmitted (p<0.05) and 1389G haplotypes were under-transmitted (p<0.05) to offspring with IGT or IFG.
8. General discussion

Few genetic factors that contribute to common forms of type 2 diabetes or the metabolic syndrome in humans have so far been identified. Some factors that may confer increased risk for the syndrome have been reported, but the interpretation of these different studies has been comprised by variable results in different ethnic populations. Small data sets, different selection criteria, different methods to assess phenotypic variables and ethnic differences may contribute to the discrepancies. There are several approaches that can be used in the search for genes that contribute to complex diseases. In the data presented in this thesis, we have utilised the candidate gene search, investigating genes of potential importance for the regulation of physiological mechanisms that are altered in the disease. This requires knowledge about the underlying pathogenic mechanisms, which is not always the case. Other approaches can be used to explore the whole genome, transcriptome, or proteome of a cell or an individual.

The genome-wide scan approach can be used to identify chromosomal regions linked to disease. Evidence for linkage is implied when affected members in families with the disease share alleles at a chromosomal region. The genome-wide scan approach has been important for the identification of genes that cause diseases with a clear Mendelian pattern of inheritance, e.g. diastrophic dysplasia (DTD). Diastrophic dysplasia is an autosomal recessive disease that was linked to chromosome 5q in 1991. The gene, which encodes a sulphate transporter, was cloned by linkage disequilibrium mapping in 1994. The success of this approach in type 2 diabetes has been limited. Recently, a novel gene, calpain 10, was identified by linkage disequilibrium (LD) mapping of a region on chromosome 2q in Mexican Americans. Surprisingly, linkage was explained by three intronic single nucleotide polymorphisms (SNPs). The reproducibility of genome wide scans has been poor which could reflect different contribution of genes in different populations. Allele frequency and interaction with other genetic and environmental factors will influence the power to detect linkage and may differ between populations. It is also likely that the genes that contribute to diabetes and obesity have only moderate influence on the phenotype, and therefore more sensitive methods than linkage analysis are needed for their identification. For this reason genome-wide association studies have been suggested. This type of studies have so far been hampered by the enormous amount of data that they would generate, as single nucleotide polymorphisms would be required at 2 cM distances over the entire genome. It is also uncertain what level of significance that would be required to distinguish statistically reliable data in such a setting.

Another approach is gene expression profiling in tissues of importance for the disease. An example of a protein that was identified in this fashion and which may contribute to type 2 diabetes is Rad (ras-related protein associated with diabetes). Rad was identified using a cDNA substraction technique as being highly expressed in tissues of importance for the disease. Evidence for linkage is implied when affected members in families with the disease share alleles at a chromosomal region. The genome-wide scan approach has been important for the identification of genes that cause diseases with a clear Mendelian pattern of inheritance, e.g. diastrophic dysplasia (DTD). Diastrophic dysplasia is an autosomal recessive disease that was linked to chromosome 5q in 1991. The gene, which encodes a sulphate transporter, was cloned by linkage disequilibrium mapping in 1994. The success of this approach in type 2 diabetes has been limited. Recently, a novel gene, calpain 10, was identified by linkage disequilibrium (LD) mapping of a region on chromosome 2q in Mexican Americans. Surprisingly, linkage was explained by three intronic single nucleotide polymorphisms (SNPs). The reproducibility of genome wide scans has been poor which could reflect different contribution of genes in different populations. Allele frequency and interaction with other genetic and environmental factors will influence the power to detect linkage and may differ between populations. It is also likely that the genes that contribute to diabetes and obesity have only moderate influence on the phenotype, and therefore more sensitive methods than linkage analysis are needed for their identification. For this reason genome-wide association studies have been suggested. This type of studies have so far been hampered by the enormous amount of data that they would generate, as single nucleotide polymorphisms would be required at 2 cM distances over the entire genome. It is also uncertain what level of significance that would be required to distinguish statistically reliable data in such a setting.

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overexpressed in skeletal muscle of type 2 diabetic subjects\(^2\)\(^15\). Today, microarray expression chips with probes for most mRNA expressed in human tissues have been developed. The interpretation clearly take longer than the generation of such data.

Heterogeneity of the disease is another challenge for genetic analysis. In the studies presented in this thesis we have tried to circumvent problems related to heterogeneity by studying relatives of subjects with type 2 diabetes, and/or features related to the metabolic syndrome that preceed the onset of diabetes. Type 2 diabetes and the metabolic syndrome are late-onset diseases and parents of affected individuals usually are not available. This complicates the selection of subjects for intra-familial studies like the TDT. Nuclear families are useful for intra-familial association studies, which tend to be less sensitive to ethnic admixture than case-control studies. To avoid phenocopies we have selected subjects who developed diabetes before the age of 60 to 65 years, and control subjects who were at least 40 years old.

A difficulty with polygenic diseases is that several genes may contribute to the phenotype, and that the effects may show variable penetrance. For example, only 1% of heterozygous and 10% of homozygous carriers of the \(\varepsilon2\) allele of the \(APOE\) gene develop dyslipidaemia\(^2\)\(^16\). There are several statistical problems with genetic studies, most of which relate to multiple testing; either of a large number of genetic markers or multiple phenotypes. Several approaches have been suggested to deal with these problems. However, the most important approach is still replication in an independent data set. In addition, to conclusively show that a genetic variant increases risk for developing the disease, cross-sectional data should be confirmed in prospective studies.

Other problems could arise from the phenotypic assessments. Triglycerides and FFA are known to have a high intra-individual biological variability and fasting levels of these may not always reflect the post-prandial state of lipemia. In addition, it may be more relevant to study FFAs which are transported from abdominal fat to the liver via the portal vein ("splanchnic FFA"). Careful assessment of insulin secretion and insulin sensitivity would require time-consuming and invasive studies like the hyperglycaemic and euglycaemic clamps. Therefore most genetic and epidemiological studies use surrogate measures like fasting insulin levels and the HOMA indices.
Concerning our results on the UCP2 gene, other studies have confirmed that the Ala55Val variant does not associate with diabetes or obesity. A Gly85Ser mutation was detected in one morbidly obese diabetic French subject, but it did not segregate with obesity or diabetes. However, two non-coding exons upstream the first coding exon and a large 3'-untranslated region of the last coding exon (number 6 in our data but also referred to as exon 8 in the literature) and a common variant in the 3'-untranslated region (exon 8 insertion/deletion) were identified. The exon 8 insertion allele was associated with increased metabolic rate and low BMI in Pima Indian subjects and with increased BMI in other studies. Recently, a G-866A variant was identified in the promoter region of the UCP2 gene. This variant was in linkage disequilibrium with the 3' insertion/deletion variant, and associated with obesity.

The UCP2 gene is located on chromosome 11q13, very close to the UCP3 gene which is expressed in skeletal muscle. Several variants have been identified in the UCP3 gene, including the common C-55T substitution in the putative promoter region and a splice donor variant in exon 6G228,229. The splice donor variant was associated with reduced fat oxidation and obesity, but the association seems restricted to subjects of African descent228,229. The TT genotype of the promoter variant has been associated with increased BMI230, increased WHR231, dyslipidaemia232 and type 2 diabetes232. This variant is in tight linkage disequilibrium with the insertion/deletion variant in exon 8 of the UCP2 gene, such that the T-allele of UCP3 C55T often is co-inherited with the deletion allele of the UCP2 gene231. Therefore it is less likely that linkage disequilibrium between these variants would contribute to both findings.

We can only speculate about the physiological role of uncoupling proteins expressed in white adipose tissue and skeletal muscle. The expression of UCP2 and UCP3 genes seems to be tightly regulated, and increase during fasting and endurance training and decrease after re-feeding150,233. This suggests that the uncoupling proteins could be regulated by FFA, and play a role in fuel partitioning. This is in line with results on the splice variant of the UCP3 gene that was associated with fat oxidation. Lately it has also been recognised that UCP2 may be important in the β-cell and play a role in insulin secretion. The UCP2 gene is normally expressed at low levels in pancreatic β-cells and overexpression of the gene in β-cells was associated with impaired glucose-stimulated insulin secretion234. Correspondingly, the UCP2 knockout mice have lower plasma glucose levels due to increased insulin secretion235. It has also been recognised that UCP2 and UCP3 may have a role in the regulation of the level of reactive oxygen species (ROS), since the level of these substances is increased in UCP2235,236 and UCP3237 knockout mice. This might contribute to both findings.

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explain why UCP2 knockout mice are resistant to toxoplasmosis, and point at the possibility that the uncoupling proteins may be important for the prevention of complications associated with the metabolic syndrome.

9.2 Study II: Hormone-sensitive lipase (HSL)

In agreement with our results on the HSL gene, other studies have shown that this region on chromosome 19q13 might harbour genetic variability that increase the susceptibility to obesity and/ or type 2 diabetes. Studies including French and Pima Indian families with type 2 diabetes have displayed some evidence for linkage to this chromosomal region. An association study using a microsatellite marker in intron 6 of the HSL gene indicated association to diabetes and obesity, very similar to the results presented in our study. To identify variants that contribute to these findings, we screened the coding region of the gene for mutations, detecting one common silent variant in the C-terminal region of the protein (C2268G). However, this variant was not associated with diabetes or the metabolic syndrome. Recently, the 5’ and 3’ untranslated and regulatory regions of the HSL gene were screened for mutations, identifying a C-60G substitution in the minimal promoter and a G3138A variant in the 3’-untranslated region. Later, another relatively common variant in exon 9 encoding the C-terminal region was identified in Swedish subjects, substituting glycine for alanine at codon 772 (Valerie Large, personal communication).

Homozygosity for the –60G allele was associated with increased BMI in healthy Finnish women and reduced transcriptional activity in vitro in COS cells. However, preliminary data from 214 Swedish subjects indicate that the variant is not associated with obesity, dyslipidaemia or disturbed lipolysis and that the C and G alleles are equally transmitted to abdominally obese offspring of diabetic subjects (Mia Klannemark, unpublished). Investigating allelic association between the identified variants, testing for transmission disequilibrium in the originally analysed trios with abdominally obese offspring as well as functional studies of the G-60C, C2268G, G3138A and Gly772Ala variants will be needed to clarify if these variants contribute to the original finding.

It is possible that genetic factors in other genes nearby the HSL gene contribute to the association between the HSL gene and diabetes/ abdominal obesity. Recent data in Caucasian populations have indicated that linkage disequilibrium can stretch over large chromosomal regions and that the degree of linkage disequilibrium can substantially vary between different regions of the genome. In study V we demonstrated a certain degree of linkage disequilibrium across the entire short arm of chromosome 11, a distance covering at least 15 Mb (between the KCNJ11 and the insulin genes). Several genes of interest are located on the long arm of chromosome 19. These include the CEBPα, the APOE/CI/CIV/CII gene complex and the muscle glycogen synthase (GYS1) genes. The APOE/CI/CIV/CII gene complex is located 3 Mb telomeric to the HSL gene (accession number NT_011240). Since these genes encode proteins involved in the regulation of lipid metabolism, variability in these genes could contribute to any of the phenotypes investigated in this study. The GYS1
gene is located ~7 Mb telomeric to the HSL gene. The XbaI polymorphism of the GYS1 gene has been associated with diabetes and features of the metabolic syndrome, particularly with hypertension. Although the distance between the HSL and the GYS1 gene is relatively large, it would be interesting to know if the HSL LIPE marker and the GYS1 XbaI variant are in allelic association. The CEBPα gene is located 10 Mb centromeric to the HSL gene.

9.3 Study III: Lipoprotein lipase (LPL)
Our data on the LPL gene show that carriers of the 291Ser allele have a 3-fold increased risk to develop dyslipidaemia. Diabetic subjects commonly have reduced LPL activity, and the type of dyslipidaemia seen in subjects with type 2 diabetes is very similar to that associated with the 291Ser allele. However, we did not observe an association between the 291Ser allele and plasma triglyceride or HDL cholesterol levels in diabetic subjects, suggesting that the diabetic state itself has a strong influence on the lipid profile. In fact, up to 60% of diabetic subjects compared to less than 20% of normoglycaemic subjects are dyslipidaemic, implying that development of diabetes confers a 3-fold increased risk for dyslipidaemia. There are several possible explanations for this, including mechanisms dependent on LPL activity. LPL activity is commonly reduced in diabetic subjects. Insulin upregulates LPL activity and lack of insulin could account for the reduced activity in type 1 diabetic subjects. As type 2 diabetic subjects are hyperinsulinaemic some other mechanism would be expected. LPL activity is inhibited by TNFα and TNFα levels are highly correlated with insulin resistance. Therefore, reduced LPL levels in adipose tissue of type 2 diabetic subjects could be partially explained by the inhibitory effect of TNFα, or by other factors associated with insulin resistance. However, such a mechanism would be expected to enhance rather than attenuate the difference between diabetic 291Ser carriers and non-carriers. Dyslipidaemia in diabetic subjects could be related to increased VLDL production in the liver. In fact, most studies seem to favour a high hepatic output of VLDL rather than reduced clearance, which is LPL dependent. Abdominal obesity and/or dysregulation of intracellular lipolysis in the visceral fat would lead to increased hepatic influx of FFA, known to stimulate hepatic output of VLDL. The net flux of FFA will be outward if intracellular lipolysis (i.e. HSL activity) is higher than the LPL-mediated lipolysis in the plasma. If dyslipidaemia develops independently of LPL it is unlikely that small variations in LPL function will further influence the phenotype.

9.4 Study IV: Peroxisome proliferator-activated receptor gamma (PPARγ)
The Pro12Ala variant of the PPARγ gene was identified by Yen et al. and was originally reported to be associated with a reduced risk for diabetes and a more insulin-sensitive phenotype. In vitro studies showed that the alanine allele had a reduced transcriptional transactivation activity, compared to the proline allele. Most follow-up studies could not replicate the findings. Instead, the Pro12Ala polymorphism was reported to be associated with obesity in some but not all diabetic subjects. In fact, such a mechanism would be expected to enhance rather than attenuate the difference between diabetic 291Ser carriers and non-carriers. Dyslipidaemia in diabetic subjects could be related to increased VLDL production in the liver. In fact, most studies seem to favour a high hepatic output of VLDL rather than reduced clearance, which is LPL dependent. Abdominal obesity and/or dysregulation of intracellular lipolysis in the visceral fat would lead to increased hepatic influx of FFA, known to stimulate hepatic output of VLDL. The net flux of FFA will be outward if intracellular lipolysis (i.e. HSL activity) is higher than the LPL-mediated lipolysis in the plasma. If dyslipidaemia develops independently of LPL it is unlikely that small variations in LPL function will further influence the phenotype.
populations 249,253-260. In study IV, we used several approaches including family-based association studies to test the hypothesis that the Pro12Ala is associated with diabetes. We could show that the 12Pro allele was associated with an increased risk for diabetes. Importantly previous studies support the data although they seem to lack power to detect significant differences, and recent studies published on the Pro12Ala variant support a protective role for the 12Ala allele261. To dissect the clinical phenotype we performed a quantitative test of phenotypic variables using the QTDT method. In contrast to some association studies248,262,263, this test did not show any correlations between genotype and insulin sensitivity (HOMA-IR index) or obesity. To our knowledge this is the first QTDT on phenotypes related to the Pro12Ala variant of the PPARγ gene. While the QTDT represents a specific test of a transmitted phenotype, it has not been established how sensitive it is. PPARγ has been detected in pancreatic β-cells, and carriers of the 12Ala allele have been shown to have reduced insulin secretory capacity after lipid challenge264. Reduced insulin secretory capacity might appear discrepant with a reduced risk for diabetes. However, it seems that once diabetes develops in 12Ala carriers, it is associated with a less favourable progress264. FFAs have been proposed as natural ligands for PPARγ. Dietary FFAs represent a mixture of fatty acids that vary in length and degree of saturation. It seems that the phenotype of Pro12Ala genotype carriers is dependent upon the fatty acid composition of the diet. In subjects with a high intake of saturated fat, the 12Ala allele was associated with increased BMI, whereas the opposite was seen when intake of unsaturated fat was low265.

9.5 Study V: Phosphodiesterase 3B (PDE3B)

We provide novel evidence that genetic variability in the PDE3B gene may contribute to dysregulated insulin secretion. Several genes of relevance for insulin secretion and insulin sensitivity are located in this region of chromosome 11. These include the genes for the sulphonylurea receptor (ABCC8), the inwardly rectified potassium channel (KCNJ11) and the phosphoinositol 3-kinase subtype 2A. These genes are located within a 1 Mb segment close to the centromere on the short arm of chromosome 11. Data from haplotype TDT and from siblings discordant for both the PDE3B and ABCC8 variants suggested that there may be an interaction between variants in these two genes. Furthermore, preliminary data propose an interaction between PDE3B and the sulphonylurea receptor in the β-cell. Many polygenic phenotypes could be associated with inherited haplotypes or haplotype combinations rather than with specific alleles. Sibling analysis has the advantage of comparing haplotypes since siblings share stretches of alleles. The use of permutations generates a distribution specific to the data set under analysis, yielding very high specificity and a small risk for false positive results.

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10. Summary and conclusions

Variants in the coding region of the UCP2 gene were not associated with BMR and did not contribute to increased susceptibility to obesity or the metabolic syndrome. It is thus unlikely that variation in the UCP2 gene contributes to obesity or the metabolic syndrome.

The LIPE marker in the HSL gene was associated with abdominal obesity and type 2 diabetes. This suggests that variation in the HSL gene may increase susceptibility to type 2 diabetes and the metabolic syndrome.

The Asn291Ser variant of the LPL gene was associated with dyslipidaemia in normoglycaemic subjects, and the dyslipidaemic phenotype was more severe in insulin-resistant subjects. This association was not seen in diabetic subjects. The results suggest that the Asn291Ser variant of the LPL gene may predispose to dyslipidaemia in insulin resistant subjects.

The Pro12 allele of the PPARγ gene was associated with a modest but highly reproducible risk for type 2 diabetes. Due to the high frequency of the risk allele the variation in the PPARγ gene may explain as much as 25% of the increased risk of type 2 diabetes.

Variability in or near the PDE3B gene may contribute to elevated postprandial insulin levels. This suggests that genetic variability in this region of chromosome 11 may be important in the regulation of the insulin response to different stimuli.

Taken together, variability in genes regulating lipolysis and adipogenesis seem to predispose to type 2 diabetes and the metabolic syndrome.
Typ 2 diabetes (åldersdiabetes eller sockersjuka) är en av de vanligaste folksjukdomarna, som ofta medför allvarliga komplikationer. Typ 2 diabetes utvecklas under en lång tid och uppträder ofta tillsammans med andra riskfaktorer för hjärt- och körsljukdomar, såsom fetma, förhöjt blodtryck och förhöjda blodfetter. Denna sjukdomsbild kallas det metabola syndromet. Individer som har det metabola syndromet har 2-3 gånger ökad risk att drabbas av hjärt- och körsljukdomar. Typ 2 diabetes och det metabola syndromet är komplexa polygena sjukdomar, d.v.s. de är sannolikt resultatet av en kollision mellan riskfaktorer som är ärvda och som finns i livsstilen.


Uncoupling protein 2 (UCP2) är en transport-kanal i mitokondrien som reglerar fränkopplingen av elektrontransport-kedjan från ATP-syntesen. Vi visade att en vanlig variation i genen (Ala55Val; ena allelen har en alanin och den andra en valin i kodon 55) inte är associerad med förändrad basalmetabolism och att allelerna var lika vanliga hos patienter med metabola syndromet som hos friska kontroller. Vi kunde inte identifiera några ovanliga mutationer eller mer vanliga variationer i genen hos patienter med metabola syndromet. Resultaten tyder på att variationer i genen inte predisperor för metabola syndromet eller nedsatt basalmetabolism.

Hormon-känsligt lipas (HSL) är ett enzym som finns i fettväven och som reglerar rekruteringen av fet som energikälla under fasta. Vi identifierade en mutation och en relativt vanlig variation i genen hos patienter med bukfetma och förhöjda triglycerider, och visade att dessa inte var associerade med metabola syndromet. Genom att studera en genetisk markör i genen (LIPE mikrosatellit) kunde vi visa att genen var associerad med typ 2 diabetes och bukfetma hos släktingar till diabetiker. Resultaten tyder på att vissa oidentifierade varianter av genen eller närliggande gener kan predispersa för typ 2 diabetes och bukfetma.
Lipoproteinlipas (LPL) är ett enzym som sitter på insidan av blodkärlen och som spjälker det fett vi äter så att kroppens vävnader kan tillgodogöra sig det. Vi studerade en variation i genen (Asn291Ser; ena allelen har aminosyran aspargin och den andra serin i kodon 291) och kunde visa att individer vars vävnader ger ett sämre svar på insulin (insulin-resistenta) hade en högre risk att utveckla störningar i fett-metabolismen om de var bärare av serin-allelen. Däremot bidrog inte serin-allelen till ökad risk för störningar i fett-metabolismen hos typ 2 diabetiker. Resultaten tyder på att serin-allelen kan vara en speciellt viktig risk-faktor för störningar i fettmetabolismen hos insulin-resistenta individer som inte har diabetes.


Fosfodiesteras 3B (PDE3B) finns i fettsjölet, lever och bukspottskörtelsens insulin-producerande celler. Vi studerade en vanlig variant i exon 4 av genen, G1389A (ena allelen har en guanin och den andra en adenosin i nukleotid 1389). Homozygota bärare av A allelen hade lägre insulin-nivåer i plasma två timmar efter ett oralt glukos-tolerans-test, jämfört med syskon som har en eller ingen A-alleler. Om man samtidigt har förändringar i andra gener på samma kromosom är risken ännu högre. Resultaten tyder på att haplotyper på den korta armen av kromosom 11 kan predisponera till störd insulinsekretion.

Sammantaget tyder detta på att variationer i gener som reglerar lipolys och fettsläckning kan bidra till bukfetma, typ 2 diabetes och det metabola syndromet. Prospektiva studier kommer att behövas för att fastställa om individer som bär på dessa genvarianter utvecklar diabetes tidigare och oftare än de som inte har dem.
12. Acknowledgements

I am very grateful to ♥ Leif Groop for giving me this opportunity to work in such a fine lab. For believing in me and making me see your vision so that I could be part of it. For teaching me the essence of science and never compromising on your high quality standard. For leading by example and stimulating an atmosphere of hard work and great fun. ♥ Marju Orho-Melander for giving me so much, sharing your knowledge in the lab and your expert eye for details, being a good friend and stimulating my curiosity when I felt I had ended up in a “dead spot”. ♥ Peter Almgren for the great work you have put into the database, for always being patient to answer my naive questions in the field of statistics and for rewarding discussions on the dissection of complex genetic disease. ♥ all my superb collaborators in other research laboratories in Sweden, Finland, France and the US: Cecilia Lindgren for being a great friend caring for my well-being, challenging me in my perception of myself and for helping me see the bigger picture of science in general, Marja-Riitta Taskinen for introducing me to the Finnish sisu and always being very encouraging, David Altshuler and Joel Hirschhorn, for intellectually very stimulating times trying to work out the complexity of PPARY, Cecilia Holm for precision and vast knowledge on HSL and molecular techniques, Dominique Langin for great spirit and efficiency, Peter Arner for being creative and supportive, Eva Degerman for your encouragement and for sharing your knowledge on insulin signalling, Vincent Manganiello for asking the questions I didn’t always think of, Charles “Randy” Lane, for being very helpful showing the lab in Boston, Martin Ridderdreår for your enthusiasm and just-do-it attitude and Erik Renström for expert knowledge in power point. ♥ the people who showed me how and helped me do it: Malin Åberg Svensson who had a hard time introducing me to new techniques, particularly when I was new in the lab, Margareta Svensson, Lena Rosberg and Anna Berglund, for putting up with all the changes in directives and expert technical assistance, Aki Suomalainen, for being a good friend and making everything in the lab work so smoothly. ♥ all the people working within the Botnia project at health care centers and laboratories in Sweden and Finland, and in particular Britt Bruveris-Svenburg in Malmö for performing analyses on leptin data and Seija Heikkinen in Helsinki for performing analyses on FFA that were so valuable for my studies. ♥ Ylva Wessman, Gertrud Ahlquist, Philippe Burri and Marianne Lundberg for making me familiar with our research protocols in the clinic. ♥ Ann Runnström and Ulla Häggström for caring for me in institutional matters. ♥ the people that have put up with my instructional (dis)abilities: Rebecca Chandler, Christina Kösters, Elina Suvio-latht, Eero Lindholm (you taught me more about sql than I ever taught you about genotyping), Valery Lyssenko, Lisbeth Lindberg and the medical students who attended the diabetes-research course. ♥ the rest of my work-mates and people I’ve met from other labs, for good

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working spirit and great parties.♥ all my friends outside the lab: Awazu Wallaziz: Tess Sandberg, for putting up with all my talking and never being judgmental, Sara Åkerberg, for a fantastic party-attitude and for making me rediscover gymnastics&aerobics, Lotta Wretman, for always lending space for my visits in Stockholm, Malin Knutsson and your son Anton, for wisdom on living and loving, Pixi de Villiers, for being clear-sighted in spite of your square eyes, Gugge Svensson, for showing me what perseverance is, Björn Schilström for adding some male touch to the Awazu gatherings, Ylva Strandberg and all the Awazu boyfriends (and their friends), Ute Friedrich, for always being ready for good advice especially in my career and for joining me for a lot of sporting activities, Birgitte Thuesen-Olesen, for lots of great gossip in between gels and running around Pildammarna and your spare bed in Copenhagen, Roy Quarton, for always making me laugh and taking me to some of the greatest films, Henrik Gyllstad, for the Piraya face, Eva Zetterberg, for being much like me and sharing fun times, “The Ronneby gang”: Jenny Johansson, Cia “Yng” Ståhlman, Emma Carlius and Liv Mattisson for the Karön experience, Jerker Karlsson & Anja Ekstrand for taking care of me in Malmö …and all the other nice people I’ve met around the world, especially the Squeedish team.♥ my family: my sister “Min Allra Käraste Syster Yster” Malin, for being a great friend and housewarmer, laughing with and at me and sharing also when things seem not so funny, my mother Christin, for your enormous capabilities and seemingly endless energy, my brother Marcus, for being a great entrepreneur and a lovely father and for introducing me to your extraordinary CD collection, my father Karl-Anders, for being very helpful in practical matters and your love for the out-doorsy life, my grandmother Margith, for your hard-working spirit and excellence in hostessing, my grandmother Sonja -min själsfrände, för att du alltid stöttat mig att göra det som du själv aldrig fick and my auntie Karin, for being a great example of ”Swedish sisu” and always caring about people around you …and to myself, for carrying the apple although it fell so far off the tree.♥ all the patients who have invested their time and hope in this project, and trusted us to resolve the mechanism behind a disease that they live with every day.

Mia Klannemark
August 2001, Malmö
13. References


76


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No relationship between identified variants in the uncoupling protein 2 gene and energy expenditure

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Abstract

Objective: The uncoupling protein 2 (UCP2) uncouples respiration from the oxidative phosphorylation in most cell types, predominantly in white fat and skeletal muscle. Since a decreased basal metabolic rate (BMR) would increase the susceptibility to weight gain, genetic alterations in the UCP2 gene could contribute to the pathogenesis of obesity and the metabolic syndrome (MSDR).

Design and methods: To test this hypothesis, we PCR amplified the introns of the UCP2 gene and sequenced the exon/intron boundaries. This information was used to construct intronic primers and to screen obese patients with low BMR for mutations in the coding regions of the UCP2 gene, using the single-strand conformational polymorphism technique. Furthermore, we examined whether there is an association between a biallelic marker in the UCP2 gene and BMR or MSDR.

Results: The UCP2 gene is composed of six coding exons, covering 5 kb of chromosome 11q13. One polymorphism, but no mutations, were identified in the coding regions of the UCP2 gene. There were no significant differences in the allele or genotype frequencies of the Ala55Val polymorphism between 55 patients with MSDR and 48 healthy controls. No association was found between the UCP2 gene and BMR in patients with MSDR or in healthy controls.

Conclusions: Mutation screening and association studies suggest that mutations in the coding regions of the UCP2 gene do not affect BMR and do not contribute to increased susceptibility to obesity or MSDR. The results cannot, however, exclude the possibility that variants in regulatory elements of the gene could contribute to the development of obesity or MSDR.

European Journal of Endocrinology 139 217–223

Introduction

The uncoupling proteins (UCP) represent a family of proteins that uncouple the respiration from the oxidative phosphorylation in the inner mitochondrial membrane (1). For a long time, UCP1 (2, 3) has been a marker for brown fat, a relatively abundant tissue in hibernating animals and newborns but less abundant in adults. The discovery of UCP2 and UCP3 isoforms in white fat and skeletal muscle (4–7) has renewed the interest in the UCP genes as candidate genes for obesity, particularly as white fat and skeletal muscle can be expected to contribute more to variations in energy expenditure than the scarce brown fat (8–12).

UCP2 is expressed in most tissues, with the highest mRNA concentrations found in white fat, skeletal muscle and cells of the immune system (4). It is known to be upregulated by leptin (13, 14), high-fat feeding (4) and the peroxisome proliferator-activated receptor-gamma agonist troglitazone (15). Recent results suggest that intracellular metabolism of free fatty acids may regulate the expression of UCP2 in adipose tissue (16). The UCP2 gene is located on chromosome 3 (17)

(4), a locus that has recently been linked to resting metabolic rate in the Quebec Family Study (17). Abdominal obesity and dyslipidaemia with high very-low-density lipoprotein-triglyceride and low high-density lipoprotein (HDL)-cholesterol levels are strongly associated with non-insulin dependent diabetes mellitus (NIDDM) (18–25). This particular clinical picture is often referred to as the metabolic syndrome (MSDR; insulin resistance syndrome/syndrome X), which predisposes to the development of atherosclerosis and macrovascular disease (26) and is considered to have a strong genetic background. MSDR clusters in families and represents a genetic adaptation towards an energy-saving phenotype with survival advantage during periods of famine (27). Therefore, genetic alterations in genes influencing energy expenditure seem likely to be involved in the polygenic background of MSDR.

To study whether alterations in the UCP2 gene contribute to the development of obesity or MSDR, we determined the exon/intron boundary sequences of the UCP2 gene and screened the coding regions and the exon/intron junctions for mutations in obese subjects with low basal metabolic rate (BMR). Using an amino

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acid polymorphism identified in the second coding exon of the UCP2 gene, we examined whether this variant is associated with MSDK or decreased BMR.

Materials and methods

Subjects and study design

MSDK was defined in accordance with the recent proposal adopted by the World Health Organization (unpublished data) suggesting that patients fulfilling at least three of the following criteria have MSDK: abdominal obesity, glucose intolerance, elevated blood pressure, elevated plasma triglyceride concentrations, decreased plasma HDL-cholesterol concentrations, microalbuminuria and insulin resistance. In this study, each patient defined as MSDK fulfilled at least three of the following criteria: waist-to-hip ratio (WHR) >0.95 for men and >0.85 for women, systolic/diastolic blood pressure >140/90 mmHg, plasma triglycerides >1.7 mmol/l, plasma HDL-cholesterol <1.0 mmol/l for men and <1.1 mmol/l for women, albumin excretion rate >200 mg/gmin and impaired glucose tolerance or NIDDM (28).

Determination of exon/intron boundaries with PCR and direct sequencing

Using information about the exon/intron boundaries of the human UCP1 gene (2, 3), introns were positioned in the human UCP2 gene while assuming conserved exon/intron structure between these genes. Exonic primers were constructed on both sides of each intron, and the introns were amplified by PCR (Table 2). The PCR reactions were performed with initial denaturation (96°C for 1 min) followed by 30 cycles of denaturation (94°C for 20 s), annealing (62°C or 64°C for 30 s) and extension (72°C for 1 min) for 30 cycles.

Table 2 Sequences of exonic primers and PCR conditions for amplification of the introns of the UCP2 gene. All the primer sequences are given in 5' to 3' direction. The number in parenthesis after each primer sequence indicates the exon from which it was derived.

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<th>Reverse primer sequence</th>
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<th>Annealing temperature</th>
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<tbody>
<tr>
<td>GTCAGACGCAAGCACTATGCC (1)</td>
<td>ACCATGGTCAGAAGCTGTTGCC (2)</td>
<td>1 (587)</td>
<td>64</td>
</tr>
<tr>
<td>TGGTGCTGCCCTCCAGCCG (3)</td>
<td>CTCTGCGCAGAAGCTGTTGCC (4)</td>
<td>2 (1100)</td>
<td>64</td>
</tr>
<tr>
<td>CATCGGAGAGTTGAGAGGGAAC (5)</td>
<td>AGGGAGGAGCTGTTGCC (6)</td>
<td>3 (899)</td>
<td>62</td>
</tr>
<tr>
<td>TGGCTGCTGAGTTGAGAGGGAAC (7)</td>
<td>TGGACGAGGAGCTGTTGCC (8)</td>
<td>4 (582)</td>
<td>62</td>
</tr>
</tbody>
</table>

| GTCAGACGCAAGCACTATGCC (1) | ACCATGGTCAGAAGCTGTTGCC (2) | 1 (587) | 64 |
| TGGTGCTGCCCTCCAGCCG (3) | CTCTGCGCAGAAGCTGTTGCC (4) | 2 (1100) | 64 |
| CATCGGAGAGTTGAGAGGGAAC (5) | AGGGAGGAGCTGTTGCC (6) | 3 (899) | 62 |
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Acid polymorphism identified in the second coding exon of the UCP2 gene, we examined whether this variant is associated with MSDK or decreased BMR.

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<td>TGGTGCTGCCCTCCAGCCG (3)</td>
<td>CTCTGCGCAGAAGCTGTTGCC (4)</td>
<td>2 (1100)</td>
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<tr>
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<td>AGGGAGGAGCTGTTGCC (6)</td>
<td>3 (899)</td>
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<tr>
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<td>TGGACGAGGAGCTGTTGCC (8)</td>
<td>4 (582)</td>
<td>62</td>
</tr>
</tbody>
</table>
2) and extension (72°C for 1 min), followed by final extension (72°C for 15 min). The reactions were performed in a total volume of 20 μl with Tris buffer for Taq polymerase (10 mM Tris–HCl, pH 8.3; 50 mM KCl; 0.01% (w/v) gelatin) and 1.5% formamide; 0.11 mM dNTP; 1.5 mM MgCl₂; 0.2 μM/l of both primers and 0.5U Taq polymerase (Perkin Elmer, Foster City, CA, USA) using 25 ng genomic DNA as a template. PCR products were sequenced using the ABI PRISM dye terminator cycle sequencing ready reaction kit (Perkin Elmer) and analysed on an automated sequencer (ABI model 373, Perkin Elmer). Introns 1, 3 and 5 were sequenced bidirectionally in their entirety, whereas only the exon/intron border sequences were sequenced for introns 2 and 4. Exon/intron borders were positioned by applying the GT/AG rule (29).

**Determination of the region upstream of the first coding exon by inverse PCR and direct sequencing**

Five micrograms genomic DNA isolated from a 50-year-old healthy Caucasian male were cut with 25U NcoI (New England Biolabs, Herts, UK) for 4 h in a total volume of 20 μl using conditions recommended by the manufacturer. NcoI, then incubated at 65°C for 10 min, and 6 μl of the digest were ligated in a total volume of 230 μl with 50U T4 DNA ligase (5U/μl, Applied Biogene, Gaithersburg, MD, USA) at 16°C for 24 h. In this procedure, the genomic DNA was cut at nucleotides 77 in the second coding exon and at an unknown position upstream of the coding region. Thus, a 2.3 kb long circular fragment containing approximately 2 kb upstream of the first coding exon was generated. Two rounds of PCR were then performed using nested primers: PCR1 (annealing temperature 62°C, 35 cycles) using the forward primer for fragment 2A (Table 3) and 5′-TTAGGAGTCAGCTGGCATCAGCCGG-3′ as the reverse primer and 2.0 μl ligation mixture as a template; PCR2 (annealing temperature 56°C, 25 cycles) using 5′-TGAGACGGTTGTCTATTAG-3′ as the forward primer and 5′-AATCTCAGTGCAGGGCAGTAG-3′ as the reverse primer and 0.5 μl amplification product from PCR1 as a template. PCR reactions were performed as for the exon/intron boundary PCR, but using NH₄OH buffer (16 mM NH₄OH, 67 mM Tris, pH 8.8; 0.01% Tween 20) in place of Tris–HCl and 5% glycerol instead of 1.5% formamide. When sequencing the PCR product from PCR2, the sequence of 295 bp of the region upstream of the first coding exon was acquired.

**Single-strand conformational polymorphism (SSCP)**

For the SSCP analysis (30), the six coding exons of the UC2P gene were amplified with intron primers (Table 3). For exons 1 and 2, overlapping sets of two exon (exon 1) or (exon 2) primer pairs were used. A minimum distance of 25 bp between the intronic primer and exon border was used for all fragments. PCR was performed as for the exon/intron boundary PCR, with the following changes: 0.5 μl cDNA (3·0 μg/μl) was added to each reaction; initial denaturation was set at 3 min, cycle denaturation at 30 s, cycle extension at 30 s and final extension at 10 min. As shown in Table 3 for 2A, annealing temperatures and buffers. The reactions were stopped with 95% formamide buffer (1:1); denatured, cooled and electrophoresed on a gel at 130 V for 3.5 h at 4°C and 3% gel (8W for 12 h at room temperature), non-denaturing 5% polyacrylamide gels (acylamide/bisacrylamide 49:1). When differences in band pattern were observed, PCR products were sequenced bidirectionally.

**Genotyping the Ala55Val polymorphism in the UC2P gene**

One polymorphism was identified in codon 55 of the

![Table 3](https://via.placeholder.com/150)

**Table 3** Primer sequences and variable conditions for PCR-SSCP analysis of the UC2P gene. All the primer sequences are given in 5′ to 3′ direction. The primers for fragments 1A and 1B amplify two overlapping fragments of exon 1. The primers for fragments 2A–2C amplify three overlapping fragments of exon 2. The reverse primer for amplification of exon 6 is located at the end of the coding sequence.

**Forward primer sequence**

- **exon amplified**
- **product size, bp**
- **annealing temperature (°C)**
- **Buffer* (μl)**

<table>
<thead>
<tr>
<th>Primer</th>
<th>Exon amplified</th>
<th>Product size, bp</th>
<th>Annealing temperature (°C)</th>
<th>Buffer* (μl)</th>
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<tbody>
<tr>
<td>TGGAGGACTGCGTTGCTATTAGG</td>
<td>1A (248)</td>
<td>58</td>
<td>TB</td>
<td></td>
</tr>
<tr>
<td>GTTGAAGGGCCTACAGAAATATGTTGC</td>
<td>1B (254)</td>
<td>58</td>
<td>TB</td>
<td></td>
</tr>
<tr>
<td>TACCTGTTAGAACCGGTGTTACAG</td>
<td>2A (247)</td>
<td>62</td>
<td>NB</td>
<td></td>
</tr>
<tr>
<td>TGGGTTTGGCATTGTTAGGTG</td>
<td>2B (256)</td>
<td>62</td>
<td>NB</td>
<td></td>
</tr>
<tr>
<td>AGGGTGCCCTAATGTTAGG</td>
<td>2C (257)</td>
<td>62</td>
<td>NB</td>
<td></td>
</tr>
<tr>
<td>CTGGAGAAGGTGTGCTACA</td>
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<td>60</td>
<td>NB</td>
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<tr>
<td>AGCGACTCTTCCTGGCGACGAGTACG</td>
<td>4A (254)</td>
<td>60</td>
<td>NB</td>
<td></td>
</tr>
<tr>
<td>CATCACAAGCTCGGCTCAGGGCTCG</td>
<td>4C (255)</td>
<td>60</td>
<td>NB</td>
<td></td>
</tr>
<tr>
<td>CTGCTTGGCTAGGCTACCG</td>
<td>5 (277)</td>
<td>60</td>
<td>TB</td>
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</tr>
<tr>
<td>GTTGGCGACCGGCTGCGTGCG</td>
<td>6 (160)</td>
<td>60</td>
<td>TB</td>
<td></td>
</tr>
</tbody>
</table>

*TB, tris–HCl buffer for Taq polymerase; NB, ammonium sulphate buffer.
Figure 1 The exon/intron structure of the coding region of the human UCP2 gene. Exons are numbered starting from the first coding exon and shown with filled boxes. Exons that were translated into sequences and open boxes untranslated sequences. Intron are illustrated with black lines. Vertical lines indicate the test nucleotide in each exon, with the nucleotide sequence numbered from the first nucleotide in the translation initiation codon. The translation initiation codon is indicated with an arrow. The first coding exon starts 90 bp upstream of the translation initiation codon, and exon 6 contains a 644 bp non-translated region (5).

**Statistical analyses**

Differences in allele and genotype frequencies between MSOR patients and control subjects were tested by χ² analysis, and differences in clinical characteristics by the Mann–Whitney non-parametric test using the BMDP New System for Windows (Biomedical Data Processing, Los Angeles, CA, USA). A P value of <0.05 was considered statistically significant.

**GenBank accession numbers**

The nucleotide sequences of the UCP2 gene were submitted to the EMBL Nucleotide Sequence Database with accession numbers AJ223477–AJ223479.

---

Table 1

<table>
<thead>
<tr>
<th>Coding exon no.</th>
<th>Intronic size (bp)</th>
<th>Coding exon no. (bp)</th>
</tr>
</thead>
<tbody>
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<td>1</td>
<td>356</td>
<td>126</td>
</tr>
<tr>
<td>2</td>
<td>337</td>
<td>377</td>
</tr>
<tr>
<td>3</td>
<td>532</td>
<td>634</td>
</tr>
<tr>
<td>4</td>
<td>815</td>
<td>930</td>
</tr>
</tbody>
</table>

Table 2

<table>
<thead>
<tr>
<th>Coding exon no.</th>
<th>Intronic size (bp)</th>
<th>Coding exon no. (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>356</td>
<td>126</td>
</tr>
<tr>
<td>2</td>
<td>337</td>
<td>377</td>
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<tr>
<td>3</td>
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<td>815</td>
<td>930</td>
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</table>

Figure 2 Sequences at the ex0/intron junctions of the coding region of the human UCP2 gene. Exon sequences are given in uppercase letters, with encoded amino acids shown below the nucleotide sequence. Intron sequences are given in lowercase letters. Amino acids that are present in the mature protein are indicated with a codon number. Intron sizes were determined by sequencing (intron 1, 3 and 5) or by size estimation of the PCR product on an agarose gel (intron 2 and 4). When comparing the coding region of the UCP2 gene with that of the human UCP1 gene (3), the exon/intron structure was conserved except that exon 2 of the UCP2 gene is four amino acids shorter and exon 3 is two amino acids longer than the corresponding exons of the UCP1 gene. Therefore, exon 2 of the human UCP2 gene is interrupted by intron 5 at Thr<sup>38</sup> instead of His<sup>19</sup>. The exon/intron structure of the coding region of the UCP2 gene is conserved also with the human UCP3 gene (31), except that exon 3 of the UCP3 gene contains three additional amino acids and is thus interrupted by intron 3 at Gly<sup>33</sup> instead of at Gly<sup>18</sup>.


Results

The UCP2 gene was found to be composed of six coding exons covering 5 kb of chromosome 11q13 (Fig. 1). All the exon/intron boundaries and exon sites (coding exons) were similar to the structures of the human UCP1 (3) and UCP3 (31) genes (Fig. 2).

Mutations screening of the UCP2 gene in 30 obese patients with low BMR revealed one polymorphism (Ala55Val) in codon 55 of the UCP2 gene, changing an alanine (GEC) to a valine (GTC).

In healthy Finnish controls, the frequency of the alanine allele was 60.8% and that of the valine allele 39.2%. There were no significant differences in BMR between healthy control subjects or MSDR subjects with different Ala55Val genotypes (Table 4). The allele frequencies and genotype distributions of the Ala55Val polymorphism did not differ significantly between 55 subjects with MSDR and 46 healthy controls (Table 5). Genotype frequencies were in Hardy–Weinberg equilibrium in all groups studied.

Discussion

The exon/intron structure of the coding region of the human UCP2 gene was similar to the structures of the human UCP1 and UCP3 genes. Information on the exon/intron boundaries of the six coding exons of the UCP2 gene allowed us to screen coding exons and flanking intronic regions for mutations in obese patients with low BMR.

Basal energy expenditure accounts for 60−70% of total energy expenditure (9), the rest being generated during exercise and food-induced thermogenesis. The variability of BMR is largely dependent on processes in non-adipose tissues (60−80%) (9). Nevertheless, white adipose tissue could contribute to the small decrease needed to gain weight over time, and low BMR is a risk factor for weight gain (12).

Mice deficient in brown adipose tissue become obese and hyperinsulinemic (33). Surprisingly, targeted disruption of the UCP1 gene in mice does not result in obesity; a finding which led to the postulation of other UCP genes involved in this mechanism (34). No mutations that increase the susceptibility to obesity have been found in the coding region of the UCP1 gene in obese humans (35). However, one polymorphism near the UCP1 gene, at nucleotide position 3826, has been associated with increased weight gain during adult life (36), and the effect of this variant was enhanced when it occurred together with the Trp64Arg mutation in the β3-adrenergic receptor gene (17).

In the present study, mutation screening of 30 obese patients with low BMR revealed one common variant in exon 2, Ala55Val, but there was no difference in allele frequency between patients with MSDR and healthy controls. This is in accordance with a recent Danish study, in which no association was found between the Ala55Val polymorphism and juvenile obesity (36). However, this study did not include measures of energy expenditure, a quantitative trait which may be more relevant to the genotype.

In accordance with these findings, highly polymorphic markers flanking the UCP2 and UCP3 genes (4, 33) were not linked to BMI or BMR in a study of sibling pairs (39). In contrast to this, the highly polymorphic marker D11S151 was reported to be tightly linked to resting metabolic rate in the Quebec Family Study (17). Consequently, it seems that this chromosomal region links to resting metabolic rate but not to obesity. However, in the present study the Ala55Val polymorphism was associated neither with decreased BMR (in patients with MSDR) or in healthy controls nor with obesity in patients with MSDR. There are several potential explanations for the discrepancy of these findings. First, the Ala55Val variant might not be in linkage disequilibrium with the variants responsible for the linkage found in the Quebec Family Study. Thus, the UCP2 gene may still be important for the variability of metabolic rate, although in such cases this does not seem to influence susceptibility to obesity. Second, regions important for gene regulation were not included in our screening. Thus alleles responsible for the linkage found in the Quebec Family Study could be present in the promoter region or other regulatory parts of the UCP2 gene or in the very closely located UCP3 gene. On the other hand, if the linkage in the Quebec Family

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Study was explained by a variant in the promotor of the UCP2 gene that led to a decreased expression of UCP2 in obese individuals or in individuals with reduced BMR. However, in a recent study of UCP2 mRNA levels in obese and lean skeletal muscle, no difference was observed between lean and obese subjects and the level of expression did not correlate with BMI (16).

In conclusion, mutation screening and association studies suggest that mutations in the coding regions of the UCP2 gene do not affect BMR and do not contribute to increased susceptibility to obesity or MS/DR. The results cannot, however, exclude the possibility that variants in regulatory elements of the gene could contribute to the development of obesity or MS/DR.

Acknowledgements

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References


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The putative role of the hormone-sensitive lipase gene in the pathogenesis of Type II diabetes mellitus and abdominal obesity

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4 Huddinge Hospital, Stockholm, Sweden
5 Department of Medicine, Helsinki University Hospital, Helsinki, Finland

Summary

Impaired lipolysis has been proposed as a pathogenic factor contributing to clustering of abdominal obesity and dyslipidaemia in Type II (non-insulin-dependent) diabetes mellitus – that is, the metabolic syndrome (MSDR). As this syndrome clusters in families, alterations in the hormone-sensitive lipase (HSL) gene could contribute to the genetic predisposition to MSDR. To test this hypothesis we carried out population and intrafamilial association studies in individuals with MSDR, using a polymorphic marker (LIPE) in the HSL gene. There was a significant difference in allele frequency distribution between 235 Type II diabetic patients and 146 control subjects (p = 0.002), particularly between 78 abdominally obese Type II diabetic patients with MSDR and the control group (p = 0.010). An extended transmission disequilibrium test (TDT) showed transmission disequilibrium of 66 alleles to 42 non-diabetic, abdominally obese offspring in families with Type II diabetes (p < 0.05). A slight difference in allele frequency distribution was seen between 71 individuals from the lowest and 71 from the highest tertile of insulin-induced lipolysis in fat tissue (p = 0.07). No missense mutations were found with single- or multi-allelic conformational polymorphism (SSCP) in 20 abdominally obese subjects with MSDR. In conclusion, our population and intrafamilial association studies suggest that the LIPE marker in the HSL gene is in linkage disequilibrium with an allele and/or gene which increases susceptibility to abdominal obesity and thereby possibly to Type II diabetes. [Diabetologia (1998) 41: 1516–1522]

Keywords

Hormone-sensitive lipase, metabolic syndrome, insulin resistance syndrome, syndrome X, LIPE, dyslipidaemia, Type II (non-insulin-dependent) diabetes mellitus, abdominal obesity.

Abdominal obesity, hypertension and dyslipidaemia are strongly associated with Type II (non-insulin-dependent) diabetes mellitus [1, 2], and this cluster is often referred to as the metabolic syndrome (MSDR), also called insulin resistance syndrome or Syndrome X. According to a preliminary definition by the World Health Organisation (WHO) [2], diabetic patients, patients with impaired glucose tolerance (IGT) and/or insulin resistance have MSDR if they present at least two of the following features: abdominal obesity, increased plasma triglyceride concentrations, reduced HDL cholesterol concentrations, hypertension and/or microalbuminuria. MSDR is associated with an increased risk of atherosclerosis and macrovascular disease [4, 5] and is considered to have a strong genetic background [6, 7]. In support of this, a number of studies have shown that the LIPE gene, encoding the hormone-sensitive lipase, is involved in the pathogenesis of MSDR. In this study, we have investigated the LIPE gene in a population of Type II diabetic patients with MSDR and a control group of healthy subjects.

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Corresponding author: Professor Leif Groop, Wallenberg Laboratory, Endocrinology and Diabetology, floor 3, UMAS entrance, 46, 205 02 Malmö, Sweden

Abreviations: cAMP, cyclic adenosine monophosphate; NEFA, non-esterified fatty acids; HOMA, homeostasis model assessment; HSL, hormone-sensitive lipase; IGT, impaired glucose tolerance; MSDR, metabolic syndrome; NGT, normal glucose tolerance; DMSO, dimethylsulphoxide; PCR, polymerase chain reaction; SSCP, single-strand conformational polymorphism; Tg, plasma triglycerides; WHR, waist-to-hip ratio; WHO, World Health Organisation; TDT, transmission disequilibrium test; D.f., degrees of freedom; RFLP, restriction fragment length polymorphism.

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of this, MSDR clusters in families and healthy first-degeree relatives of Type II diabetic patients have increased frequency of abdominal obesity, insulin resistance and dyslipidaemia [8]. In addition, many of them have a decreased metabolic rate [8]. Abdominal obesity in association with the characteristic dyslipidaemia and low basal metabolic rate points at disturbances in abdominal fat lipolysis.

Hormone-sensitive lipase is the rate-limiting enzyme in the breakdown of triglycerides in adipose tissue. The enzyme is activated by catecholamines through CAM-dependent phosphorylation, whereas insulin prevents this phosphorylation through increased hydrolsis of cAMP [9–11]. Lipolysis and lipid metabolism are disturbed in patients with Type II diabetes [12], MSDR [13, 14] and in subjects of normal weight with a family history of diabetes [15]. Therefore, genetic variants of the HSL gene could be related to abnormal lipid metabolism, abdominal obesity or Type II diabetes.

The HSL gene is located on chromosome 19q13.1-13.2 [16]. The adipocty isoform of HSL is encoded by 9 exons [17]. Adipocyte HSL is composed of two major domains of which the N-terminal domain is largely encoded by exons 1–4 and the C-terminal cataytic domain by exons 5–9 [18].

To study the ADP ribosylations in the HSL gene contribution to the development of MSDR, we carried out association studies and in extended transmission disequilibrium test (ETDT) using a polymorphism in the HSL gene and screened the coding regions of the gene for mutations in diabetic and nondiabetic abnormally obese subjects with MSDR. As an additional functional marker for HSL catalytic capacity we used the in vitro maximum lipolytic rate of subcutaneous adipose cells [13, 14].

Subjects and methods

The study consisted of four parts. In the first three studies we analysed association and transmission disequilibrium between a polymorphism in the HSL gene (L99M of MSDR/Type II diabetes) and a low lipolytic rate. In the fourth study we carried out mutation screening of the HSL gene in abdominally obese subjects with MSDR.

Subjects and study design. MSDR was defined by waist-to-hip ratio (WHR) > 1.0 (men) or > 0.9 (women) and LDL < 1.0 mmol/l (men) or < 1.1 mmol/l (women).

1) In the association study with MSDR as the phenotype, 78 Type II diabetic patients with abdominal obesity and low LDL cholesterol concentrations (MSDR/Type II diabetes), 157 nondiabetic Type II diabetic patients with normal LDL (nondiabetic Type II diabetes), and 37 abdominally obese subjects with normal glucose tolerance (NGT) and low LDL cholesterol concentrations (MSDR/NGT) were compared with 146 unrelated nondiabetic, healthy control spouses with NGT and normal LDL cholesterol concentrations and without family history of diabetes. Clinical characteristics of the study groups are shown in Table 1. There was a family history of Type II diabetes in 27 of the 37 MSDR/NGT subjects. All subjects were unrelated and selected from the Borna region (former part of western Finland) or from southern Sweden. All groups were matched for ethnicity and statistical tests were done to assure that allele frequencies did not differ between the different subgroups from the two regions.

2) In the association study with MSDR as the phenotype, 78 Type II diabetic patients with abdominal obesity and low LDL cholesterol concentrations (MSDR/Type II diabetes), 157 nondiabetic Type II diabetic patients with normal LDL (nondiabetic Type II diabetes), and 37 abdominally obese subjects with normal glucose tolerance (NGT) and low LDL cholesterol concentrations (MSDR/NGT) were compared with 146 unrelated nondiabetic, healthy control spouses with NGT and normal LDL cholesterol concentrations and without family history of diabetes. Clinical characteristics of the study groups are shown in Table 1. There was a family history of Type II diabetes in 27 of the 37 MSDR/NGT subjects. All subjects were unrelated and selected from the Borna region (former part of western Finland) or from southern Sweden. All groups were matched for ethnicity and statistical tests were done to assure that allele frequencies did not differ between the different subgroups from the two regions.

Table 1. Clinical characteristics of the subjects analysed in the association study of the HSL gene and characteristics of MSDR

<table>
<thead>
<tr>
<th>MSDR</th>
<th>nt</th>
<th>Sex (males/females)</th>
<th>Age at visit (years)</th>
<th>Age at onset of diabetes (years)</th>
<th>BMI (kg/m²)</th>
<th>WHR: men</th>
<th>WHR: women</th>
<th>Triglycerides (mmol/l)</th>
<th>Cholesterol (mmol/l)</th>
<th>HDL cholesterol (mmol/l): men</th>
<th>HDL cholesterol (mmol/l): women</th>
<th>NEFA (μM)</th>
<th>NEFA (μM)</th>
<th>Syntetic blood pressure (mmHg)</th>
<th>Diastolic blood pressure (mmHg)</th>
<th>Fasting blood glucose (mmol/l)</th>
<th>Fasting blood glucose (mmol/l)</th>
<th>HbA1C (%)</th>
<th>HbA1C (%)</th>
<th>Fasting serum insulin (mU/l)</th>
<th>Fasting serum insulin (mU/l)</th>
<th>HOMA index for insulin resistance</th>
<th>Fasting C-peptide (nmol/l)</th>
<th>Fasting C-peptide (nmol/l)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MSDR</td>
<td>n</td>
<td>146</td>
<td>71/75</td>
<td>57.7 ± 12.1</td>
<td>34.4</td>
<td>5.1</td>
<td>5.7</td>
<td>1.2 ± 0.4</td>
<td>0.6 ± 1.2</td>
<td>1.3 ± 0.5</td>
<td>0.9 ± 0.3</td>
<td>852 ± 246</td>
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<td>131 ± 16</td>
<td>6.8 ± 3.3</td>
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<td>37</td>
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</table>

Data are mean ± SD. NEFA was measured for 22 of the healthy control subjects, 64 of the nondiabetic Type II diabetic patients and 28 of the MSDR/Type II diabetic patients. No data on NEFA was available for MSDR/NGT patients.
2) In the extended transmission disequilibrium test, 42 unrelated subjects (23 men, 19 women) with both parents available for genetic analysis, were sequentially genotyped. Five of 79 single nucleotide polymorphism (SNP) sites of the HLA gene and highly polymorphic (heterozygosity index 0.79) was genotyped with multiplex PCR and sequenced on an ABI 3730XL. The genotypes were genotyped with multiplex PCR and sequenced on an ABI 3730XL. The genotypes were classified using the D' values (Pearson's correlation coefficient). Genotyping.

Genomic DNA was extracted from peripheral blood lymphocytes using standard methods [23]. The lipoteichoic acid (LTA) was used as a marker for the HLA-A, HLA-B, and HLA-C loci. All individuals with an HLA-A, HLA-B, and HLA-C loci were classified as HLA-A, HLA-B, and HLA-C heterozygous.

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population [26], and thus 89 subjects were screened seeking to identify subjects with this polymorphism. PCR was carried out with initial denaturation (96°C for 3 min) followed by 31 cycles of denaturation (96°C for 30 s), annealing (30 s, see Table 3 for variable annealing temperatures) and extension (72°C for 30 s), followed by final extension at 72°C for 10 min. The reactions were done in a total volume of 20 μl with 16 mM NH4SO4, 67 mM Tris (pH 8.8), 0.1% Tween 20, 0.13 mM dNTPs, 1.5 mM MgCl2, 0.2 μM of both primers; 0.5 μM α-32P-dCTP and 0.5 μM Taq polymerase using 21 ng genomic DNA as template. Either 1% DMSO, 1.5% formamide or 5% glycerol (Table 3) was used to increase PCR-sensitivity. The reactions were stopped with 95% formamide buffer (1:1, denatured, cooled and electrophoresed on glycerol-free 3% for 3.5 h at 4°C and 5% glycerol (8W for 12 h at room temperature), nondenaturating 5% polyacrylamide gels (acylamide/bisacrylamide 49:1). When different band patterns were observed, PCR products were sequenced bidirectionally using the ABI PRISM dye terminator cycle sequencing kit (Perkin Elmer, Foster City, Calif., USA) and analysed on an automated sequencer (ABI model 373, Perkin Elmer). Heterozygous variants were confirmed by using the restriction fragment length polymorphism technique (PCR-RFLP). Using this procedure, the estimated degree of mutation detection is approximately 95% in our laboratory. Statistical analysis. Differences in clinical characteristics were tested by Mann-Whitney nonparametric test statistics using the BMDF New System for Windows statistical package (Biomedical Data Processing, Los Angeles, Calif., USA). P-values of less than 0.05 were considered statistically significant. Allele frequency distribution was tested by χ2-analysis, and alleles with expected frequencies of less than 5.0 were pooled to assure the validity of the χ2-test. Extended TDT analysis was calculated using the ETDT software package 1.4 for multilocus markers [27], whereby logistic regression was done to estimate parameters for transmitted and non-transmitted alleles from heterozygous parents. With these parameters, log likelihood was calculated for the allele-wise and genotype-wise model and deviation from the null-hypothesis tested by the McNemar Z-test.

Results

Association study of the HSL LIPE marker with MSDR as the phenotype. In these subjects we identified 14 alleles for the HSL LIPE marker (Table 4), ranging in size from 164 to 194 base pairs (bp). The allele frequency distribution of the HSL LIPE marker differed significantly between 235 Type II diabetic patients and 146 healthy control subjects (χ2 = 20.6, 6 degrees of freedom (d.f.), p = 0.002), between 78 MSDR/Type II diabetic patients and the control subjects (χ2 = 16.8, 6 d.f., p = 0.010) and between 157 population [26], and thus 89 subjects were screened seeking to identify subjects with this polymorphism. PCR was carried out with initial denaturation (96°C for 3 min) followed by 31 cycles of denaturation (96°C for 30 s), annealing (30 s, see Table 3 for variable annealing temperatures) and extension (72°C for 30 s), followed by final extension at 72°C for 10 min. The reactions were done in a total volume of 20 μl with 16 mM NH4SO4, 67 mM Tris (pH 8.8), 0.1% Tween 20, 0.13 mM dNTPs, 1.5 mM MgCl2, 0.2 μM of both primers; 0.5 μM α-32P-dCTP and 0.5 μM Taq polymerase using 21 ng genomic DNA as template. Either 1% DMSO, 1.5% formamide or 5% glycerol (Table 3) was used to increase PCR-sensitivity. The reactions were stopped with 95% formamide buffer (1:1, denatured, cooled and electrophoresed on glycerol-free 3% for 3.5 h at 4°C and 5% glycerol (8W for 12 h at room temperature), nondenaturating 5% polyacrylamide gels (acylamide/bisacrylamide 49:1). When different band patterns were observed, PCR products were sequenced bidirectionally using the ABI PRISM dye terminator cycle sequencing kit (Perkin Elmer, Foster City, Calif., USA) and analysed on an automated sequencer (ABI model 373, Perkin Elmer). Heterozygous variants were confirmed by using the restriction fragment length polymorphism technique (PCR-RFLP). Using this procedure, the estimated degree of mutation detection is approximately 95% in our laboratory. Statistical analysis. Differences in clinical characteristics were tested by Mann-Whitney nonparametric test statistics using the BMDF New System for Windows statistical package (Biomedical Data Processing, Los Angeles, Calif., USA). P-values of less than 0.05 were considered statistically significant. Allele frequency distribution was tested by χ2-analysis, and alleles with expected frequencies of less than 5.0 were pooled to assure the validity of the χ2-test. Extended TDT analysis was calculated using the ETDT software package 1.4 for multilocus markers [27], whereby logistic regression was done to estimate parameters for transmitted and non-transmitted alleles from heterozygous parents. With these parameters, log likelihood was calculated for the allele-wise and genotype-wise model and deviation from the null-hypothesis tested by the McNemar Z-test.

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nonobese Type II diabetic patients and the control subjects (χ² = 15.1, 6 d.f., p = 0.020). No difference was seen between MSDR/Type II diabetic and nonobese Type II diabetic patients (χ² = 2.2, 6 d.f., p = 0.19). No significant difference in allele frequency distribution was observed between MSDR/NGT and healthy control subjects (χ² = 7.4, 5 d.f. and p = 0.19). The combined group of diabetic and nondiabetic individuals with MSDR, however, differed from control subjects (χ² = 15.1, 6 d.f. and p = 0.019) but not from the pooled group of nonobese Type II diabetic and control subjects (χ² = 6.5, 7 d.f., p = 0.48). To exclude ethnic distortion we also carried out the analysis in the Botnia population only. We observed significant differences in allele frequency distribution between all Type II diabetic patients and control subjects (p = 0.007), between MSDR/Type II diabetic patients and control subjects (p = 0.010) and a smaller difference between nonobese Type II diabetic patients and control subjects (p = 0.06).

Extended transmission disequilibrium test (ETDT) in abdominally obese offspring. We genotyped 42 abdominally obese offspring and their parents for the HLIE marker. Of these offspring 39 had a diabetic parent and the remaining three had at least one diabetic sibling. There were eighteen homoyzygous parents who were thus not informative for transmission of alleles. Transmission was informative for sixty-six parental alleles, and in this set of families eleven different alleles of the HLIE gene were transmitted. Results from both the allele-wise (χ² = 20.0, 10 d.f., p = 0.029) and the genotype-wise (χ² = 35.1, 23 d.f., p = 0.002) model indicated that certain alleles were preferentially transmitted to abdominally obese offspring in families with Type II diabetes.

The result from the two models does not significantly differ (χ² = 15.1, 13 d.f., p = 0.30). No individual allele explained the transmission disequilibrium, although allele 5 accounted for the greatest deviation from the expected transmission (p = 0.14, after correction for multiple comparisons).

Association study of the HLIE gene marker with low lipolytic rate as the phenotype. The difference in allele frequency distribution (Table 5) of the HLIE gene marker between subjects with high (n = 71) and low (n = 71) lipolytic activity did not reach statistical significance (χ² = 8.6, 4 d.f., p = 0.072).

SSCP mutation screening in abdominally obese patients with MSDR. We did not identify any missense nonobese Type II diabetic patients and the control subjects (χ² = 15.1, 6 d.f., p = 0.020). No difference was seen between MSDR/Type II diabetic and nonobese Type II diabetic patients (χ² = 2.2, 6 d.f., p = 0.19). No significant difference in allele frequency distribution was observed between MSDR/NGT and healthy control subjects (χ² = 7.4, 5 d.f. and p = 0.19). The combined group of diabetic and nondiabetic individuals with MSDR, however, differed from control subjects (χ² = 15.1, 6 d.f. and p = 0.019) but not from the pooled group of nonobese Type II diabetic and control subjects (χ² = 6.5, 7 d.f., p = 0.48). To exclude ethnic distortion we also carried out the analysis in the Botnia population only. We observed significant differences in allele frequency distribution between all Type II diabetic patients and control subjects (p = 0.007), between MSDR/Type II diabetic patients and control subjects (p = 0.010) and a smaller difference between nonobese Type II diabetic patients and control subjects (p = 0.06).

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SSCP mutation screening in abdominally obese patients with MSDR. We did not identify any missense
mutations in the HSL gene in 20 abdominally obese patients with type II diabetes. In lower frequencies, a silent variant was found in codon 765 (exon 9), changing a GCC (alanine) to a GCT (alanine). Furthermore, in another subject we identified a variant changing a G to T in nucleotide +41 relative to the transcription between these extreme groups detected no noticeable difference. On the other hand, when comparing groups below and above the median of the lipolytic rate there was no difference at all between the groups (p = 0.52). It is therefore still possible that a biallelic marker in the HSL gene could show an association with a low lipolytic rate.

The coding regions of the HSL gene and the non-coding exon 4 were screened for mutations in abdominally obese patients with NDSR using the SSCP technique. Despite the positive association between MSDR and the HSL gene, no missense mutations were identified. A silent mutation (Ala756 GCC→GCT) and a non-coding mutation (exon B, bp 41 G→T) were found, but the prevalence of these mutations was very low.

Few previous studies have examined the role of the HSL gene in the development of obesity and MSDR. In a Japanese population, a polymorphism has been observed in the coding regions of the HSL gene [26], changing an arginine to a cysteine in codon 309. We observed a low frequency of this variant in our population, and there was no difference in the allele frequency between Type II diabetic patients and healthy subjects. Serum triglyceride and HDL-cholesterol concentrations were lower in Type II diabetic subjects with either arginine or cysteine in this position, while total serum cholesterol concentration were higher in Type II diabetic subjects heterozygous for Arg309-Cys [26]. The polymorphism in codon 309 could not be identified in our study group. In a more recent study, a polymorphic marker in intron 6 of the HSL gene was associated with Type II diabetes rather than to abdominal obesity or MSDR. The intragenic association study, however, could provide some more insight into the phenotype associated with the HSL gene.

The ETDT study clearly showed distorted transmission of alleles to abdominally obese offspring in families with Type II diabetes. As abdominal obesity is a risk factor for Type II diabetes [8], it seems likely that the HSL marker in the HLE gene is in linkage disequilibrium with a gene increasing susceptibility to abdominal obesity and thereby possibly to Type II diabetes.

Acknowledgements. We would like to thank A.Suomalainen and P.Almgren for computational and statistical expertise, and M.Aberg for technical support. This work was supported by grants from the Sigrid Juselius Foundation, the Albert Pålén Foundation, the University Hospital, the Medical Faculty of Lund University, the Swedish Medical Research Council, the Nordic Foundation, the Swedish Diabetes Foundation and the European Diabetes Foundation and EEC grant BMH4-CT95-0962.

Note added in proof. Of the subjects analyzed in the association study with MSDR as the phenotype, six of the 78 NIDDM/Type II diabetes patients (7.7%) and seven of the 146 controls (4.8%) had the C→T (codon 765 variant

which at least in part is due to impaired function of HSL. This suggests that individuals from the lowest tertile of lipolysis we observed a slight difference in allele frequency distribution between the groups (p = 0.07). Given the number of repeating tests, however, this difference is not significant. These variants were confirmed by PCR-RFLP using restriction enzymes BclI, for the codon 765 variant) and MboI (for codon 41 variant). The codon 765 variant was detected in one of 60 subjects screened, and the position + 41 variant in one of 30 subjects screened. No additional mutations were identified in the 10 hypertriglyceridemic subjects screened for all exons. Neither did we detect any mutations in the 30 abdominally obese subjects or in the 29 hypertriglyceridemic subjects screened for exons 4, 6 and 8. A polymorphism described previously in exon 4 of the HSL gene (Arg309Cys), seen in 5.2% of Japanese control subjects [26], could not be detected in 89 Scandinavian subjects.

Discussion

The allele frequency distribution of the HSL LIPE polymorphic marker showed a considerable difference between abdominally obese Type II diabetic patients and healthy control subjects. This was also true when we compared non-obese Type II diabetic patients without signs of NDSR and healthy control subjects, whereas no notable difference was observed between obese and nonobese Type II diabetic patients. Neither was there any important difference in the allele frequency distribution between nonobese diabetic patients with features of MSDR and lean control subjects. This was also reported before [28], and it could thus mean that the HSL LIPE polymorphism increases susceptibility to Type II diabetes rather than to abdominal obesity or MSDR. The intrafamilial association study, however, could provide some more insight into the phenotype associated with the HSL gene.

The ETDT study clearly showed distorted transmission of alleles to abdominally obese offspring in families with Type II diabetes. As abdominal obesity is a risk factor for Type II diabetes [8], it seems likely that the HSL marker in the HLE gene is in linkage disequilibrium with a gene increasing susceptibility to abdominal obesity and thereby possibly to Type II diabetes.

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References


Interaction between the Asn291Ser variant of the LPL gene and insulin resistance on dyslipidaemia in high risk individuals for Type 2 diabetes mellitus

M. Klannemark*§, L. Suurinkeroinen†§, M. Orho-Melander*, L. Groop*† and M. -R. Taskinen†

Abstract

Aims Lipoprotein lipase (LPL) is a major regulator of triglyceride clearance. A genetic variant of the LPL gene on chromosome 8p22, Asn291Ser, has previously been associated with dyslipidaemia and an increased frequency of cardiovascular disease as well as familial disorders of lipoprotein metabolism. The aim of this study was to test whether the phenotypic expression of the LPL Asn291Ser variant is dependent upon glucose tolerance and insulin resistance. Therefore, the Asn291Ser variant was examined in 192 patients with Type 2 diabetes, 278 subjects with normal glucose tolerance who are first degree relatives of patients with Type 2 diabetes and 226 healthy control spouses without family history of diabetes.

Methods The subjects were genotyped with an allele-specific minisequencing method. Insulin resistance was estimated using the homeostasis model assessment (HOMA) index.

Results The frequency of the Asn/Asn genotype was significantly increased in normoglycaemic subjects with hypertriglyceridaemia (>1.7 mmol/l), and was associated with dyslipidaemia and increased systolic blood pressure. There was a significant interaction between Asn291Ser and insulin resistance in normoglycaemic subjects, indicating that dyslipidaemia is more severe in Asn/Asn carriers with reduced insulin sensitivity. The frequency of the Asn/Asn genotype was not increased in diabetic subjects with hypertriglyceridaemia, but was associated with increased systolic blood pressure.

Conclusions The Asn291Ser genotype of the LPL gene is associated with dyslipidaemia in normoglycaemic subjects, and the dyslipidaemic phenotype is more severe in insulin resistant subjects. This association is not seen in diabetic subjects.


Keywords dyslipidaemia, lipoprotein lipase, LPL291, Type 2 diabetes mellitus

Abbreviations ANOVA, analysis of variance; CI, confidence interval; CV, coefficient of variance; HDL, high density lipoprotein; HOMA, homeostasis model assessment; LDL, low density lipoprotein; LPL, lipoprotein lipase; NGT, normal glucose tolerance; OR, odds ratio; PCR, polymerase chain reaction; VLDL, very low density lipoprotein; WHO, World Health Organization

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599
Introduction

The key features of dyslipidaemia in Type 2 diabetes are high levels of plasma triglycerides and very low density lipoproteins (VLDL) and low levels of high density lipoproteins (HDL) [1]. Hypertriglyceridaemia is seen in 20-60% of Type 2 diabetic patients and two to three times more common than in non-diabetic populations [1]. Importantly, these lipid abnormalities are also observed in glucose-tolerant relatives of Type 2 diabetic patients [2-8] in whom they seem to cluster with other features of the metabolic syndrome, i.e. insulin resistance, abdominal obesity and hypertension.

A number of studies have shown that both genetic and environmental factors can modulate lipid levels in man [6]. Genes encoding for enzymes regulating key steps in the conversion of VLDL to low density lipoproteins (LDL) represent potential candidate genes that could modulate the expression of dyslipidaemia. Lipoprotein lipase (LPL) has a central role in both VLDL and HDL metabolism [7,8]. Low LPL activity has been associated with raised plasma triglyceride and low HDL cholesterol levels. In Type 2 diabetes, LPL activity is commonly subnormal and contributes to the elevation of serum triglycerides [9,10]. A prior report showed that post-heparin plasma LPL activity is reduced to insulin-resistant first degree relatives of patients with Type 2 diabetes [11]. Thus, genetic variants of the LPL gene could modulate the magnitude of dyslipidaemia in high-risk individuals for Type 2 diabetes. Several genetic defects of the LPL gene have been reported in exons 4, 5 or 6 of the LPL gene [12]; most of these are rare and cause severe dyslipidaemia. However, a common asparagine to serine substitution at residue 291 (Asn291Ser, exon 6) has an allele frequency of 2-5% [11-15]. In most studies, the Asn291Ser variant has been associated with decreased HDL cholesterol and elevated triglyceride concentrations, although normal lipid values have also been reported in carriers of this variant [13-21].

The variability of the Asn291Ser genotype indicates that other genes or factors, such as the presence of insulin resistance or diabetes, may modulate the expression of the genotype.

To test the hypothesis that the phenotypic expression of the LPL Asn291Ser variant is dependent upon glucose tolerance and insulin resistance, the Asn291Ser variant was examined in 192 Type 2 diabetic patients, 278 subjects with normal glucose tolerance who are first degree relatives of patients with Type 2 diabetes and 226 healthy control spouses without family history of diabetes.

Subjects and methods

Subjects

Subjects were selected from the Botnia region of western Finland [22]. Allele frequency comparisons were made between 192 unrelated Type 2 diabetic patients, 278 unrelated subjects with normal glucose tolerance (NGT) who are first degree relatives of patients with Type 2 diabetes (NGT-ref) and 226 unrelated healthy control spouses without family history of diabetes. Genes encoding for enzymes regulating key steps in the conversion of VLDL to low density lipoproteins (LDL) represent potential candidate genes that could modulate the expression of dyslipidaemia. Lipoprotein lipase (LPL) has a central role in both VLDL and HDL metabolism [7,8]. Low LPL activity has been associated with raised plasma triglyceride and low HDL cholesterol levels. In Type 2 diabetes, LPL activity is commonly subnormal and contributes to the elevation of serum triglycerides [9,10]. A prior report showed that post-heparin plasma LPL activity is reduced to insulin-resistant first degree relatives of patients with Type 2 diabetes [11]. Thus, genetic variants of the LPL gene could modulate the magnitude of dyslipidaemia in high-risk individuals for Type 2 diabetes. Several genetic defects of the LPL gene have been reported in exons 4, 5 or 6 of the LPL gene [12]; most of these are rare and cause severe dyslipidaemia. However, a common asparagine to serine substitution at residue 291 (Asn291Ser, exon 6) has an allele frequency of 2-5% [11-15]. In most studies, the Asn291Ser variant has been associated with decreased HDL cholesterol and elevated triglyceride concentrations, although normal lipid values have also been reported in carriers of this variant [13-21].

Clinical investigations and laboratory assays

Clinical investigations and laboratory assays were performed as previously described [22]. Briefly, fasting plasma triglycerides and HDL cholesterol were measured by standard enzymatic methods. Lipid profile was determined at the Laboratory Services, Helsinki University Hospital, Helsinki, Finland.

Table 1. Clinical characteristics of the study groups

<table>
<thead>
<tr>
<th>Subjects (n = 496)</th>
<th>Control (n = 226)</th>
<th>NGT-ref (n = 278)</th>
<th>Type 2 DM (n = 192)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>56 ± 10</td>
<td>55 ± 13</td>
<td>63 ± 12&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>Triglycerides (mmol/L)</td>
<td>1.4 ± 0.8</td>
<td>1.8 ± 0.9</td>
<td>2.1 ± 1.2&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>HDL cholesterol (mmol/L)</td>
<td>1.33 ± 0.32</td>
<td>1.42 ± 0.32</td>
<td>1.03 ± 0.17</td>
</tr>
<tr>
<td>Cholesterol (mmol/L)</td>
<td>5.9 ± 1.2</td>
<td>6.2 ± 1.3</td>
<td>6.0 ± 0.1</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>25.8 ± 3.6</td>
<td>26.6 ± 3.4</td>
<td>28.3 ± 4.6&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Systolic blood pressure (mmHg)</td>
<td>123 ± 26</td>
<td>128 ± 26</td>
<td>133 ± 29&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Diastolic blood pressure (mmHg)</td>
<td>68 ± 15</td>
<td>74 ± 18</td>
<td>78 ± 18&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Fasting glucose (mmol/L)</td>
<td>5.0 ± 0.5</td>
<td>5.1 ± 0.5</td>
<td>6.4 ± 2.5&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>HOMA-IR index for insulin resistance*</td>
<td>2.09 ± 1.46</td>
<td>2.27 ± 1.37</td>
<td>3.80 ± 5.31&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Fasting C-peptide (mmol/L)</td>
<td>0.42 ± 0.20</td>
<td>0.50 ± 0.22</td>
<td>0.36 ± 0.24&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>HbA&lt;sub&gt;1c&lt;/sub&gt; (%)</td>
<td>5.6 ± 0.4</td>
<td>5.5 ± 0.4</td>
<td>7.3 ± 1.2&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

Data is mean ± SE. *P < 0.05, P < 0.001, P < 1 x 10<sup>-6</sup> vs control subjects and P = 0.05, P < 0.01, P = 1 x 10<sup>-6</sup> vs NGT-ref subjects. **HOMA index values are reported for Type 2 diabetic patients without insulin treatment (n = 147).
Genotyping
Subjects were genotyped for the LPL Ams291Ser variant with an allele-specific mini-multiplexing method as previously described [21], using the upstream primer 5'-ATC TITG TGT TCT TTT TAC CC-3' and a biotinylated downstream primer 5'-AGT TTG CAT GAT TGC GCT-3' to amplify this region by polymerase chain reaction (PCR). The biotinylated PCR fragment was linked to a streptavidin-coated well, incubated with detection primers (5'-CA A ATG CTA GGG TCA GAT CAA-3') and [3'H]dNTP, and a liquid scintillation counter was used to detect allelic variants with an A at the second position of codon 291.

Statistical analyses
Descriptive clinical data were compared with the Student's t-test (mean ± 50) and differences in clinical characteristics of the different Ams291Ser genotype carriers were tested by the Mann-Whitney non-parametric test, using the BMDO New System for Windows statistical package (Biomedical Data Processing, Los Angeles). Data from non-parametric analyses was expressed as median (interquartile range) unless otherwise stated. A P-value < 0.05 was considered statistically significant. Bonferroni correction for multiple comparisons was calculated when specified, although the corrected P-value is too conservative when variables are not independent. Frequencies were compared with Pearson χ²-analysis, and Fisher's exact test (two-tailed) when expected numbers were too low (< 1) to ensure the validity of the χ². Comparative risk was estimated with the odds ratio (OR) and 95% confidence intervals (CI95%). Genetic interaction with physiological parameters was calculated by two-way analysis of variance (ANOVA).

Results
Frequency of the Ams/Ser in subjects with normal glucose tolerance, Type 2 diabetes and hypertetiglyceridaemia
The serine allele of the LPL Ams291Ser variant was present in 13 of 384 (3.4%) chromosomes from Type 2 diabetic patients, in 26 of 556 (4.7%) chromosomes from NGT-REL subjects and in 13 of 452 (2.9%) chromosomes from control subjects. All identified carriers of the serine allele were heterogeneous for the variant, and the corresponding Ams/Ser genotype frequencies were 8.9% in Type 2 diabetic patients, 9.4% in NGT-REL subjects and 5.3% in control subjects (Table 2). Allele and genotype frequencies were in Hardy-Weinberg equilibrium in all three groups studied. Neither Type 2 diabetic patients nor NGT-REL subjects had increased frequency of the Ams/Ser genotype compared to control subjects.

When the groups were divided by fasting plasma triglyceride levels, genotype frequencies differed significantly between non-diabetic groups with high (HTg) and normal (Nog) triglyceride levels (Table 2). The frequency of the Ams/Ser genotype was higher among HTg control subjects (11.5%) than among Nog control subjects (6.5%) (P = 0.07), and the Ams/Ser frequency was higher among HTg NGT-REL subjects (13.5%) than among Nog NGT-REL subjects (5.5%) (P = 0.022). In addition, the frequency of the Ams/ Ser genotype was increased in NGT-REL subjects as compared to Nog control subjects (9.4 vs. 3.6%, P = 0.05).
Figure 1 Frequency (%) of ApoA/Per genotype carriers in diabetic (closed bars) and non-diabetic (open bars) subjects according to plasma triglyceride quartiles (cut-off levels were based on the pooled group of normoglycemic and diabetic subjects and are shown on the y-axis). The number of ApoA/Per genotype carriers in each quartile is given above the bar.

P = 0.02. There was no difference between HTg NGT-rel subjects and HTg control subjects (13.5 % vs. 11.5 %), or between HTg Type 2 diabetic patients and Normoglycemic diabetic patients.

There were no differences in plasma triglycerides, HDL-cholesterol or apolipoprotein AI concentrations in ApoA/Per genotype carriers and non-carriers (Table 2). However, Type 2 diabetic carriers of the ApoA/Per genotype had increased systolic (P = 0.004) and diastolic (P = 0.03) blood pressure compared to diabetic non-carriers (Table 4). Male, but not female, diabetic carriers of the ApoA/Per genotype had significantly increased systolic blood pressure (P = 0.01). Excluding subjects on lipid-lowering treatment did not change the results in diabetic subjects.

Genetic interaction between the ApoA/Per genotype and features of the metabolic syndrome

Interaction between genotype and physiological parameters was investigated by comparing fasting plasma triglyceride levels or systolic blood pressure between carriers and non-carriers of the ApoA/Per genotype and between each quartile of BMI and HOMA index for insulin resistance using a two-way ANOVA. In normoglycemic subjects, a significant interaction between the ApoA/Per genotype and triglyceride levels was seen (P = 0.05, Fig. 2) but not systolic blood pressure (data not shown). A significant interaction was seen between the ApoA/Per genotype and BMI (Fig. 2). In Type 2 diabetic subjects, however, there was no significant interaction between the ApoA/Per genotype and BMI on triglyceride levels or systolic blood pressure (data not shown). There were too few carriers without insulin treatment in each quartile to allow such analysis for HOMA index in the diabetic subjects.

Phenotypic characteristics of ApoA/Per genotype carriers among subjects with normal glucose tolerance and Type 2 diabetes

As shown in Table 3, normoglycemic carriers of the ApoA/Per genotype (NGT-rel and control subjects) had increased concentrations of fasting plasma triglycerides (P = 0.00009) and reduced concentrations of HDL-cholesterol (P = 0.0009) and apolipoprotein AI (P = 0.05), compared with non-carriers. The reduction of HDL-cholesterol concentration was accounted for by a reduction of both the HDL2 (P = 0.01) and the HDL3 (P = 0.03) subfractions. In addition, carriers of the ApoA/Per genotype had significantly higher systolic blood pressure (P = 0.01) than non-carriers. There were no significant differences in body mass index (BMI) or HOMA index between normoglycemic ApoA/Per genotype carriers and non-carriers. In female normoglycemic carriers of the ApoA/Per genotype, triglyceride concentrations (P = 0.0004) were increased and HDL cholesterol concentrations reduced (P = 0.003) compared to female non-carriers (Table 2). In male normoglycemic ApoA/Per genotype carriers, triglyceride concentrations (P = 0.04) and systolic blood pressure (P = 0.05) were increased compared to male non-carriers (Table 3).

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In Type 2 diabetic patients there were no differences in plasma triglycerides, HDL-cholesterol or apolipoprotein AI concentrations between ApoA/Per genotype carriers and non-carriers (Table 4). However, Type 2 diabetic carriers of the ApoA/Per genotype had increased systolic (P = 0.004) and diastolic (P = 0.03) blood pressure compared to diabetic non-carriers (Table 4). Male, but not female, diabetic carriers of the ApoA/Per genotype had significantly increased systolic blood pressure (P = 0.01). Excluding subjects on lipid-lowering treatment did not change the results in diabetic subjects.
### Table 3 Comparisons between normoglycaemic subjects with AnS/AnS and AnS/Se genotypes of the LPL, APOE4 variant

<table>
<thead>
<tr>
<th></th>
<th>Ant/An (n = 465)</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Sex (women/men)</td>
<td>227/236</td>
<td>16/23</td>
</tr>
<tr>
<td>Age (years)</td>
<td>54 (46-65)</td>
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</tr>
<tr>
<td>Triglycerides (mmol/l)</td>
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<tr>
<td>Waist-to-hip ratio</td>
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### Table 4 Comparisons between Type 2 diabetic subjects with AnS/AnS and AnS/Se genotypes of the LPL, APOE4 variant

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<td>Age (years)</td>
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<td>67 (60-72)</td>
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<tr>
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HOMA-index was analysed for Type 2 diabetic patients without insulin treatment. 
*Insulin alone or in combination with hypoglycaemic agents.

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diabetes, glucose-tolerant first degree relatives of patients with Type 2 diabetes and control spouses. The A/G pattern was most frequent in hypertensive, diabetic subjects with normal glucose tolerance, approximately 2:3 times more common than in the general population, but it was not significantly increased in hypertensive, diabetic subjects with Type 2 diabetes. It is possible that diabetic A/G genotype carriers could be under-represented as a result of increased mortality, although this seems unlikely as carriers and non-carriers were of similar age in all groups. It is more likely that the effect of the A/G genotype on renal function in diabetic patients, in whom several diabetes-specific factors can modify plasma triglyceride levels. In normoglycaemic subjects the A/G genotype was associated with higher triglyceridemia and increased systolic blood pressure, whereas in diabetic subjects only an association with increased blood pressure was observed. As previously described [13], the phenotypic expression of the A/G genotype was dependent upon sex. In the diabetic patients, loss of glucose control could have attenuated differences in triglyceride levels. In control spouses from the Botnia region (n = 405), a fasting plasma triglyceride level of 1.7 mmol/l represents the upper quartile, whereas in diabetic subjects from the same region (n = 841) the corresponding value is 2.4 mmol/l. Therefore, each group was divided into quartiles according to plasma triglyceride levels and the prevalence of A/G genotype carrier in each group was examined. In the normoglycaemic group, there was a significant increase of A/G genotype carriers with increasing plasma triglycerides, whereas this could not be seen among the diabetic subjects.

Thus, the LPL 291 A/G genotype is not associated with dyslipidemia in Type 2 diabetic subjects.

Few previous studies have investigated blood pressure in relation to the LPL gene. The present study found that the A/G genotype is associated with increased blood pressure in both normoglycaemic and diabetic subjects. A recent study reported that three polymorphic markers at the LPL locus on chromosome 8p22 were linked to systolic blood pressure [32]. It is possible that the LPL 291 A/G genotype, or a variant in linkage disequilibrium with the serine allele, could be related to the development of increased blood pressure.

In general, there seems to be a large variability in the A/G 291 Ser phenotype indicating that other genes or factors, such as the presence of diabetes, obesity or insulin resistance may modulate the expression of this genotype. It was found that dyslipidaemia is more severe in insulin-resistant non-diabetic carriers of the A/G genotype than in insulin sensitive carriers, indicating that the phenotype is dependent upon insulin sensitivity. This interaction might be the result of the insulin resistance of cells important for lipoprotein metabolism [28], or to other genetic factors influencing insulin resistance.

Thus, the LPL 291 A/G genotype is not associated with dyslipidaemia in Type 2 diabetic subjects.
References


The common PPARG Pro12Ala polymorphism is associated with decreased risk of type 2 diabetes

David Altschuler1,2,3,4, Joe N. Hirshhorn1,2,3,4, Mia Klanneskar1,2,3,4, Cecilia M. Lindgren1,2,3,4, Marie-Claude Vohl1,2, James Nemesh1, Charles R. Lane1, Stephen F. Schaffner1, Stacey Boik1, Carl Brewster1, Tainanama Tuomio1,2, David Gaudet3, Thomas J. Hudson1,2,4, Mark Daly1, Leaf Groop1, and Eric S. Lander1,2

*These authors contributed equally to this report

Genetic association studies are viewed as problematic and plagued by irreproducibility1, many associations have been reported for type 2 diabetes (T2D), but none have been confirmed in independent populations with comprehensive controls. We evaluated 16 published genetic associations to type 2 diabetes and related sub-phenotypes using a family-based design to control for population stratification, and replication samples to increase power. We were able to confirm only one association, that of the common Pro12Ala polymorphism in peroxisome proliferator-activated receptor γ (PPARG) with type 2 diabetes. By analysing over 3,000 individuals, we found a modest (1.25-fold) but significant (P < 0.002) increase in relative risk associated with the more common proline allele (−85% frequency). Moreover, our results resolve a controversy about common variation in PPARG. An initial study found a trend for effect2, but four of five subsequent publications3–5 failed to confirm the association. All six studies are consistent with the odds ratio we describe. The data implicate a polymorphism in PPARG in the pathogenesis of type 2 diabetes. Because the risk allele occurs at such high frequency, its modest effect translates into a large population attributable risk—increasing as much as 25% of type 2 diabetes in the general population. Many factors may contribute to variable association results: multiple hypothesis testing, publication bias, ethnic stratification, population-specific linkage disequilibrium between markers and causal variants, inadequate statistical power, and gene-gene and gene-environment interactions. To evaluate reported associations to type 2 diabetes and test newly discovered alleles, we designed a study to address as many of these confounders as possible. We used a multi-layered design (Table 1). Associations were first tested in 333 Scandinavian parent-offspring trios with type 2 diabetes or abnormal glucose homeostasis using transmission disequilibrium testing (TDT; ref 23) to eliminate false positives due to population stratification. Alleles showing nominal association in the initial sample (P < 0.05 in the direction of the original report) were tested for replication in three additional samples: 11,130 individuals from Scandinavian sibships discordant for type 2 diabetes, 48 case-control pairs from Scandinavia and 127 case-control pairs from the Sagamour-Lac-Saint Jean region of Quebec, Canada. The use of siblings further addresses stratification (by sib-TDT; ref 24 or related methods), whereas the case-control sample assesses population risk. At least 14 common single-nucleotide polymorphisms (SNPs) have been associated with type 2 diabetes or related sub-phenotypes4–7,8. Notably, family-based controls were not used (except in a single report7). We genotyped the 16 variants in the initial 333 parent-offspring trios (Table 2). Three variants were rare or absent (<1% allele frequency). Our data cannot exclude a biological effect of these variants, but such low frequency rules out a significant impact on diabetes risk in our population. Of the remaining 13 variants, 11 showed either non-significant deviation from 50:50 transmission from heterozygous parents or a trend in the opposite direction from the original report. Because some of these variants were originally associated with quantitative phenotypes rather than diabetes itself, we genotyped a random sample of 379 parent-offspring trios in which the offspring had normal glucose tolerance using the TDTQ method8,9, we found no association with the relevant phenotype (Table 2). Of course, such data do not rule out small effects, the statistical power

Table 1: Characteristics of study populations

<table>
<thead>
<tr>
<th>Sex (male)</th>
<th>Age (y)</th>
<th>Fastig plasma glucose (mmol/L)</th>
<th>BMI (kg/m²)</th>
<th>Haemoglobin A1c (%)</th>
<th>Plasma glucose at 2 h (mmol/L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TDT trios (Scandinavia)</td>
<td>DMD/ART</td>
<td>179/157</td>
<td>38/9</td>
<td>37/9</td>
<td>27/5</td>
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<tr>
<td>NCT</td>
<td>245</td>
<td>5.1/0.3</td>
<td>5.1/0.3</td>
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<td></td>
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<tr>
<td>Staphylococcus (Scandinavia)</td>
<td>DMD/ART</td>
<td>282/229</td>
<td>65/10</td>
<td>34/7</td>
<td>28/5</td>
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<tr>
<td>NCT</td>
<td>242</td>
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<td>DMD/ART subjects</td>
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Data are presented as numbers of cases and controls. Plasma glucose was measured at baseline (fasting) and 2 h after an oral glucose tolerance test (OGTT). DM, type 2 diabetes; ITP, impaired glucose tolerance; IG, impaired fasting glucose; NGT, normal glucose tolerance.}

References: 1Whitehead Institute/MIT Center for Genome Research, Cambridge, Massachusetts, USA. 2Diabetes Unit, Massachusetts General Hospital, Boston, Massachusetts, USA. 3Harvard Medical School, Boston, Massachusetts, USA. 4Division of Endocrinology, Vårbyhus Hospital and Sundsvall University Hospital, University of Linköping, Sweden. 5Department of Epidemiology and Biostatistics, Johns Hopkins School of Public Health, Baltimore, Maryland, USA. 6Department of Biology, University of Massachusetts, Amherst, Massachusetts, USA. 7Department of Biology, University of Massachusetts, Amherst, Massachusetts, USA. 8Department of Biological Sciences, University of Warwick, Coventry, West Midlands, UK. 9Correspondence should be addressed to E.S. (e-mail: E.S@sangerlab.org.uk).
obtained is represented in the upper limits of the confidence intervals (Table 2). Two variables showed nominally significant association in the initial sample: a missense variant in PPARG (Pro12Ala) and a silent missense polymorphism in exon 22 of ARCC8 (Table 2). PPARG encodes PPARγ, a nuclear hormone receptor that regulates adipogenesis and is a target for thiazolidinediones, medications used to treat diabetes. The less frequent allele (1%) was associated with increased diabetes risk (26.12, odds ratio 2.2, 95% CI 1.3-3.6 oned-tailed, Table 2). For both variables, transmission ratios were not significantly different from 50:50 in non-diabetic trios, ruling out transmission ration distortion (data not shown).

We attempted to further replicate these results in additional samples. The ARCC8 association was not confirmed, as the trend in the additional samples was in the opposite direction from our initial result. The T2D-Scorers study (41), a case-control study in Scandinavian case genotypes were CC375, CT47, TT1, and control genotypes were CC363, CT53, TT2. These data suggest that the initial result was statistically significant but not unexpected when testing 13 hypotheses. By contrast, we confirmed the PPARG association (Table 2): the three follow-up samples demonstrated similar odds ratios, (0.74, 0.68, and 0.92) with a pooled P-value of 0.0012. Combining our initial and replication samples, the P-Value is 0.002. Because our analysis was prompted by a previously reported association, and given the biological role of PPARG, we believe these data constitute strong replication.

We then estimated the genotype relative risk (GRR) and population attributable risk of PPARG Pro12Ala. The transmission ratio (TDT) and genotype counts (case-control) of the proline allele are consistent with codominant, additive, multiplicative or recessive models. Under any of these scenarios, the GRR of the proline allele is estimated as approximately 1.25. Because this risk allele is so common (frequency=0.87% in our samples), a GRR of 1.25 corresponds to a population attributable risk of approximately 25%. That is, these data indicate that if the population were monomorphic for the protective alanine allele, the prevalence of type 2 diabetes would be 25% lower.

We also examined this association with other phenotypes by applying the TDTQ method to the T2D offspring in the T2D trio samples. This analysis suggested that the initial result may be an artifact of increasing the number of testing 13 hypotheses. By contrast, we confirmed the PPARG association (Table 2); the three follow-up samples demonstrated similar odds ratios (0.74, 0.68, and 0.92) with a pooled P-value of 0.0012. Combining our initial and replication samples, the P-Value is 0.002. Because our analysis was prompted by a previously reported association, and given the biological role of PPARG, we believe these data constitute strong replication.

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The table shows the results of a study on the effects of dietary fiber on cholesterol levels in human volunteers. The study involved two groups of participants, one consuming a high-fiber diet and the other a low-fiber diet. The data are presented as mean ± standard deviation (SD) for each group and at different time points (before and after the intervention). The table includes the following columns:

- Group: Indicates the dietary group (High-Fiber or Low-Fiber).
- Time (Before): Cholesterol levels before the intervention.
- Time (After): Cholesterol levels after the intervention.
- Change: Difference between the Before and After values.
- P-value: Statistical significance of the change (significant if ≤ 0.05).

The text suggests that the high-fiber diet significantly reduced cholesterol levels compared to the low-fiber diet. The study highlights the potential of dietary interventions in improving cardiovascular health.
Tri populations. Because transmission disequilibrium testing requires two living parents, a parent-offspring trio population is biased towards patients of young age. When studied, such individuals may not yet manifest the complex and multi-factorial disorder such as 2 type 2 diabetes. For this reason, we chose to include patients with IGT and IIF in one trio population. Therefore, we chose that these disorders often constitute a ‘pre-diabetic’ state; between 25 and 50% of all subjects with IGT convert to type 2 diabetes within 10 years, and patients with IIF convert to type 2 diabetes at a similar rate. Because our patients with IGT or IIF are young (average age 30) and are selected from families with multiple diabetic members, their abnormal glucose homeostasis serves as a strong predictor of eventual development of diabetes. We identified 335 such trio young offspring had IGT, 108 had IIF and 126 had type 2 diabetes. To investigate phenotypes in a non-diabetic population, we studied a non-overlapping sample of 379 parent-offspring trios; all offspring were NGT. The offspring have a waist-to-hip ratio from either the upper quintile or the lowest decile as defined in a healthy control population.

Replication samples. To evaluate findings with a nominal P-value < 0.05 in the initial trio population, we also selected two independent replication samples from the Framingham Heart Study, each including all subjects with age at onset of type 2 diabetes ≤ 30 years, we identified 481 cases with type 2 diabetes or severe IGT (181 patients ≤ 30 years; ≤ 120 mmol glucose ≥ 8.5 mmol/l). Because there was no requirement for parental DNA in these samples, older subjects and a more stringent definition of affection status were used. In our experience, patients with severe IGT have a very high risk (29%) of conversion to overt type 2 diabetes within a three-year follow-up period (P. Almgren and L.G., unpublised data). We then assembled 481 age-, gender- and geographically matched normal glucose tolerance (NGT) controls. Specifically, affected individuals were matched to controls from the same geographic region (Boston cases were matched with controls from Boston, and so on). In addition, 612 diabetics and 518 NGT subjects were recruited. Because NGT subjects were selected at random, the type 2 diabetic siblings had ages of onset ≥ 30 years and the non-diabetic (NGT) siblings were all older than 45. The same criteria for excluding cumulating risk factors were used for these samples. In addition, we tested a case-control sample from a geographically distant population. These samples were unrelated adults (above 19) recruited from the region of Saguenay–Lac-St-Jean (Northeastern Quebec) of French Canadian descent. Patients newly diagnosed with type 2 diabetes (using WHO90 criteria following a 75 g oral glucose load) were included, and each patient was age- and sex-matched with an individual from the same population having a normal glucose tolerance.

Genotyping. Genotyping was performed by either single-base extension (SBE) or fluorescence resonance energy transfer (SBE-FRET) (ref 37) or single-base extension with fluorescence polarization (SBE-FPF, ref 37), using modifications of the MicroSeq SBE protocol (Promega, Madison, WI). PCR primers, SBE primers and PCR conditions are available on request. A mix (5 μl) containing 1 U shrimp alkaline phosphatase (Roche), 2 U exonuclease 1 (Fermentas), 150 μM Tris HCl, pH 8.3 and 15 mM MgCl2 was added to 10 μl PCR product in a 384-well black polystyrene plate (MI Research) and incubated at 56°C for 1 min. SBE reaction mixture (5 μl) was added containing 0.5 U Thermosequenase DNA polymerase (Amersham, 200 μM Tris HCl, pH 8.3, 85 μL MgCl2), 1.6 μl SBE primer and 0.2 μl each of ROX, and TAMRA labeled dNTPs specific to the alleles being assayed. Reactions were denatured for 2 min at 92°C, followed be 50 cycles of a 92°C for 30 s, a 55°C for 30 s, and a 60°C for 30 s. Plates were read on an Analyst Fluorescent Plate reader (IBS Biosystems); polymorphic fluorochrome (ROX and TAMRA) were used to assign genotypes. For SBE-FRET, the SBE mix contained 5-FAM-labeled SBE primer.

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Association Between A Variant In The Phosphodiesterase 3B Gene And Hyperinsulinemia In Genotype-Discordant Sibling Pairs

Mia Klannemark, Marju Orho-Melander, Peter Almgren, Eva Degerman, Vincent Manganiello and Leif Groop

Subjects with type 2 diabetes and their first degree relatives show elevated postprandial FFA levels. Output of FFA from adipose tissue is downregulated by insulin via activation of phosphodiesterase 3B (PDE3B). PDE3B is also expressed in pancreatic β-cells and could be involved in postprandial regulation of insulin secretion. The aim of this study was to investigate if variants in the PDE3B gene increase susceptibility to type 2 diabetes or prediabetic phenotypes. Mutation screening of the gene in 41 subjects identified no novel variants in addition to a known variant in exon 4 (G1389A). Phenotypic characteristics were compared in 266 sibling pairs discordant for this variant. Two hours after an oral glucose tolerance test insulin concentrations were elevated in GG/GA vs AA siblings (57.4 vs 44.2 mU/L, p=0.0015). Quantitative transmission disequilibrium test (TDT) in 157 parent offspring trios with abnormal glucose tolerance did not indicate association with two hour insulin levels. Hapotype TDT including other variants near the PDE3B locus revealed unequal transmission of several PDE3B/G1389A haplotypes to offspring with abnormal glucose tolerance. Analysis of sibling pairs discordant for genotype combinations in PDE3B and the sulphonylurea receptor gene further strengthened the result (p=0.000035), suggesting interaction between these two loci. In conclusion, data from siblings discordant for the G1389A variant in the PDE3B gene suggest that variability in or near the PDE3B gene may contribute to elevated insulin levels.

Type 2 diabetes (non-insulin dependent, NIDDM) is a multifactorial and most likely polygenic disease defined by chronic elevation of plasma glucose (1). Several more or less monogenic forms of type 2 diabetes have been identified (2), representing about 5% of subjects with diabetes. Genetic factors that contribute to the disease in a polygenic fashion are expected to be more frequent. Such factors could influence insulin sensitivity or the capacity to compensate for increased insulin demands by increasing insulin secretion (3).

Phosphodiesterases hydrolyse cAMP, which is a key second messenger in intracellular signalling of hormones (4). Phosphodiesterase 3B (PDE3B) is specifically expressed in adipocytes, liver and pancreatic β-cells (5-6). In the adipocyte, PDE3B is activated postprandially in response to insulin to compensate for increased insulin demands by increasing insulin secretion (3).

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decrease the output of free fatty acids (FFA) in vivo (7). Subjects with type 2 diabetes have an impaired ability to downregulate FFA output in response to insulin (8), resulting in increased serum levels of FFA which in turn could promote peripheral insulin resistance. In the hepatocyte PDE3B could influence endogenous glucose production, and in the β-cell PDE3B could modulate the regulation of insulin secretion (9-11). The presence of the PDE3B gene is located on chromosome 11p15.1 (6), close to the sulphonylurea receptor (ABCC8) gene (Figure 1). Variants in this chromosomal region (11p15) have been associated with hyperinsulinemia and type 2 diabetes as summarized by Vionnet et al. (12) and Lömbert et al. (6). Mexican Americans homozygous for the 3819A allele of the ABCC8 gene were characterized by hyperinsulinemia (13). To exclude that the effect seen in our study was due to the concomitant presence of the G3819A variant in the ABC8 gene, we also stratified for the G3819A genotype frequency in Hardy-Weinberg equilibrium ($\chi^2 = 1.2$, p=0.27). From 1840 siblings we identified 266 sibling pairs discordant for G1389A. The siblings had similar fasting plasma levels of lipids and FFA, and similar body composition (Table 1). Insulin resistance, determined by the homoeostasis model assessment (HOMA-IR) index, fasting serum insulin and FFA levels two hours after an oral glucose tolerance test (OGTT) did not significantly differ between the siblings (Table 1).

The levels of serum insulin two hours after OGTT were higher in GG/AG siblings than in AA siblings ($57\pm 4$ vs $44\pm 2$ mU/l, p=0.0015), particularly after correcting for plasma glucose levels (Table 1). This difference was seen in 168 non-diabetic pairs ($57\pm 12$ vs $43\pm 7$ mU/l, p=0.00057) but not in 19 diabetic pairs without insulin-treatment ($48\pm 10$ vs $52\pm 13$, p=0.72). The effect was less pronounced in 97 non-diabetic siblings matched for degree of glucose tolerance (both siblings had normal or impaired IGTT) glucose tolerance, p=0.031, indicating that this variant could be associated with or interact with IGTT.

To try to replicate the findings in another family-based material, 157 parent-offspring trios (404 subjects from 126 nuclear families) were genotyped for the G1389A variant in intron 4 (G1389A) (5) was selected for phenotypic analysis in genotype-discordant siblings and parent-offspring trios. To identify new variants within the gene, we screened the entire coding region and flanking intronic segments in 40 subjects (including 20 subjects with type 2 diabetes) and one healthy control subject, shifting in intron 6 of the PDE3B gene for novel variants and examined if such variants are associated with type 2 diabetes and abnormal glucose tolerance or prediabetic phenotypes like insulin resistance or impaired β-cell function. To avoid confounding by ethnic admixture and family-based approaches to study association in genotype-discordant siblings and parent-offspring trios.

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preserved in 112 sibling pairs concordant for ABCC8/G3819A (Table 2, \(p=0.048\), one-sided test). Analysis of non-diabetic siblings discordant for both variants showed that 27 siblings AA for PDE3B/1389A and 27 siblings AA for ABCC8/G3819A allele previously associated with higher insulin levels (Table 2, \(31\pm4\) vs \(80\pm15\), \(p=0.000035\)). Analysis of non-diabetic siblings discordant for both variants in the opposite direction showed that 35 siblings that were GG for ABCC8/3819 and AA for PDE3B/1389 did not statistically differ with respect to insulin levels compared to their discordant siblings (Table 2, \(47\pm9\) vs \(60\pm17\), \(p=0.53\)). This implies that in our Scandinavian population the ABCC8/3819G allele interacts with PDE3B/1389G to increase serum insulin levels, either representing a physiological interaction or linkage disequilibrium with a third genetic factor.

To test if the PDE3B/G1389A variant is associated with type 2 diabetes or abnormal glucose tolerance we used the transmission disequilibrium test (TDT). A alleles were slightly overtransmitted to unrelated offspring with type 2 diabetes or abnormal glucose tolerance (113 transmitted and 86 untransmitted A alleles of totally 392 transmissions, \(\chi^2=3.7, p=0.056\)). We also looked at the interaction between the PDE3B/G1389A locus and other variants in this chromosomal region (Figure 1: KCNJ11/Leu270Val (14), KCNJ11/Ile337Val (14), ABCC8/Ser1370Ala (15), ABCC8/G3819A (15), ABCC8/exon 22 C/T (15), ABCC8/exon 24 T/C (15), INS/I-23T (16) by following the transmission of haplotypes. PDE3B/1389A was overtransmitted together with KCNJ11/270Leu (p=0.012) and INS/-23A (p=0.028) to 108 offspring with abnormal glucose tolerance (Table 3). Vice versa, PDE3B/1389G was undertransmitted together with KCNJ11/270Val (p=0.0056), KCNJ11/I-337Ile (p=0.0094), ABCC8/exon 22C (p=0.029) and INS/-23T (p=0.012) to these offspring. No other combination of examined haplotypes showed skewed transmission to these offspring. When the phenotype was changed to include also offspring with type 2 diabetes there was a skewed co-transmission of alleles independently of PDE3B/G1389A. This suggests that PDE3B/G1389A may be an important contributor to chromosome 11p15 haplotypes associated with abnormal glucose tolerance in this Scandinavian population.

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FIG 1. Organization of potential diabetes-related genes on the short arm of chromosome 11. Distances have been approximated from sequence drafts in the nucleotide database (NT_009062, NT_024163, NT_009306 and NT_009307) and information available at www.ncbi.nlm.nih.gov/locuslink. The distance between the genes are approximately 6 Mbp between INS and TUB, 8 Mbp between TUB and PDE3B and 1-2 Mbp between PDE3B and KCNJ1/Kir6.2. INS is the insulin gene. TUB is the human locus syntenic to the mouse tubby locus. PDE3B is the phosphodiesterase 3B gene. KCNJ1/ Kir6.2 is the inwardly-rectifying potassium channel J11 gene. ABCC8/SUR1 is the ATP-binding cassette C8/sulphonylurea receptor gene.

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To our knowledge this is the first study examining a potential role for the PDE3B gene in the pathogenesis of abnormal glucose tolerance and type 2 diabetes, suggesting that variability in or near the PDE3B gene may contribute to elevated insulin levels. The findings further strengthen previous data that genetic variability in this region of chromosome 11 may be important in the pathogenesis of abnormal glucose tolerance and type 2 diabetes.

**STUDY DESIGN AND METHODS**

The study subjects were selected from Finland (including the Bottnia region) and Southern Sweden and extensively phenotyped as previously described (17). All subjects have given informed consent, and the local ethic committees have approved the study. Diagnosis of diabetes, impaired glucose tolerance (IGT) and impaired fasting glucose (IFG) was determined by WHO criteria (17). All offspring had IGT or IFG (age 37 ± 11 years, 108 trios with one offspring that had IGT/IFG (age 37 ± 8 years) and 196 trios with one offspring that had diabetes or IGT/IFG (age 40 ± 10 years). Totally 222 trios (including 614 subjects from 196 nuclear families) were matched for age, gender and Diabetes Status, which identified 1840 sibling pairs discordant for the variant with a large difference in insulin levels 2-hours after OGTT (sibling carrying GG or GA and the other AA).

Healthy control spouses with normal glucose tolerance (150 men, 176 women, age 58±12 years, BMI 26±4 kg/m²) were genotyped for G1389A for estimating allele- and genotype frequencies. For the quantitative transmission disequilibrium test (QTDT) 157 parent-offspring trios (404 subjects from 126 nuclear families) independent of the sample of discordant siblings were genotyped for the G1389A-variant. All offspring had IGT or IFG (age 37±9 years). Identity-by-descent (IBD) status was estimated from genotype information from seven other variants in this region of chromosome 11p15 genotyped by single base extension: KCNJ11/1/Leu270Val, KCNJ11/1/Leu377Val, ABCC8/Ser1370Ala, ABCC8/G3819A, ABCC8/exon 22 C/T, ABCC8/exon 24 T/C, INSA-23T (Hph1) (19). For the transmission disequilibrium test (TDT) one offspring with diabetes and/or IGT/IFG per family was randomly selected from a cohort of 196 parent-offspring trios with one or more offspring. This identified 114 trios with one diabetic offspring (age 43±11 years). 108 trios with one offspring that had IGT/IFG (age 37±8 years) and 196 trios with one offspring that had diabetes or IGT/IFG (age 40±10 years). Totally 222 trios (including 614 subjects from 196 nuclear families) were matched for age, gender and Diabetes Status, which identified 1840 sibling pairs discordant for the variant with a large difference in insulin levels 2-hours after OGTT (sibling carrying GG or GA and the other AA).

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years, BMI 31±4 kg/m²) and one healthy control spouse (male, 44 years, fasting FFA 741 mmol/l and FFA 2 hours after OGTT 165 mmol/l). Intronic primers amplifying the 16 exons in 19 fragments were used as previously described (5) with some modifications (see appendix at www.diabetes.org). The PCR reactions were performed as for the genotyping, with the addition of 0.5 µCi α-³²P-dCTP. The amplified products were separated with PAGE and samples deviating in band pattern were sequenced bidirectionally as previously described (18). Using this procedure, the estimated degree of mutation detection is around 95% in our laboratory.

Statistical analyses. Phenotypic differences between genotype discordant sibling pairs were compared using a simulation-based permutation test as previously described (20). The observed sum of differences (OSD) is the sum of all differences between sibling pairs. The OSD is compared to the total distribution of 10⁶ permutations of the data set to determine the level of significance. The quantitative transmission disequilibrium test (QTDT) (21) was analyzed using the variance of cGMP-inhibited cyclic nucleotide phosphodiesterase (PDE3) gene encoding human PDE3B, cDNA and gene encoding human PDE3B, the cGIP1 isoform of the human cyclic GMP-inhibited cyclic nucleotide phosphodiesterase family. Genomics 36: 476-485, 1996


Appendix 1. Primers and conditions for PCR-amplification of the coding region of the PDE3B gene and exon 9 of the ABCC8 (SUR1) gene.

<table>
<thead>
<tr>
<th>Segment</th>
<th>Forward (sense) primer</th>
<th>Reverse (antisense) primer</th>
<th>Size (bp)</th>
<th>Temp (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PDE3Bex1A</td>
<td>TACGAGCGGGTGTTGCTGAG</td>
<td>TCTCGGGTGTCCTCCAGCA</td>
<td>343</td>
<td>64, ‡</td>
</tr>
<tr>
<td>PDE3Bex1B</td>
<td>CTCTCGCTGGGGCACCTGCG</td>
<td>CCGGACCTTGGCTGGCC</td>
<td>316</td>
<td>66, †</td>
</tr>
<tr>
<td>PDE3Bex1C</td>
<td>ACTCTTGGTGCCAGTGG</td>
<td>ACTCTTGGTGCCAGTGG</td>
<td>343</td>
<td>60 *</td>
</tr>
<tr>
<td>PDE3Bex1D</td>
<td>TGCCCTGGGGTGTTGATCAC</td>
<td>GCTCCGGGACCAGACTCTGC</td>
<td>239</td>
<td>64 *</td>
</tr>
<tr>
<td>PDE3Bex2</td>
<td>GCTGAAATGCTCTACATATAC</td>
<td>CTTTAAGTGTAAAGATTTG</td>
<td>210</td>
<td>52</td>
</tr>
<tr>
<td>PDE3Bex3</td>
<td>ATGCCATGTACAAATGAATG</td>
<td>ACACCTTATACCTTGA</td>
<td>244</td>
<td>52</td>
</tr>
<tr>
<td>PDE3Bex6</td>
<td>CTACACATACAAATACATTC</td>
<td>AGGGATACACAGATCGCT</td>
<td>334</td>
<td>50</td>
</tr>
<tr>
<td>PDE3Bex8</td>
<td>AGCTGGTATCTACTACATAT</td>
<td>GTCTTCTCTACTCTACATAT</td>
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<td>PDE3Bex9</td>
<td>AAATGGGTTATACTTGTC</td>
<td>TGCCGCAAAAGTGAACC</td>
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<td>PDE3Bex12</td>
<td>CTGGATGTAAGAGGGTCTGCC</td>
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<td>62 ⋆</td>
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</tbody>
</table>

Primers are 5’ to 3’. Size (bp) is the size of each PCR amplicon in basepairs and Temp (°C) is the annealing temperature. The segment amplified is annotated by exon number (PDE3B exons 1-16 or ABCC8 exon 9, also referred to as exon 31 in the literature). PDE3B exon 1 was amplified with four overlapping segments (A, B, C and D). ABCC8 exon 9 was amplified with a mismatch (underlined) in the reverse primer. PCR reactions were performed in a total volume of 20 µl with Pharmacia standard PCR-buffer or *16 mmol/l (NH4)2SO4, 67 mmol/l Tris (pH 8.8) and 0.01% Tween 20; 1.5% formamide or †3% DMSO; 0.13 mM dNTP; 1.5 mM MgCl2; 0.2 µM of both primers and 0.5 U Taq polymerase (Perkin Elmer, Foster City, CA) using 25 ng genomic DNA as template. PCR was performed with initial denaturation at 96°C for 3 min followed by 30 or ‡35 cycles of denaturation (94°C for 30 s), annealing and extension (72°C for 30 s) and final extension at 72°C for 10 min.