

Variants in the Hepatocyte Nuclear Factor-1 α and -4 α Genes in Finnish and Chinese Subjects With Late-Onset Type 2 Diabetes

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OBJECTIVE — To determine the role of the hepatocyte nuclear factor (HNF)-1 α and HNF-4 α genes in the etiology of late-onset type 2 diabetes in Finnish and Chinese subjects.

RESEARCH DESIGN AND METHODS — The whole coding regions of the genes encoding for HNF-1 α and HNF-4 α , including ~800 bp of the HNF-1 α promoter, were investigated in 40 Finnish subjects (fasting C-peptide 50–570 pmol/l) and 47 Chinese subjects with type 2 diabetes by single-strand conformation polymorphism (SSCP) analysis. Frequencies of the variants of these genes were analyzed by restriction fragment–length polymorphism analysis in additional samples of 100 Finnish diabetic patients and 82 Finnish control subjects and in 58 Chinese diabetic patients and 51 Chinese control subjects.

RESULTS — No previously reported gene defects were detected, but one novel functionally silent GCC→GCG variant (nucleotide 73, exon 10) was observed in the HNF-4 α gene in a Chinese diabetic patient. Interestingly, the Ala98Val substitution of the HNF-1 α gene occurred at a significantly higher frequency in 140 Finnish diabetic patients compared with 82 control subjects ($P = 0.014$). The Ala98Val variant was not, however, associated with abnormalities in insulin secretion evaluated by oral and intravenous glucose tolerance tests in subjects with normal ($n = 295$) or impaired ($n = 38$) glucose tolerance.

CONCLUSIONS — Variants in the HNF-1 α and HNF-4 α genes are unlikely to play a major role in the pathogenesis of late-onset type 2 diabetes in Finnish and Chinese subjects. However, the association of the Ala98Val variant of the HNF-1 α gene with type 2 diabetes in Finnish subjects may indicate a diabetogenic locus close to the HNF-1 α gene.

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Late-onset type 2 diabetes is a complex familial disease characterized by varying degrees of β -cell dysfunction and insulin resistance. Recently, gene defects in the hepatocyte nuclear factor (HNF)-1 α and HNF-4 α genes have been identified in patients with dominantly inherited and insulin-deficient subtypes of type 2 diabetes (i.e., types 3 and 1, respectively, maturity-onset diabetes of the young [MODY]) (1,2). Furthermore, a population-specific variant in the HNF-1 α gene is a common cause of early-onset type 2 diabetes in the Canadian Oji-Cree population (3). Based on the linkage of late-onset type 2 diabetes close to the HNF-1 α gene on chromosome 12q in Finnish subjects with low insulin secretion, it has been hypothesized that different alleles of the HNF-1 α gene may cause MODY3 and common late-onset type 2 diabetes (4). To date, only a few defects in the HNF-1 α and HNF-4 α genes have been described in subjects with late-onset type 2 diabetes from Japan, the U.S., the U.K., Denmark, and France (5–10). These defects have not been described in Finnish (11,12) or Chinese subjects with late-onset type 2 diabetes. To elucidate whether variants of the HNF-1 α and HNF-4 α genes contribute to late-onset type 2 diabetes, we screened the whole coding regions of the HNF-1 α and HNF-4 α genes in Finnish and Chinese diabetic patients and ~800 bp of the putative promoter of the HNF-1 α gene in Finnish diabetic patients, and investigated the effect of the amino acid substitutions on insulin secretion in nondiabetic subjects.

RESEARCH DESIGN AND METHODS

Subjects

For the initial screening of the HNF-1 α and HNF-4 α genes, 40 Finnish subjects with late-onset type 2 diabetes (16 men and 24 women, age 65 ± 1 years, BMI 28.3 ± 0.7 kg/m², age at diagnosis 55 ± 1 years) with the lowest tertile of fasting insulin levels at the 10-year follow-up (fasting C-peptide level 380 ± 20 pmol/l, range 50–570) were

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Abbreviations: AUC, area under the curve; HNF, hepatocyte nuclear factor; IGT, impaired glucose tolerance; IVGTT, intravenous glucose tolerance test; MODY, maturity-onset diabetes of the young; NGT, normal glucose tolerance; OGTT, oral glucose tolerance test; PCR, polymerase chain reaction; SSCP, single-strand conformation polymorphism; WHO, World Health Organization.

A table elsewhere in this issue shows conventional and Système International (SI) units and conversion factors for many substances.

chosen from our previous population-based study (13). The patients were newly diagnosed type 2 diabetic patients who were ascertained from health centers in the county of Kuopio, Finland, from 1979 to 1981 and were examined for glucose tolerance and other cardiovascular risk factors at baseline and 5 and 10 years of follow-up. For the additional screening of the variants of the HNF-1 α and HNF-4 α genes, a random sample of 100 subjects from our previous studies was included (56 men and 44 women, age 62 ± 1 years, BMI 28.8 ± 0.5 kg/m², age at diagnosis 55 ± 1 years); the total study population comprised 140 subjects with late-onset type 2 diabetes (14). All subjects with type 2 diabetes were unrelated, reported a positive family history of diabetes (at least one first-degree relative with type 2 diabetes), and were diagnosed with type 2 diabetes according to World Health Organization (WHO) criteria (15).

For the association study, a random sample of 82 unrelated Finnish control men (age 54 ± 1 years, BMI 27.2 ± 0.5 kg/m²) who had reported a negative family history of diabetes were included from our previous population study (16). These subjects did not have any chronic diseases or drug treatment that could influence carbohydrate metabolism. Because allele frequency for an autosomal polymorphism should be independent of sex, these healthy men could be examined for the estimation of allele frequencies of the HNF-1 α and -4 α genes in the Finnish population. In addition, a random sample of 295 subjects with normal glucose tolerance (NGT) (150 men and 145 women, age 44 ± 1 years, BMI 25.6 ± 0.2 kg/m²) and 38 subjects with impaired glucose tolerance (IGT) (15 men and 23 women, age 51 ± 2 years, BMI 28.4 ± 0.8 kg/m²) from our previous population studies (17) were used to study the effects of the variants of the HNF-1 α and HNF-4 α genes on insulin secretion in oral glucose tolerance tests (OGTTs) and intravenous glucose tolerance tests (IVGTTs).

For the initial screening of the HNF-1 α and HNF-4 α genes, 47 Chinese subjects with late-onset type 2 diabetes (22 men and 25 women, age 49 ± 1 years, BMI 23.6 ± 3.1 kg/m², age at diagnosis 46 ± 1 years) were randomly chosen from diabetic patients attending outpatient clinics in the Jiangsu Province of China. All of these diabetic patients reported a positive family history of diabetes. For an association study, an additional sample of 58 Chinese subjects with late-onset type 2 diabetes was included (24

men and 34 women, age 60 ± 1 years, BMI 25.3 ± 4.7 kg/m², age at diagnosis 55 ± 1 years). All subjects with type 2 diabetes were diagnosed according to WHO criteria (15).

The Chinese control group consisted of 51 healthy unrelated subjects (15 men and 36 women, age 52 ± 1 years, BMI 26.8 ± 0.1 kg/m²) with NGT based on an OGTT and without a family history of diabetes. The protocol was approved by the ethics committees of Kuopio University Hospital and Jiangsu Province and was in accordance with the Helsinki Declaration.

Identification of variants in the HNF-1 α and HNF-4 α genes

We investigated ~800 bp of the putative promoter and all 10 exons of the HNF-1 α gene and 12 exons (exons 1A–C and exons 2–10) of the HNF-4 α gene and flanking introns with polymerase chain reaction (PCR) using primers described previously (1) or designed by us (the HNF-4 α gene: 5' 1A–F GGCCTGGAGGCAGGGAGAAT; 1A–R, CACTGGCACACCTGGGCACA; 1B–F, GCAACATGTCCGTTTGTCTC; 1B–R, GACACAGAAGGAAGCAGGGT; 1C–F, CATTCTGGGTGAAGGGAGGC; 1C–R, CCTTGCCGTCTCTGAACC; 2F GCTGAAGAAATTGAGGCTCC; 2R, CCTCACTCCCTTCTCTCCTG; 3F, GTGTCTTCTCCATCCAACCA; 3R, GTTGAAATGACTGTCCGGG; 4F, TACTCCATCCTGTCTTCCC; 4R, AGAATGGAGGTGAGGAGGT; 5F, GCCCGGACATCTCCAGCATT; 5R, ACCATCCACGCCCATCCTCA; 6F, CAGATGGCA AACACTGTTCC; 6R, GCCACATGTAATCTCCTT; 7F, TCAACCAAGGTGACTTCCC; 7R, GGATGGCTTAGGAGGTGTGC; 8F, CCTTGCCCACCCTTTCAT; 8R, GCCAAGGAGCTGAGGGGTGA; 9F, GATCGACCTTCTCTACTGC; 9R, CTTTCTCCTGCCTCCTGTCT; 10F, GTCTGTCTGTTTGTCTTCC; and 10R, ATCACCAGGTGCTCTTTAG). PCR was carried out in a volume of 10 μ l. Each reaction contained 50 ng genomic DNA, 5 pmol each primer, 10 mmol/l Tris-HCl (pH 8.8), 50 mmol/l KCl, 1.5 mmol/l MgCl₂, 0.1% Triton X-100, 100 μ mol/l dNTP, 0.14 U DNA polymerase (Dynazyme DNA polymerase; Finnzymes, Espoo, Finland), and 0.55 μ Ci [α -³²P]dCTP (NEN Life Science Products, Boston, MA). PCR reaction included a denaturation step at 94°C for 3 min, followed by 30–35 cycles starting with denaturation at 94°C for 30 s, annealing for 30 s (~2°C under the melting temperature of

the primer with a lower melting temperature), extension at 72°C for 30 s, with final extension at 72°C for 4 min. PCR products were cut to 150- to 250-bp fragments before single-strand conformation polymorphism (SSCP) analysis that was performed in a 5–6% nondenaturing polyacrylamide gel containing 10% of glycerol at 2 different gel temperatures: 38°C for ~4 h and 29°C for ~5 h (18). Variant forms of samples in the SSCP were identified by direct sequencing (Thermo Sequenase Radiolabeled Terminator Cycle Sequencing Kit; USB, Cleveland, OH) and verified by restriction fragment–length polymorphism analysis on a 3% agarose gel (NuSieve GTG; FMC Bioproducts, Rockland, ME).

OGTTs and IVGTTs

All study subjects underwent an OGTT (75 g glucose) after a 12-h overnight fast. The first-phase insulin secretion in 295 subjects with NGT and 38 subjects with IGT was evaluated by an IVGTT after a 12-h overnight fast. We took two successive samples of blood glucose (5 min apart) for the measurement of fasting blood and plasma insulin levels. An intravenous glucose bolus (0.3 g glucose/kg body wt as a 50% solution administered for 90 s) was then injected via the cannula in the nonsampled arm. Additional samples for measurements of blood glucose and plasma insulin were taken at 4, 6, 8, 10, 19, 22, 29, 37, 67, 90, and 180 min. The first-phase insulin secretion was evaluated by calculating the area under the insulin response curve during the first 10 min of the IVGTT. Glucose utilization was analyzed using the minimal model of glucose disappearance according to Bergman et al. (19). The equations of this model provide measurements of the sensitivity of glucose elimination to insulin (the insulin sensitivity index inversely proportional to insulin resistance) and glucose-dependent glucose elimination (as measured by the glucose sensitivity index).

Statistical analysis

The significance of differences in allele frequencies and clinical variables according to the genotypes was tested by Pearson's χ^2 test (noncontinuous variables) and Student's two-tailed *t* test (continuous variables) when appropriate. For comparison of more than two groups, analysis of variance was applied; if needed, confounding factors were adjusted with analysis of covariance. Because of the skewed distribution, insulin was logarithmically transformed before statistical analysis. All data are presented as means \pm SE.

Table 1—Allele frequencies (95% CI) of the variants in the HNF-1 α and -4 α genes in Chinese and Finnish subjects

Location	Codon	Substitution	Amino acid	Chinese subjects		Finnish subjects		P_1^*	P_2^\dagger	P_3^\ddagger
				Control subjects (n = 51)	Type 2 diabetic subjects (n = 105)	Control subjects (n = 82)	Type 2 diabetic subjects (n = 140)			
HNF-1 α gene										
Exon 1	Codon 17	CTC→CTG	—	ND	ND	ND	ND	—	—	—
	Codon 27	ATC→CTC	Ile→Leu	0.39 ± 0.13	0.50 ± 0.10	0.40 ± 0.10	0.46 ± 0.08	NS	NS	NS
	Codon 98	GCC→GTC	Ala→Val	—	0.02 ± 0.03	0.04 ± 0.04	0.09 ± 0.05	—	0.014§	—
Exon 4	Codon 288	GGG→GGC	—	—	—	0.24 ± 0.09	0.25 ± 0.07	—	NS	—
Exon 7	Codon 459	CTG→TTG	—	0.48 ± 0.14	0.52 ± 0.10	0.30 ± 0.09	0.36 ± 0.08	NS	NS	<0.001
		CTG→CTA	—	—	0.01 ± 0.01	—	—	—	—	—
Intron 1	Codon 487	AGC→AAC	Ser→Asn	0.50 ± 0.14	0.51 ± 0.10	0.29 ± 0.09	0.36 ± 0.08	NS	NS	<0.001
		Nucleotide -42	G→A	—	0.32 ± 0.13	0.44 ± 0.10	0.40 ± 0.10	0.42 ± 0.08	NS	NS
Intron 2	Nucleotide +91	A→G	—	ND	ND	ND	ND	—	—	—
		Nucleotide -23	C→T	—	0.46 ± 0.14	0.51 ± 0.10	0.30 ± 0.09	0.36 ± 0.08	NS	NS
Intron 5	Nucleotide +9	C→G	—	0.12 ± 0.10	0.01 ± 0.10	—	—	NS	—	—
		Nucleotide -42	G→T	—	0.46 ± 0.14	0.50 ± 0.10	—	—	NS	—
Intron 7	Nucleotide +7	A→G	—	0.48 ± 0.14	0.53 ± 0.10	0.41 ± 0.10	0.56 ± 0.08	NS	NS	NS
Intron 9	Nucleotide -24	T→C	—	0.46 ± 0.14	0.53 ± 0.10	0.38 ± 0.10	0.44 ± 0.08	NS	NS	NS
HNF-4 α gene										
Exon 1C	Nucleotide 57	GTG→ATG	Val→Met	0.52 ± 0.14	0.38 ± 0.09	0.09 ± 0.06	0.15 ± 0.06	NS	NS	<0.001
Exon 2	Nucleotide 86	GCC→GCT	—	—	—	0.04 ± 0.04	0.04 ± 0.03	—	NS	—
Exon 4	Nucleotide 31	ACT→ATT	Thr→Ile	0.04 ± 0.05	—	—	—	—	—	—
Exon 10	Nucleotide 73	GCC→GCG	—	—	0.01 ± 0.01	—	—	—	—	—
Intron 1B	Nucleotide -5	C→T	—	0.15 ± 0.10	0.24 ± 0.08	0.20 ± 0.09	0.16 ± 0.06	NS	NS	NS

*Significance for the difference in genotype distribution between Chinese control subjects (n = 51) and type 2 diabetic patients (n = 140) (χ^2 test); †significance for the difference in genotype distribution between Finnish control subjects (n = 82) and type 2 diabetic patients (n = 140); ‡significance for the distribution in genotype distribution between Chinese (n = 51) and Finnish control subjects (n = 82); §P = 0.126 after adjustment for the number of tests conducted; ||HNF-4 α transcript with exons 1 and 1C has not been observed to be expressed in β -cells. ND, not determined; NS, not significant.

RESULTS — In the initial screening of the HNF-1 α and HNF-4 α genes, we found similar variants, including three amino acid polymorphisms (Ile27Leu, Ala98Val, and Ser487Asn), four silent variants (Leu17 [CTC→CTG], Gly288 [GGG→GGC], Leu459 [CTG→TTG], and Leu459 [CTG→CTA]), and seven intronic variants (Table 1), in 40 Finnish and 47 Chinese subjects with type 2 diabetes. These findings are similar to those which have been previously described in subjects with late-onset type 2 diabetes (1). The Gly288 variant was observed only in Finnish subjects, whereas the Leu459 (CTG→CTA) variant and nucleotide variants in intron 5 of the HNF-1 α gene were found in Chinese subjects. In the HNF-4 α gene, we identified two amino acid polymorphisms, Val→Met (nucleotide 57 exon 1C) and Thr→Ile (nucleotide 31 exon 4); two silent variants, GCC→GCT (nucleotide 86 exon 2) and GCC→GCG (nucleotide 73 exon 10); and one intron variant in Finnish or Chinese subjects with type 2 diabetes. From these, the GCC→GCT (nucleotide 86 exon 2) variant was found in Finnish subjects only, whereas

the Thr→Ile (nucleotide 31 exon 4) substitution and the silent GCC→GCG (nucleotide 73 exon 10) variant were observed in Chinese subjects. The Leu 459 (CTG→TTG), Ser487Asn, and C→T (nucleotide -23, intron 2) of the HNF-1 α gene, and the Val→Met substitution (nucleotide 57 exon 1C) of the HNF-4 α gene occurred statistically more frequently in Chinese control subjects than in Finnish control subjects (Table 1).

The Ala98Val variant of the HNF-1 α gene was more frequent among 140 Finnish subjects with type 2 diabetes (allele frequency 0.09) than among 82 control subjects (allele frequency 0.04) ($P = 0.014$ for genotype distribution) (Table 1). The genotype frequencies of the Ala98Val variant did not deviate from Hardy-Weinberg expectations in subjects with type 2 diabetes or in control subjects. Allele frequencies of other variants of the HNF-1 α and HNF-4 α genes did not differ significantly between subjects with type 2 diabetes and Finnish and Chinese control subjects.

Among 140 Finnish subjects with type 2 diabetes, 24 individuals were heterozygous

for the Ala98Val variant (17.1%) and among 82 Finnish control subjects, 4 individuals were heterozygous (4.9%) and 1 was homozygous (1.2%) for the Ala98Val variant. This 56-year-old individual had a fasting glucose level of 5.3 mmol/l (mean level 5.6 ± 0.1 mmol/l, n = 82), a 1-h glucose level of 4.0 mmol/l (7.1 ± 0.2 mmol/l), a 2-h glucose level of 4.1 mmol/l (5.2 ± 0.3 mmol/l), a fasting insulin level of 49.2 pmol/l (55.9 ± 4.0 pmol/l), a 1-h insulin level of 250.8 pmol/l (429.3 ± 42.3 pmol/l), a 2-h insulin of 88.8 pmol/l (209.2 ± 25.9 pmol/l), and an insulin area under the curve (AUC) at 2 h during an OGTT of 19,188 pmol · min (37,660 ± 18,593 pmol · min) and the rates of whole-body glucose uptake of 74.7 $\mu\text{mol} \cdot \text{kg}^{-1} \cdot \text{min}^{-1}$ (57.7 ± 7.0 $\mu\text{mol} \cdot \text{kg}^{-1} \cdot \text{min}^{-1}$).

Subjects with or without the heterozygous Ala98Val variant did not differ significantly with respect to age; BMI; fasting, 1-h, or 2-h plasma glucose or insulin levels in an OGTT or during peak insulin concentration at 4 min; or AUC during the first 10 min of insulin secretion in an IVGTT among subjects with NGT (n = 295) or IGT (Table 2). Furthermore, the heterozygous Ala98Val

Table 2—Effect of the Ala98Val variant of the HNF-1 α gene on insulin secretion and insulin sensitivity during an OGTT and an IVGTT in Finnish subjects with NGT (n = 295) or IGT (n = 38)

	Subjects with NGT		P_1	Subjects with IGT		P_2
	AA98 (n = 253)	AV98 (n = 42)		AA98 (n = 35)	AV98 (n = 3)	
Sex (M/F)	128/125	19/23	0.52	7/18	1/2	0.61
Age (years)	44.3 \pm 0.8	43.4 \pm 1.7	0.66	52.1 \pm 1.7	45.0 \pm 4.4	0.24
BMI (kg/m ²)	25.6 \pm 0.2	24.9 \pm 0.5	0.26	28.6 \pm 0.8	31.3 \pm 3.7	0.38
OGTT						
Fasting glucose (mmol/l)	5.1 \pm 0.0	5.1 \pm 0.3	0.68	6.1 \pm 0.1	6.1 \pm 0.4	0.90
2-h glucose (mmol/l)	5.3 \pm 0.0	5.5 \pm 0.2	0.31	8.6 \pm 0.2	8.7 \pm 0.6	0.93
Fasting insulin (pmol/l)	54.4 \pm 1.7	62.5 \pm 6.7	0.40	80.8 \pm 6.4	90.0 \pm 35.6	0.91
1-h insulin (pmol/l)	379.7 \pm 15.1	422.9 \pm 58.9	0.77	526.6 \pm 70.9	534.0 \pm 174.9	0.72
2-h insulin (pmol/l)	241.1 \pm 10.3	255.8 \pm 25.8	0.49	466.9 \pm 53.3	504.8 \pm 174.3	0.69
IVGTT						
4-min insulin (pmol/l)	369.1 \pm 14.5	356.1 \pm 46.0	0.37	322.0 \pm 40.4	274.6 \pm 39.6	0.90
Insulin AUC during 0–10 min (pmol \cdot l ⁻¹ \cdot min)	2,596.1 \pm 99.6	2,595.6 \pm 303.3	0.73	2,453.2 \pm 283.6	2,196.8 \pm 348.1	0.87
$S_I \cdot 10^{-4}$ (min ⁻¹ \cdot μ U \cdot ml ⁻¹)	4.3 \pm 0.1	4.5 \pm 0.4	0.54	2.4 \pm 0.4	1.2 \pm 0.3	0.42

Data are n or means \pm SE. None of the comparisons between the AA98 and AV98 genotypes among subjects with NGT (P_1) or IGT (P_2) were statistically significant. S_I , insulin sensitivity index.

variant was not associated with age at onset of diabetes (n = 140) or the degree of insulin resistance, systolic or diastolic blood pressure, serum total cholesterol, or triglyceride levels in the control group (n = 82) (data not shown). We also investigated the impact of other amino acid substitutions of the HNF-1 α and HNF-4 α genes (Ile27Leu, Ser487Asn, and Val \rightarrow Met in nucleotide 57 of exon 1C) on insulin secretion in Finnish subjects with NGT. None of the substitutions was associated with insulin secretion abnormalities evaluated by an OGTT or IVGTT (data not shown).

CONCLUSIONS — Defects in the HNF-1 α and -4 α genes have been observed to underlie the development of dominantly inherited and early-onset type 2 diabetes in several populations worldwide (1–3,5,20). Because the role of these genes in determining the genetic susceptibility to late-onset type 2 diabetes is unknown, we screened the HNF-1 α and the HNF-4 α genes for variants in Finnish and Chinese subjects with late-onset type 2 diabetes. No specific gene defects for diabetic patients were identified in these genes, but the previously reported Ala98Val variant of the HNF-1 α gene was associated with late-onset type 2 diabetes in Finnish subjects.

The Val98 allele of the HNF-1 α gene occurred at two to three times higher frequency in Finnish subjects with type 2 diabetes than in the corresponding control subjects. Previously, the Val98 allele has

even been found at a three- to fourfold higher prevalence in Finnish patients with early-onset diabetes (allele frequency 0.132), but at a similar frequency in patients with late-onset diabetes (0.042) compared with control subjects (0.035) in an independent sample from western Finland (21). Since the Finnish population is largely inhabited by the settlers from the south and west (22), the east–west difference in the prevalence of the Val98 allele in subjects with type 2 diabetes may reflect the migratory origin of Finns. This may have led to differences in the founder mutations defining disease susceptibility in these regions.

The heterozygous Val98 allele has been reported to be associated with decreased 30-min C-peptide and insulin responses during an OGTT, but not with reduced insulin secretion during an IVGTT in healthy subjects (23). The results of our study support the view that the heterozygous Ala98Val variant is not associated with disturbances in insulin secretion in response to an intravenous glucose load in subjects with NGT or IGT. Ingested glucose is known to be a stronger physiologic stimulator of insulin secretion than glucose administered intravenously. Therefore, the discrepancy between the results obtained by an OGTT and IVGTT may result from methodological differences or from the impact of the Ala98Val variant on stimulation of insulin secretion during the ingestion of glucose. We observed one homozygous individual for

the Val98 allele who was characterized by relatively low fasting and postchallenge insulin levels but a concomitantly high degree of insulin sensitivity and normoglycemia. In this individual, insulin secretion is likely to be normal, given the high insulin sensitivity. Alternatively, a subtle impairment in insulin secretion in response to glucose or nonglucose secretagogues, compensated with high insulin sensitivity in the homozygous Val98 individual, cannot be ruled out and should be examined directly.

An alternative hypothesis is that the association of the Ala98Val variant with type 2 diabetes is attributed to linkage disequilibrium between the Ala98Val variant and a gene defect near the HNF-1 α gene, because the whole coding region of the HNF-1 α and the putative \sim 800 bp of the promoter of the HNF-1 α gene did not reveal any other variants associated with type 2 diabetes. Relative homogeneity of the Finnish population due to a limited number of founders, isolation, and rapid expansion of population enables us to detect linkage disequilibrium that originates far from ancestors. Recently, a dominantly acting gene for type 2 diabetes was mapped close to the HNF-1 α locus in Caucasian subjects (4,24). Therefore, it is possible that the Ala98Val variant is in linkage disequilibrium with a diabetogenic variant locating at the near chromosomal region.

Screening of the HNF-1 α and HNF-4 α genes in Finnish and Chinese normoglycemic subjects showed minor differ-

ences in the occurrence of variants, but it also showed major differences in the prevalence of the variants. The allele frequencies of the variants of the HNF-1 α gene tended to be higher in Chinese control subjects compared with Finnish control subjects, with the exception of the silent codon 288 polymorphism (GGG→GGC) and the Ala98Val variant that were uncommon in Chinese patients with late-onset type 2 diabetes, as previously found in Chinese patients with early-onset type 2 diabetes (20). The Val→Met (nucleotide 57, exon 1C) of the HNF-4 α gene occurred at a higher frequency in Chinese versus Finnish control subjects. The Thr→Ile variant (nucleotide 31, exon 4) of the HNF-4 α gene was not observed in Finnish subjects in this screening but was previously described in Finnish subjects (11).

To our knowledge, this is the first systematic screening of Chinese subjects with late-onset type 2 diabetes for variants in the HNF-1 α and HNF-4 α genes. No gene defects were detected in a representative sample of 47 Chinese subjects with type 2 diabetes, which is in accordance with the previous findings of a low mutation frequency in the HNF-1 α gene (<1% in Japanese subjects with late-onset type 2 diabetes) (6). Similarly, no previously reported amino acid substitutions were observed in the HNF-1 α and HNF-4 α genes in Finnish subjects with late-onset type 2 diabetes, which is consistent with the previous screening of the HNF-1 α (12) and HNF-4 α (11) genes. Therefore, it is unlikely that variants in the HNF-1 α and HNF-4 α genes could substantially contribute to the pathogenesis of late-onset type 2 diabetes in Finnish or Chinese subjects. However, the association of the Ala98Val with type 2 diabetes in Finnish subjects may indicate a possible diabetogenic locus near the HNF-1 α gene.

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