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Variants of transcription factor 7-like 2 (TCF7L2) gene and incident glucose intolerance in Japanese-Brazilians

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Variants of transcription factor 7-like 2 (*TCF7L2*) gene and incident glucose intolerance in Japanese-Brazilians

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Abstract

Common variants of the transcription factor 7-like 2 (*TCF7L2*) gene have been found to be associated with type 2 diabetes in different ethnic groups. The Japanese-Brazilian population has one of the highest prevalence rates of diabetes. Therefore, the aim of the present study was to assess whether two single-nucleotide polymorphisms (SNPs) of *TCF7L2*, rs7903146 and rs12255372, could predict the development of glucose intolerance in Japanese-Brazilians. In a population-based 7-year prospective study, we genotyped 222 individuals (72 males and 150 females, aged 56.2 ± 10.5 years) with normal glucose tolerance at baseline. In the study population, we found that the minor allele frequency was 0.05 for SNP rs7903146 and 0.03 for SNP rs12255372. No significant allele or genotype association with glucose intolerance incidence was found for either SNP. Haplotypes were constructed with these two SNPs and three haplotypes were defined: CG (frequency: 0.94), TT (frequency = 0.027) and TG (frequency = 0.026). None of the haplotypes provided evidence for association with the incidence of glucose intolerance. Despite no associations between incidence of glucose intolerance and SNPs of the *TCF7L2* gene in Japanese-Brazilians, we found that carriers of the CT genotype for rs7903146 had significantly lower insulin levels 2 h after a 75-g glucose load than carriers of the CC genotype. In conclusion, in Japanese-Brazilians, a population with a high prevalence of type 2 diabetes, common *TCF7L2* variants did not make major contributions to the incidence of glucose tolerance abnormalities.

Key words: *TCF7L2*; Glucose intolerance; Japanese-Brazilians

Introduction

Population groups with defined characteristics have been studied to assess the role of environmental and genetic factors in the etiology of non-communicable diseases such as diabetes mellitus. A previous study on Japanese-Brazilians showed that 22.6% of this population had diabetes in the first phase of the study. In the second phase of the study, 7 years later, this prevalence had increased to 36.1%, being one of the highest worldwide (1). This situation could be reflecting the strong genetic susceptibility of this population associated with an unfavorable environment.

It is well known that type 2 diabetes has a strong genetic background. At present, it is not well understood how many genes are involved and what their relative contributions are to the development of diabetes mellitus. In 2006, Grant et al. (2) identified a microsatellite marker (DG10S478) in the

transcription factor 7-like 2 gene (*TCF7L2*) that showed strong association with type 2 diabetes in Icelandic individuals, with replication in Danish and US cohorts. The single-nucleotide polymorphisms (SNPs) with the strongest correlation with DG10S478 were rs7903146, rs12255372, rs7901695, rs11196205, and rs7895340. After this initial finding many other studies have found consistent associations between *TCF7L2* variants and type 2 diabetes in populations of different ethnic groups (3-10).

The *TCF7L2* gene product is a transcription factor involved in the Wnt signaling pathway. This pathway is considered to be critical for multiple developmental and growth-regulating processes of the cell (11). Reduced insulin secretion might be the essential component by which *TCF7L2* polymorphisms increase the risk of diabe-

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tes. However, the precise molecular mechanism(s) remain to be elucidated. Since in a previous study Yi et al. (12) described the role of *TCF7L2* in the regulation of the proglucagon gene, which encodes glucagon, glucagon-like peptide 1 (GLP-1) and GLP-2, it had been suggested that the association with type 2 diabetes may involve an impaired incretin effect (2). Despite the role of *TCF7L2* in the transcriptional regulation of the proglucagon gene, plasma GLP-1 concentrations during oral glucose tolerance or mixed meal tests were not significantly influenced by the *TCF7L2* polymorphisms (13,14). Therefore, the lower incretin-mediated insulin response seems to be the result of an under-responsiveness of pancreatic β -cells rather than a reduction in GLP-1 secretion (14,15).

The aim of the present study was to assess whether two SNPs of the *TCF7L2* gene, rs7903146 and rs12255372, could predict the development of glucose intolerance in a Japanese-Brazilian population.

Material and Methods

The study population consisted of individuals recruited from the Japanese-Brazilian Diabetes Study Group, a survey designed to estimate the prevalence and incidence of diabetes and associated diseases in a Japanese-Brazilian population living in Bauru, São Paulo State, Brazil. Details on the selection and recruitment of the sample population have been previously reported (1). Briefly, the first phase of the study involved all individuals aged 40-79 years from the first generation (Issei) and a random sample (one third plus 20%) of those from the second generation (Nisei) from the same age group. A total of 647 individuals were examined and submitted to an oral glucose tolerance test (OGTT). In the second phase of the study, seven years later, the glucose tolerance status of 394 subjects was reexamined (follow-up rate: 61%). For the present study, we enrolled 222 individuals (72 males and 150 females aged 56.2 ± 10.5 years) with normal glucose tolerance in the first phase of the study and suitable DNA samples.

The glucose tolerance status was based on the 1999 WHO criteria (16). Plasma glucose was determined by the glucose-oxidase method. Insulin and proinsulin were determined by a monoclonal antibody-based immunofluorimetric assay (17,18). Homeostasis model assessment (HOMA) was used to assess β -cell function (HOMA- β) and insulin resistance (HOMA-IR) (19).

Genotyping *TCF7L2* rs7903146 and rs12255372

Blood samples were obtained from each subject and genomic DNA was extracted from peripheral blood leukocytes using a commercial kit (Puregene DNA Isolation Kit, Gentra System, USA). Both SNPs were genotyped using TaqMan SNP Genotyping Assays (Applied Biosystem, USA) according to manufacturer instructions. The genotyping success rate was 96.4%

for rs7903146 and 92.8% for rs12255372. The quality control for these assays was assessed by direct sequencing of 10 samples with different genotypes. The concordance observed between genotyping assays was 100%.

This study was approved by the Ethics Committee of Escola Paulista de Medicina, Universidade Federal de São Paulo, and all subjects gave written informed consent to participate.

Statistical analysis

All statistical analyses were performed using the Stata version 9.1 software (Statacorp, USA). Continuous data are reported as means \pm SD unless otherwise specified. Variables with skewed distributions were log transformed to satisfy assumptions of normality and back-transformed values are shown. The Student *t*-test, χ^2 or Fisher test was used as appropriate. Haplotype frequency, Hardy-Weinberg equilibrium, and linkage disequilibrium statistics were obtained using the Haploview software.

Results

The comparison of subjects' baseline characteristics showed a worse metabolic profile among those who progressed to glucose intolerance at the 7-year follow-up (Table 1). Subjects who continued to have normal glucose tolerance had lower mean values of body mass index, waist circumference, fasting plasma glucose concentrations, and HOMA-IR.

Of the 214 individuals genotyped for the rs7903146 variant, 191 (89%) had the CC genotype and 23 (11%) had the CT genotype. Of the 206 individuals genotyped for the rs12255372 variant, 192 (93%) had the GG genotype and 14 (7%) had the GT genotype. The genotypic distribution of both SNPs was in Hardy-Weinberg equilibrium. The minor allele frequency of SNP rs7903146 was 0.05 and

Table 1. Baseline characteristics of individuals who continued to have normal glucose tolerance (NGT) and individuals who progressed to glucose intolerance.

Characteristics	NGT (N = 50)	Glucose intolerance (N = 172)
Age (years)	58.4 \pm 11.0	55.5 \pm 10.5
Body mass index (kg/m ²)	22.7 \pm 3.0	24.6 \pm 3.6*
Waist circumference (cm)	79.4 \pm 11.0	86.0 \pm 9.0*
Fasting plasma glucose (mg/dL)	87.8 \pm 7.3	92.4 \pm 8.6*
HOMA- β	47.9 \pm 34	68.7 \pm 97.5
HOMA-IR	0.67 \pm 0.8	1.18 \pm 1.8*

Data are reported as means \pm SD. HOMA- β = homeostasis model assessment of β -cell function; HOMA-IR = homeostasis model assessment of insulin resistance. *P < 0.05 compared to individuals with normal glucose tolerance (Student *t*-test).

that of SNP rs12255372 was 0.03. The genotype and allele frequencies of both SNPs of subjects who continued to have normal glucose tolerance and the ones who progressed to glucose intolerance are shown in Table 2. No significant allele or genotype association was found with the incidence of glucose intolerance. Linkage disequilibrium analysis showed that the alleles of the two polymorphisms were moderately associated ($D' = 0.76$). Haplotypes were constructed with these SNPs and three haplotypes were defined: CG (frequency = 0.94), TT (frequency = 0.027) and TG (frequency = 0.026). None of the haplotypes provided evidence for an association with the incidence of glucose intolerance (Table 3).

The relationship of rs7903146 and rs12255372 with β -cell function measures was assessed at baseline. Carriers of the CT genotype for rs7903146 had lower 2-h insulin levels after the OGTT than carriers of the CC genotype (CC = 138.30 ± 133.73 pmol/L, CT = 81.40 ± 78.70 pmol/L, $P = 0.02$). Also, a trend towards lower 2-h insulin levels was observed in GT carriers of rs12255372 (GG = 130.40 ± 125.90 pmol/L, GT = 77.00 ± 75.44 pmol/L, $P = 0.07$; Table 4).

Discussion

In this study, we tested for associations between incidence of glucose intolerance and SNPs of the *TCF7L2* gene in a cohort of Japanese-Brazilians. Although *TCF7L2* variants have been consistently associated with an increased risk for type 2 diabetes in diverse populations (3-10), the present study showed that the presence of SNPs rs7903146

and rs12255372 did not predict glucose intolerance in Japanese-Brazilians. Guo et al. (20), in a large study group of Pima Indians, also did not find an association between *TCF7L2* polymorphisms and type 2 diabetes. Also, Florez et al. (21) reported associations of the *TCF7L2* gene with increased risk of developing diabetes in the Diabetes Pre-

Table 2. Genotype and allele frequencies of single-nucleotide polymorphisms (SNPs) rs7903146 and rs12255372 of subjects who remained with normal glucose tolerance (NGT) and those who progressed to glucose intolerance.

SNP	Genotype		Allele		
rs7903146	CC	CT	C	T	
	NGT	44 (89.8)	5 (10.2)	93 (94.9)	5 (5.1)
	Glucose intolerance	147 (89.1)	18 (10.9)	312 (94.5)	18 (5.5)
rs12255372	GG	GT	G	T	
	NGT	44 (93.6)	3 (6.38)	91 (96.8)	3 (3.2)
	Glucose intolerance	148 (93.1)	11 (6.92)	307 (96.5)	11 (3.5)

Data are reported as number (N) with percent in parentheses. All P values were >0.05 when comparing NGT and glucose intolerance (Fisher exact test).

Table 3. Haplotype frequencies of subjects who remained with normal glucose tolerance (NGT) and those who progressed to glucose intolerance.

Haplotype rs7903146, rs12255372	Glucose intolerance	NGT
CG	0.940	0.939
TT	0.027	0.025
TG	0.026	0.026

All P values were >0.05 when comparing NGT and glucose intolerance (chi-square test).

Table 4. Baseline characteristics by genotypes for the *TCF7L2* single-nucleotide polymorphisms of the subjects studied.

Characteristics	rs7903146		rs12255372	
	CC (N = 191)	CT (N = 23)	GG (N = 192)	GT (N = 14)
Age (years)	56.4 \pm 9.9	57.4 \pm 10.5	56.5 \pm 9.9	57.4 \pm 11.2
Body mass index (kg/m ²)	24.3 \pm 3.6	23.5 \pm 3.2	24.3 \pm 3.7	23.1 \pm 2.5
Fasting glucose (mg/dL)	91.8 \pm 8.5	88.8 \pm 9.4	92.0 \pm 8.4	88.5 \pm 9.8
2-h glucose (mg/dL)	100.8 \pm 20.8	92.1 \pm 23.3	99.1 \pm 21.2	96.2 \pm 26.3
Fasting insulin (pmol/L)	15.8 \pm 13.1	10.0 \pm 8.0	14.4 \pm 11.8	8.1 \pm 6.3
2-h insulin (pmol/L)	138.3 \pm 133.7	81.4 \pm 78.7*	130.4 \pm 125.9	77.0 \pm 75.4
Fasting proinsulin (pmol/L)	3.3 \pm 2.2	2.9 \pm 2.0	3.4 \pm 2.3	2.5 \pm 1.8
2-h proinsulin (pmol/L)	13.1 \pm 10.6	12.6 \pm 10.4	13.1 \pm 10.6	12.2 \pm 10.2

Data are reported as means \pm SD. * $P < 0.05$, CT compared to CC (Student t-test).

vention Program cohort. However, in the Asian subgroup analysis there were no associations of the polymorphisms with type 2 diabetes. Our findings suggest that this particular population has a different set of genetic risk factors for type 2 diabetes. In this scenario, this population may be used as a resource to identify new genetic risk factors for this complex phenotype.

The underlying mechanism by which intronic variations of the *TCF7L2* gene without obvious function in gene regulation contribute to the development of type 2 diabetes in most populations remains to be elucidated. One possibility is that the association with type 2 diabetes reflects a linkage disequilibrium with more distant functional alleles. A difference in linkage disequilibrium pattern with a putative functional variant in Japanese-Brazilians may be an explanation for the lack of association between the SNPs studied and the incidence of glucose intolerance in this population. Similarly, Chang et al. (22) studying a Han Chinese population, found no associations between SNPs rs7903146 and rs12255372 and type 2 diabetes, but identified a novel risk-conferring SNP, rs290487.

The frequencies of minor alleles of the two SNPs, which are the high-risk alleles for diabetes in most populations, were very low in this Japanese-Brazilian population. Similarly, Horikoshi et al. (10) and Chang et al. (22), studying samples of Japanese and Chinese populations, found that the minor allele frequencies of these SNPs were lower than those previously reported for Caucasians, meaning that studies on Asians have less power. In fact, one limitation of the present study was the relatively small statistical power derived from both low minor allele frequency and small sample size. Nonetheless, if one analyzes the point estimate of risk (in our case the presence of a T allele was associated with an RR of only 1.01, 95%CI = 0.81-1.28) it is interesting to observe that there was no tendency of association in our sample. Indeed, in most studies able to show an association between the T allele of this SNP and the prevalence or incidence of type 2 diabetes, the presence of the risk allele was associated with a 30% increased risk. This suggests that other factors are responsible for not detecting an association than only a reduced statistical

power in the present study.

Despite the lack of association between incidence of glucose intolerance and SNPs of *TCF7L2* gene in Japanese-Brazilians, we found that carriers of the CT genotype for rs7903146 had lower insulin levels at 2 h after a 75-g glucose load than carriers of the CC genotype. Saxena et al. (6), studying non-diabetic individuals, found a significant reduction in the area under the curve for insulin during the OGTT in homozygous carriers of the rs7903146 risk allele. Also, Pilgaard et al. (13) found in young healthy men a reduced 24-h insulin concentration and a reduced insulin secretion during a mixed meal in carriers of the T allele for rs7903146. These findings indicate that *TCF7L2* variants may increase diabetes risk by reduced insulin secretion rather than by reduced insulin action.

In summary, in Japanese-Brazilians, a population with a high prevalence of type 2 diabetes, common *TCF7L2* variants did not make a major contribution to the incidence of glucose tolerance abnormalities.

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