

the ER Ca^{2+} -ATPase inhibitors (21) thapsigargin and cyclopiazonic acid, the ryanodine receptor activator 4-chloro-*m*-cresol, and the protein *N*-glycosylation inhibitor tunicamycin all induced WFS1 protein as shown in Fig. 3. Only brefeldin A had no effect. Ionomycin only weakly induced WFS1 protein. The differing effects of these chemicals, which have different mechanisms of action, may provide insights into the functions of Wfs1. The lack of WFS1 induction with brefeldin A, a Golgi apparatus disruptor, may be related to its instability in solution (22). Although we did not perform Northern blot analysis for each of these

reagents, A23187 induced WFS1 mRNA in fibroblasts (data not shown).

Effects of thapsigargin and tunicamycin on Wfs1 expression in MIN6 cells

We next examined the effects of thapsigargin and tunicamycin on the expression of *Wfs1* mRNA in MIN6 cells. Thapsigargin and tunicamycin treatments are known to induce ER stress, and Chop/GADD153 is a transcription factor that plays a role in ER stress-induced apoptotic cell death (23, 24). Phosphorylation of the α -subunit of translation initiation factor-2 (eIF2- α) attenuates protein translation upon ER stress. Although the ER chaperone Bip/GRP78 expression did not change in MIN6 cells (Fig. 4B) probably due to its strong basal expression, thapsigargin and tunicamycin clearly generated ER stress as demonstrated by Chop induction and eIF2- α phosphorylation (Fig. 4A, B). Under these conditions, ER stress-induced caspase-3 activation, an event at the initiation of apoptosis (25), was evidenced by the cleavage of PARP (Fig. 4C). PARP is one of the substrates cleaved by caspase-3. Upon thapsigargin or tunicamycin treatment, the 113 kDa band decreased, and instead, the proteolytic PARP fragment (89 kDa) appeared (Fig. 4C). In association with ER stress induction and caspase-3 activation, *Wfs1* mRNA expression increased (Fig. 4A,D). With thapsigargin, *Wfs1* mRNA started to increase after 6 h and was maximal after 12 h. With tunicamycin, *Wfs1* mRNA induction peaked at 6 h, and then declined. Wfs1 protein was also increased by thapsigargin treatment (Fig. 4B). In contrast, tunicamycin, despite the mRNA induction, did not increase the Wfs1 protein, but decreased it after 24 h (Fig. 4B). This is probably due to the instability of unglycosylated Wfs1 protein (6, 16).

Thapsigargin and tunicamycin enhance human WFS1 promoter activity in MIN6 cells

To determine the mechanism of *WFS1* expression, we examined the effects of thapsigargin and tunicamycin on human *WFS1* gene promoter activity by employing transient transfection assays in MIN6 cells. We used a *WFS1* promoter-luciferase construct that contained a 3 kb DNA sequence upstream from the human *WFS1* gene transcription initiation site. The human *WFS1* gene promoter was active in MIN6 cells. Introduction of the *WFS1* promoter-reporter plasmid produced a 20-fold increase in luciferase activity as compared with the promoterless pGL3-Basic vector. Treatment of the cells with thapsigargin or tunicamycin resulted in further 1.3- and 1.5-fold increases in luciferase activity respectively (Fig. 5). We conducted these experiments again using a 1 kb (–1000 to +20) *WFS1* promoter-luciferase reporter gene. The results were essentially the same but the promoter activity was weaker than with the 3 kb construct (data not shown).

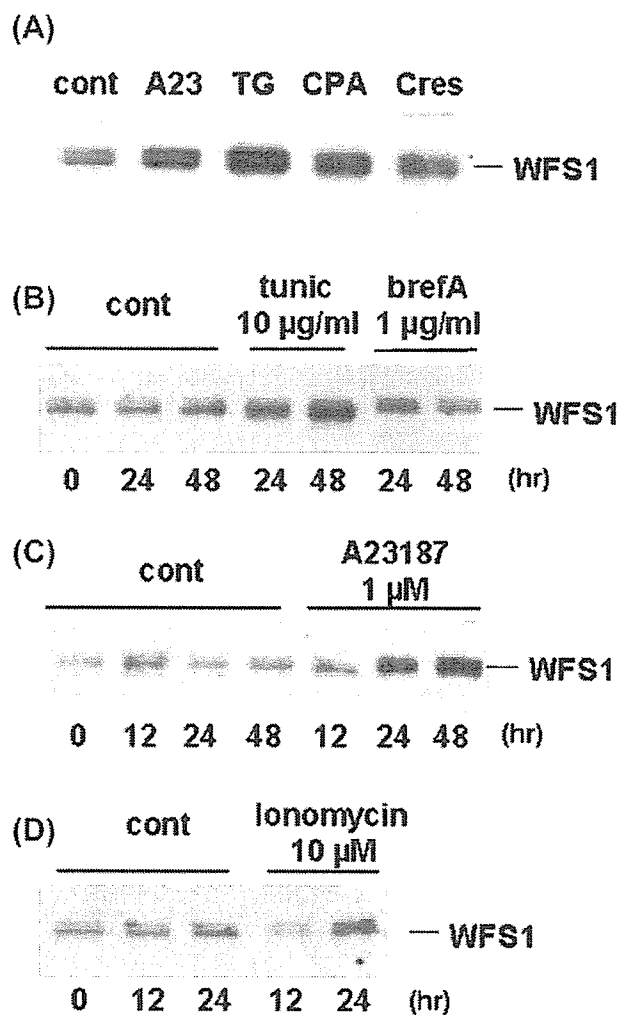


Figure 3 ER stress induces WFS1 protein in fibroblasts. Primary skin fibroblasts were cultured in the presence of (A) A23187 (A23, 1 $\mu\text{mol/l}$), thapsigargin (TG, 1 $\mu\text{mol/l}$), cyclopiazonic acid (CPA, 10 $\mu\text{mol/l}$) and 4-chloro-*m*-cresol (cres, 50 $\mu\text{mol/l}$) for 48 h. (B–D) Cells were treated for the indicated time periods with (B) tunicamycin (tunic), brefeldin A (brefA), (C) A23187, and (D) ionomycin. cont indicates control. Control samples included a vehicle (DMSO), also administered with all of the drugs. Cells were harvested after the incubation periods, and total cell lysates containing 20 μg protein were subjected to Western blot analysis using anti-WFS1c antibody.

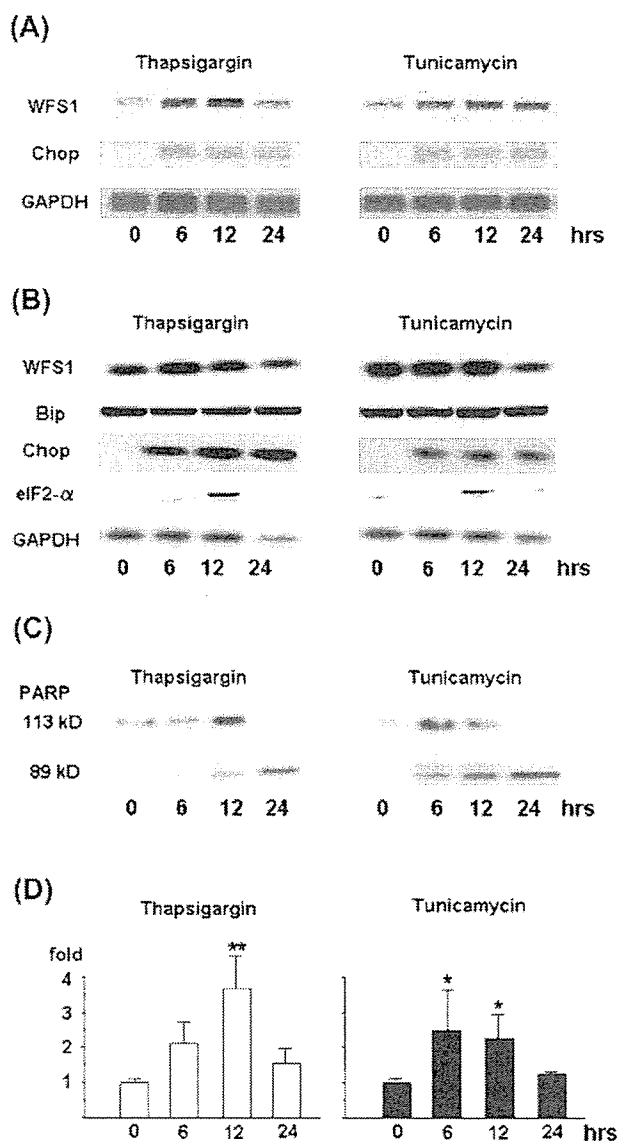


Figure 4 Thapsigargin and tunicamycin increase *Wfs1* mRNA expression in MIN6 cells in association with ER stress and apoptosis induction. MIN6 cells were placed in culture dishes and serum-starved in serum-free DMEM for 12 h, and then treated with thapsigargin (1 μ mol/l) or tunicamycin (10 μ g/ml) for 6, 12 or 24 h. Dimethyl sulfoxide (DMSO) was used to dissolve thapsigargin and tunicamycin, and the same concentration of DMSO (final, 0.05%) was employed in all experiments, including controls. After incubation, cells were washed once with ice-cold phosphate-buffered saline, and harvested. (A) Ten micrograms RNA were subjected to Northern blot analysis. (B) Total cell lysates containing equal amounts of protein (50 μ g) were separated on 10% SDS-PAGE and analyzed by immunoblotting using anti-*Wfs1*n, anti-Bip (GRP74), anti-Chop or anti-phosphorylated eIF2- α . (C) Total cell lysates containing equal amounts of protein (50 μ g) were separated on 10% SDS-PAGE and analyzed by immunoblotting using the anti-PARP antibody. Activated caspase-3 cleaves the 113 kDa PARP, resulting in the appearance of the 89 kDa fragment. (D) Quantification of the *Wfs1* mRNA from the results obtained in (A), shown as means \pm S.E. ($n = 4$). Statistical analysis, conducted using analysis of variance, indicated that the thapsigargin and tunicamycin treatments significantly increased *Wfs1* mRNA expression at 12 h and at 6 h and 12 h respectively (* $P < 0.05$, ** $P < 0.001$).

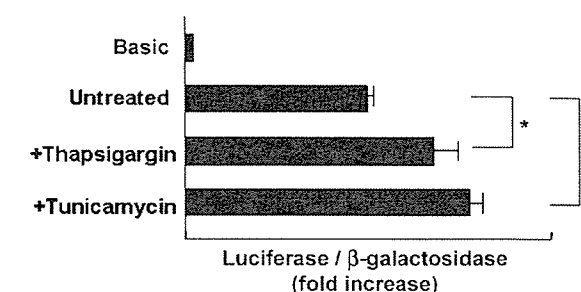


Figure 5 ER stress enhances *WFS1* promoter activity in MIN6 cells. MIN6 cells were transfected with a luciferase reporter plasmid containing a 3.0 kb human *WFS1* gene 5' flanking promoter region (from -3000 to +20) and were exposed to thapsigargin (1 μ mol/l) or tunicamycin (10 μ g/ml) for 6 h. Beta-galactosidase activity from the co-transfected expression vector pCMV β was used to calibrate for transfection efficiency. Basic represents luciferase activity from pGL3-Basic (promoterless) vector-transfected cells. Results are expressed as the fold increase as compared with basic (means \pm S.E. of four independent experiments, each performed in triplicate). P values for comparison of results with versus without drug treatments are 0.034 (thapsigargin, *) and 0.005 (tunicamycin, **) (analysis of variance).

Wfs1 expression is transcriptionally upregulated in β -cells with intrinsic ER stress

In the Akita mouse, the C96Y mutation of the *ins2* gene disturbs intramolecular disulfide bond formation, resulting in progressive β -cell loss (12). ER stress and subsequent apoptosis are at least partially responsible for this progressive β -cell loss (14). To further examine the association between increased *Wfs1* expression and ER stress, we used mouse insulinoma cells derived from an Akita mouse homozygous for the *ins2* gene C96Y mutation (*Ins2*^{96Y/Y} cell) as a model. *Ins2*^{WT/WT} cells derived from normal littermates served as controls. Doubling of the ER chaperone Bip/GRP78 in *Ins2*^{96Y/Y} cells indicated persistent ER stress in these cells (Fig. 6A). In *Ins2*^{96Y/Y} cells, *Wfs1* protein increased sixfold as compared with that in *Ins2*^{WT/WT} cells (Fig. 6B). *Wfs1* mRNA expression was also increased twofold (data not shown). We next examined *WFS1* promoter activity in these cells. Introduction of the *WFS1* promoter-reporter plasmid into *Ins2*^{96Y/Y} cells approximately doubled luciferase activity as compared with that in wild type *Ins2*^{WT/WT} cells (Fig. 7). Luciferase activity after transfection of the SV40 promoter-reporter plasmid did not differ between *Ins2*^{96Y/Y} and *Ins2*^{WT/WT} cells.

Discussion

Herein, we have documented the localization of *Wfs1* expression in the mouse pancreatic islet. Insulin-producing β -cells are the major site of *Wfs1* expression, as shown in Ishihara *et al.* (15). *Wfs1* expression is also evident in somatostatin-producing δ -cells, but is absent from glucagon producing α -cells and PP-cells. No *Wfs1* expression is observed in pancreatic exocrine acinar

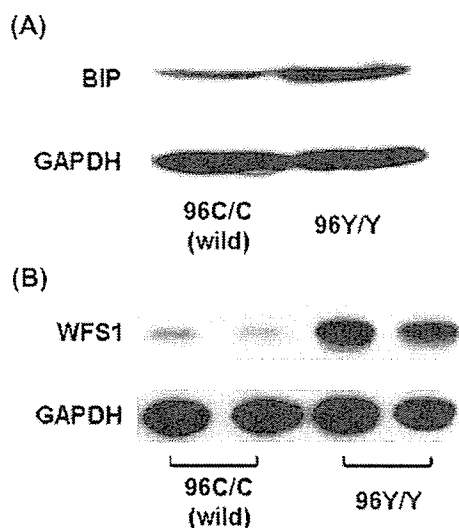


Figure 6 *WFS1* expression is increased in Akita mouse-derived *Ins2*^{96Y/Y} cells. Cell extracts of *Ins2*^{96Y/Y} cells containing equal amounts of protein (50 µg) were separated on 10% SDS-PAGE and analyzed by immunoblotting using (A) anti-Bip, and (B) anti-WFS1 and anti-GAPDH antibodies. Insulinoma cells derived from wild type littermates (wild) were used as the control. In (B), cell extracts were prepared on two separate occasions from cells derived from the same mutant mouse.

cells. A histopathological study of pancreatic islets from Wolfram syndrome patients showed selective loss of insulin-producing β -cells and an apparent preservation of glucagon-producing α -, somatostatin-producing δ -, and PP-cells (26, 27). The histochemical evidence of *Wfs1* protein localization in insulin-producing β -cells might provide a histological background explaining the insulin deficiency caused by *WFS1* mutations in Wolfram syndrome patients and suggests that *WFS1* protein is necessary for β -cell (28, 29), but not δ -cell survival.

We have also presented evidence herein that ER stress induces *Wfs1* gene expression. Treatment of fibroblasts with A23187, ionomycin, thapsigargin, cyclopiiazonic acid, 4-chloro-*m*-cresol or tunicamycin increased *Wfs1* protein levels. Chemical insults by these reagents are known to induce ER stress via disruption of Ca^{2+} homeostasis or inhibition of N-linked glycosylation. Thapsigargin and tunicamycin treatments also induced *Wfs1* mRNA expression in a mouse β -cell line, MIN6 cells. In accordance with the mRNA change, thapsigargin increased *Wfs1* protein expression. However, the *Wfs1* protein level in MIN6 cells did not change with tunicamycin. This is probably due to *Wfs1* being an N-glycosylated protein, and inhibition of glycosylation by tunicamycin decreases its stability (6, 16). Increased *Wfs1* expression in association with ER stress was further demonstrated in another β -cell model with ER stress: *Ins2*^{96Y/Y} cells derived from the Akita mouse. The Akita mouse spontaneously develops early-onset non-obese diabetes with a reduced β -cell mass, which is caused by a conformation-altering missense mutation

(Cys96Tyr) in the insulin-2 gene (12, 13). Intramolecular disulfide-bond formation is disrupted in the mutant insulin molecule. It was reported that this misfolded mutant insulin expression constitutively induced ER stress in Akita mouse β -cells (14). We have indeed confirmed increased Bip protein expression in *Ins2*^{96Y/Y} cells as compared with wild type *Ins2*^{WT/WT} cells derived from normal littermates. In *Ins2*^{96Y/Y} cells, *Wfs1* mRNA (data not shown) and protein levels (Fig. 6) were both increased. The increased *Wfs1* mRNA (two-fold, data not shown) was consistent with the increased *Wfs1* promoter activity (Fig. 7). Our results provide further evidence, i.e. a detailed analysis, that *Wfs1* expression increases in association with ER stress, especially in the pancreatic β -cells selectively lost in patients with Wolfram syndrome. It is noteworthy that the increase in *Wfs1* protein was marked (sixfold) as compared with the modest increase in Bip expression (two-fold) in *Ins2*^{96Y/Y} cells. Mechanisms other than ER stress might have further increased *Wfs1* protein expression in this cell line.

The increase in *Wfs1* expression is attributable, at least in part, to enhanced *Wfs1* transcription, because both ER stress-inducing chemical insults (MIN6 cells) and intrinsic ER stress (*Ins2*^{96Y/Y} cells) stimulated *WFS1* promoter activity as demonstrated by a transient transfection assay using a human *WFS1* promoter-luciferase reporter construct. A cis-acting ER stress responsive element (ERSE) has been identified in the proximal promoter regions of chaperone-encoding genes. This element consists of a consensus sequence of

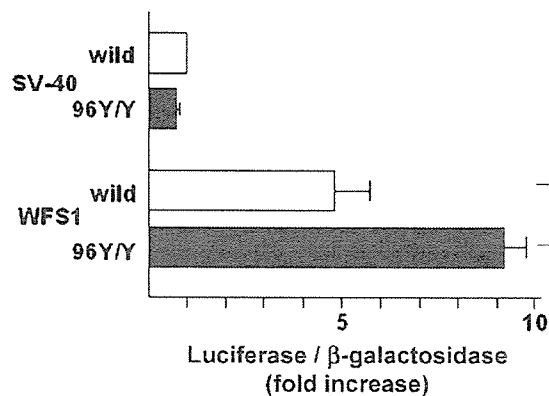


Figure 7 *WFS1* promoter activity is enhanced in *Ins2*^{96Y/Y} cells. *Ins2*^{96Y/Y} cells or wild type (wild) control cells were transfected with a luciferase reporter plasmid containing the 3.0 kb human *WFS1* gene 5' flanking promoter region (from -3000 to +20), or a control plasmid containing the SV40 promoter-luciferase reporter. The expression vector pCMV β was co-transfected, and β -galactosidase activity was used to calibrate for transfection efficiency. Results are expressed as fold-increases relative to luciferase/ β -galactosidase activities in *Ins2*^{96Y/Y} cells as compared with control *Ins2*^{WT/WT} cells in four independent experiments (means \pm S.E.), each performed in triplicate. *WFS1* promoter activity was significantly increased in *Ins2*^{96Y/Y} cells as compared with control *Ins2*^{WT/WT} cells (* P = 0.014, Student's *t*-tests).

CCAAT-N9-CCACG (30). The general transcriptional factor, NF-Y/CBF, binds to the CCAAT motif of the ERSE (31). Once ER stress ensues, p50ATF6 (active form of transcriptional factor ATF6) binds to the CCACG motif of the ERSE (31, 32) resulting in transcriptional induction of ER chaperones. Another ERSE (ERSE-II) with a consensus sequence of ATTGG-N-CCACG has also been identified (32). Although there are six CCAAT motifs in the -2800 to -2300 region of the putative human *WFS1* promoter, we found no ERSE consensus sequences within 3 kb upstream from the transcription initiation site. Further studies will be required to elucidate the mechanism of transcriptional regulation of the *Wfs1* gene via ER stress.

The observations made in this study suggest that *Wfs1* protein may be involved in the ER stress response pathway, i.e. the unfolded protein response, in which cells respond by inducing chaperones, attenuating protein translation, and inducing apoptosis. Pancreatic β -cells suffer under chronic ER stress, striving to meet the increasing demands of insulin biosynthesis and secretion. In patients with Wolfram syndrome (26) and in *Wfs1* knock-out mice (15), β -cells were selectively lost from pancreatic islets. Moreover, islets from *Wfs1*^{-/-} mice were highly susceptible to ER stress (thapsigargin and tunicamycin)-induced apoptosis (15). It is tempting to speculate that *Wfs1* protein is upregulated in response to ER stress and that it plays a physiological role in protecting cells from ER stress-induced apoptosis. Loss of function mutations of the *Wfs1* gene may cause β -cell loss due to disruption of this protective function. It was recently reported that *Wfs1* protein expressed in oocytes exhibited a cation-selective ion channel activity (7). Expression of *Wfs1* protein in oocytes increased cytosolic Ca²⁺ levels (7), and islets from *Wfs1*^{-/-} mice exhibited attenuated glucose-stimulated intracellular Ca²⁺ responses (15). *Wfs1* protein may be involved in the maintenance of ER and intracellular Ca²⁺ homeostasis, and its expression is induced under conditions of perturbed homeostasis, including ER stress.

The current findings that *Wfs1* protein, which is predominantly expressed in pancreatic islet β -cells, is transcriptionally upregulated by ER stress indicate a link between *Wfs1* protein function and ER stress responses. Further investigations utilizing *Wfs1*^{-/-} mice and *Wfs1*^{-/-} β -cells will provide insights into *Wfs1* protein function and the pathophysiology of Wolfram syndrome.

Acknowledgements

We thank Professor Junichi Miyazaki, Osaka University, Japan, for providing us with MIN6 cells. This study was supported in part by Grants-in-Aid for Scientific Research (14370338 and 16390096 to Y Tanizawa)

from the Ministry of Education, Culture, Sports, Science and Technology of Japan, grant no.15591228 (to J Kawano) from the Japan Society for Promotion of Science, and a grant from Takeda Science Foundation.

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Received 24 January 2005

Accepted 7 April 2005

β_2 - and β_3 -Adrenergic Receptor Polymorphisms Are Related to the Onset of Weight Gain and Blood Pressure Elevation Over 5 Years

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Background—The genes responsible for obesity are candidate genes for obesity-related diseases, such as hypertension. Functional polymorphisms in the β_2 - and β_3 -adrenergic receptors have been reported to be associated with hypertension and obesity.

Methods and Results—To longitudinally clarify the relevance to alterations in β -adrenergic receptor polymorphisms related to weight gain, blood pressure (BP) elevation, and sympathetic nerve activity as measured by plasma norepinephrine level, we studied 160 young, nonobese, normotensive men. Changes in body weight, BP, plasma norepinephrine levels, and β_2 -adrenergic (Arg16Gly, Gln27Glu) and β_3 -adrenergic (Trp64Arg) receptor polymorphisms were measured periodically over a 5-year period. Weight gain and BP elevation were defined as $\geq 10\%$ increases from entry levels over 5 years in body mass index or mean BP. The presence of the Gly16 allele of Arg16Gly was associated with a higher frequency of weight gain and BP elevation over the 5-year period. The subjects carrying the Glu27 allele of Gln27Glu and the Trp64 allele of Trp64Arg had a higher frequency of BP elevation. Significantly higher levels of plasma norepinephrine at entry and at year 5 were observed in the subjects with the Gly16 allele of Arg16Gly and the Glu27 allele of Gln27Glu compared with those without the Gly16 or the Glu27 alleles.

Conclusions—These results demonstrate that the Gly16 allele is related to greater weight gain and BP elevation. Additionally, Glu27 and Trp64 alleles are linked to BP elevation. The subjects carrying the β_2 -polymorphisms linked to weight gain and BP elevation also have higher plasma norepinephrine levels that are present at entry before weight gain and BP elevation. These findings suggest that β_2 -adrenergic receptor polymorphisms in association with a heightened sympathetic nerve activity could predict the future onset of obesity and hypertension, as shown in the 5-year longitudinal study. (*Circulation*. 2005;111:3429-3434.)

Key Words: hypertension ■ norepinephrine ■ obesity

Obesity and obesity-related cardiovascular disease are a rapidly growing public health problem,¹ and there is evidence that human obesity and hypertension have strong genetic as well as environmental determinants.²⁻⁴ Reduced energy expenditure and resting metabolic rate are predictive of weight gain, and the sympathetic nervous system participates in regulating energy balance through thermogenesis. The thermogenic effects in obesity have been mainly attributed to the activity of the β_1 - and β_2 -adrenergic receptors in humans. However, reports of an association of β_2 -adrenergic receptor polymorphisms with hypertension and obesity have been discordant.⁵⁻⁷ Several observations have shown that the Trp64Arg polymorphism of the β_3 -adrenergic receptor gene can also be associated with obesity⁸⁻¹⁰; however, this finding has not been confirmed in other studies.^{11,12} Few studies have

simultaneously taken into account obesity and hypertension as related to polymorphisms of β -adrenoceptor genes in the same study population followed longitudinally for several years. Additionally, plasma norepinephrine levels, as an index of sympathetic nerve activity (SNA), are also included in the present study.

Thus, this study examines the associations of polymorphisms of β -adrenergic receptors with plasma norepinephrine level (index of SNA), weight gain (obesity), and blood pressure (BP) elevation (hypertension) over 5 years in 160 subjects who at entry were young, nonobese, and normotensive.

Methods

Subjects

Subjects were recruited from a cohort of 1121 men who work in a single company in Osaka, Japan, as part of their annual medical

Received November 5, 2004; revision received February 23, 2005; accepted March 4, 2005.

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Circulation is available at <http://www.circulationaha.org>

DOI: 10.1161/CIRCULATIONAHA.104.519652

TABLE 1. Polymorphism Genotypic Frequencies in Subjects With Significant Weight Gain ($\geq 10\%$) and Mean BP Elevation ($\geq 10\%$) Over 5 Years

	Genotypes			χ^2 Test for 3 Genotypes	χ^2 Test for Alleles
Arg16Gly of β_2 -adrenoceptor gene	Arg16/Arg16	Arg16/Gly16	Gly16/Gly16		
Frequency					
With weight gain (n=59)	9 (15.3)	33 (55.9)	17 (28.8)	$\chi^2=7.98, P=0.019$	$\chi^2=6.31, P=0.012$
Without weight gain (n=101)	36 (35.6)	46 (45.5)	19 (18.8)		
With BP elevation (n=41)	4 (9.8)	20 (48.8)	17 (41.4)	$\chi^2=15.43, P<0.001$	$\chi^2=14.42, P<0.001$
Without BP elevation (n=119)	41 (34.5)	59 (49.6)	19 (16.0)		
Gln27Glu of β_2 -adrenoceptor gene	Gln27/Gln27	Gln27/Glu27	Glu27/Glu27		
Frequency					
With weight gain (n=59)	50 (84.7)	9 (15.3)	0 (0.0)	...	$\chi^2=2.89, P=0.089$
Without weight gain (n=92)	87 (94.6)	5 (5.4)	0 (0.0)	...	
With BP elevation (n=41)	32 (78.0)	9 (22.0)	0 (0.0)	...	$\chi^2=8.36, P=0.004$
Without BP elevation (n=110)	105 (95.5)	5 (4.5)	0 (0.0)		
Trp64Arg of β_3 -adrenoceptor gene	Trp64/Trp64	Trp64/Arg64	Arg64/Arg64		
Frequency					
With weight gain (n=59)	46 (78.0)	11 (18.6)	2 (3.4)	$\chi^2=7.41, P=0.025$	$\chi^2=2.39, P=0.122$
Without weight gain (n=99)	60 (60.6)	38 (38.4)	1 (1.0)		
With BP elevation (n=41)	35 (85.4)	5 (12.2)	1 (2.4)	$\chi^2=9.16, P=0.010$	$\chi^2=5.25, P=0.022$
Without BP elevation (n=117)	71 (60.7)	44 (37.6)	2 (1.7)		

Values in parentheses are percentage of subjects.

evaluation. Subjects at study entry were excluded who were aged >50 years, had obesity (body mass index [BMI] ≥ 25 kg/m²),^{13,14} had diabetes mellitus (fasting glucose level >100 mg/dL), and had hypertension ($\geq 140/90$ mm Hg). We also excluded subjects who were taking medication for hypertension, hyperlipidemia, hyperuricemia, or other illness. Only subjects who had steady body weight (weight had not changed significantly [$<5\%$] over the past year before the entry period) were enrolled in this study.^{15,16} After exclusion, 160 young, nonobese (BMI <25 kg/m²), normotensive ($<140/90$ mm Hg) men on no medications were enrolled in the present study. Informed consent was obtained from each subject, as approved by the Ethics Committee of Osaka University Graduate School of Medicine, Osaka, Japan.

Measurements

After an overnight fast of >12 hours, BMI, total body fat mass, ratio of waist circumference to hip circumference (waist-to-hip ratio), BP, heart rate, venous sampling for plasma norepinephrine, and extraction of genomic DNA from leukocytes were taken every year for 5 years. BP and heart rate were measured with the subject in the recumbent position with an automated sphygmomanometer (TM-2713, A&D) with an adjusted cuff size, which had been standardized against a mercury sphygmomanometer. The percent body fat mass was determined with impedance measurements (BF-102, Tanita), and total body fat mass (kg) was calculated according to the following formula: (percent body fat mass/100) \times body weight (kg).

Laboratory Determinations

Plasma norepinephrine was measured by high-performance liquid chromatography with a fluorometric method as previously described for this laboratory¹⁷ (intra-assay coefficient of variation=2.1%; interassay coefficient of variation=3.6%; sensitivity=0.06 to 120 nmol/L).

Genotyping

Genotyping was performed by the TaqMan assay as previously described.¹⁸ Two polymorphisms in the β_2 -adrenergic receptors (arginine/glycine substitution, Arg16Gly; glutamine/glutamate substitution, Gln27Glu) of the β_2 -adrenoceptor gene were studied.⁶ One

polymorphism (tryptophan/arginine substitution, Trp64Arg) of the β_3 -adrenoceptor gene was also studied.^{19,20} The probes and primers used in the TaqMan assay were as follows. For single-nucleotide polymorphisms in the β_2 -adrenergic receptor gene, the probes and primers were as follows: for Arg16Gly, the probes were CGCATG-GCTTCCATTGGGTGC and CGCATGGCTTCTATTGGGTGC, and the primers were GGAACGGCAGCGCCTTCT and CAGGAC-GATGAGAGACATGACGAT; for Gln27Glu, the probes were CTCGTCCCTTTCCTGCGTGACGT and CTCGTCCCTTTGCT-GCGTGACGT (the primers used in this assay were the same as those used for Arg16Gly). For the Trp64Arg single-nucleotide polymorphism in the β_3 -adrenergic receptors, the probes were TCTCGGAGTCCAGGCGATGGCCA and CTCGGAGTC-CGGGCGATGGCC, and the primers were GGAGGCAACCTGCT-GGTCAT and CACGAACACGTTGGTTCATGGT.

Statistical Analysis

Genotype frequencies and the Hardy-Weinberg equilibrium were estimated with χ^2 test. Values are shown as mean \pm SD. All data analyses were performed with SPSS 8.0 for Windows programs. Changes in measured parameters within each group and differences among groups were examined by 2-way ANOVA. When these differences were significant, the Dunnett test was used to determine whether the differences of the mean measured variables at entry and 5 years were significant within the groups and among the groups compared from baseline. Values of $P<0.05$ were considered significant.

Results

Significant weight gain and BP elevation over 5 years were defined as a $\geq 10\%$ increase in BMI or mean BP compared with values at entry.^{16,21} Fifty-nine subjects had significant weight gain over 5 years, and 41 subjects had significant BP elevation. Table 1 shows the prevalence of weight gain and BP elevation at year 5. No subjects with the Glu27/Glu27 polymorphism of the β_2 -adrenoceptor were detected in the present study. The allele frequency of Glu27 of the β_2 -

TABLE 2. Characteristics of Subjects at Entry and at Year 5

	Subjects With Weight Gain		Subjects Without Weight Gain		Subjects With BP Elevation		Subjects Without BP Elevation	
	At Entry	At Year 5	At Entry	At Year 5	At Entry	At Year 5	At Entry	At Year 5
Subjects, n	59	59	101	101	41	41	119	119
Smoker/nonsmoker, n	15/44	10/49	22/79	13/88	13/28	8/33	24/95	15/104
Age, y	39±4	44±4	40±5	45±5	40±4	45±4	40±5	45±5
BMI, kg/m ²	22.2±1.8	24.6±2.0*§	22.9±1.7	22.4±1.9	22.6±1.6	24.3±2.1†§	22.7±1.7	22.8±1.9
Waist-to-hip ratio	0.92±0.11*	0.97±0.13*§	0.88±0.12	0.91±0.13	0.92±0.09†	0.94±0.11	0.89±0.11	0.92±0.12
Total fat mass, kg	14.1±2.1*	15.6±2.2*§	12.5±1.9	12.9±2.0	13.7±2.0†	15.1±2.0†§	12.8±2.0	13.4±2.2
Systolic BP, mm Hg	127±6	141±8*	128±6	131±7	132±7†	146±9‡	126±6	131±7
Diastolic BP, mm Hg	77±5*	80±5*	74±5	75±5	74±5	83±6‡	76±4	75±6
Mean BP, mm Hg	94±5	101±6*§	93±5	94±6	93±6	104±6‡	92±6	94±6
Heart rate, bpm	70±5*	72±5	66±5	71±5§	71±4†	73±5	66±5	71±6§
Plasma norepinephrine, pmol/mL	1.18±0.11*	1.41±0.21*§	1.00±0.20	1.26±0.19	1.14±0.12†	1.43±0.24†§	1.01±0.16	1.27±0.18§

Data are mean±SD; n=160.

* $P<0.05$ vs subjects without weight gain; † $P<0.05$, ‡ $P<0.01$ vs subjects without BP elevation; § $P<0.05$, || $P<0.01$ vs values at entry.

adrenoceptor polymorphism was 4.6%, and that of Arg64 of the β_3 -adrenoceptor polymorphism was 17.4%, but all studied loci allele and genotype frequencies were in accordance with the Hardy-Weinberg equilibrium. The frequency distributions for homozygosity for the Arg16 and Gly16 alleles in this study were 28.1% and 22.5%. The frequency distributions for homozygosity for the Gln27 and Glu27 were 90.7% and 0.0%, and the frequency distributions for the Trp64 and Arg64 were 67.1% and 1.9%. The frequency distributions for homozygosity for the Glu27 and the Arg64 in our subjects were similar to those in previous studies in Japanese cohorts but lower than those found in studies in white subjects.^{5,6,9,10,22,23} The frequency of Gly16 allele of the β_2 -adrenoceptor gene was greater in subjects with weight gain than in those without weight gain. Additionally, the frequency of the Gly16 allele of the β_2 -adrenergic receptor gene was significantly greater in subjects who showed a significant BP elevation over 5 years. The frequencies of the Glu27 and Trp64 alleles were higher in subjects with BP elevation than in those without BP elevation (Table 1).

Furthermore, to evaluate the relationships between the β -adrenoceptor alleles and weight gain-related BP elevation, we compared the frequencies of alleles between the groups with and without BP elevation in subjects who significantly gained body weight versus those without weight gain. In subjects who had a significant weight gain, those who also had a significant BP elevation carried a higher frequency of the Gly16 and Glu27 alleles compared with those without a significant BP elevation ($\chi^2=4.73$, $P=0.030$; $\chi^2=6.35$, $P=0.012$, respectively). In subjects who did not gain weight over the 5-year period, the allele frequencies in the 3 genotypes that were studied were similar in subjects with and without a BP elevation over time.

Table 2 shows the demographic characteristics of the 2 groups subdivided by significant weight gain ($\geq 10\%$) over 5 years or BP elevation at entry and at year 5. At both periods, waist-to-hip ratio, total fat mass, heart rate, and plasma norepinephrine were higher in the group who had significant weight gain and in the group who had a significant rise in

mean BP compared with those without weight gain or BP elevation. It is important to note that at entry, BMI and BP were similar between the groups with and without weight gain and BP elevation. Among the 41 subjects with a significant BP elevation, 32 of these individuals also had a significant weight gain.

Subjects were divided into the 2 subgroups in each studied genotype according to the dominant allele. Characteristics between those with and without the dominant allele are shown in Tables 3, 4, and 5. Total body fat mass and waist-to-hip ratio at entry in the subjects carrying the Gly16 allele and Glu allele of the β_2 -adrenoceptor gene were greater than in the other genotypes (Tables 3 and 4). BMI and total body fat mass increased significantly in the subjects with the Gly16 allele and Glu27 allele of the β_2 -adrenoceptor genes. Subjects who had the Gly16 and Glu27 of the β_2 -adrenoceptor gene and the Trp64 of the β_3 -adrenoceptor gene had significant increments in mean BP over the 5 years (Tables 3, 4, and 5).

As we have previously reported,^{15,16,21} subjects with the most significant weight gain and BP elevation had the highest levels of plasma norepinephrine at entry compared with subjects without weight gain or BP elevation (Table 2). Plasma norepinephrine levels at both entry and year 5 were greater in subjects carrying Gly16 allele and Glu27 allele of the β_2 -adrenoceptor genes than in the other genotypes (Tables 3 and 4). Plasma norepinephrine levels increased significantly over the 5-year period in those subjects with the abnormal β -adrenoceptor alleles. The same subjects also had higher plasma norepinephrine levels at entry.

Discussion

The present study shows that the Arg16Gly and the Gln27Glu of the β_2 -adrenoceptor and the Trp64Arg of the β_3 -adrenoceptor polymorphisms have a substantial influence on future gain in body weight or BP elevation in male subjects who were originally nonobese and normotensive. The subjects carrying the polymorphism for the Gly16, Glu27, and Trp64 alleles show higher frequency in those who had a

TABLE 3. Characteristics of Subjects According to Genotype of Arg16Gly at Entry and at 5 Years

	Without Gly16 Allele (Arg16Arg)		With Gly16 Allele (Arg16Gly+Gly16Gly)	
	At Entry	At Year 5	At Entry	At Year 5
Subjects, n	45	45	115	115
Smoker/nonsmoker, n (%)	10/35 (22.2/77.8)	7/38 (15.6/84.4)	27/88 (23.5/76.5)	16/99 (13.9/86.1)
BMI, kg/m ²	22.6±1.9	22.4±2.8	22.7±1.8	23.5±2.1*‡
Waist-to-hip ratio	0.87±0.10	0.88±0.11	0.91±0.10‡	0.95±0.12*‡
Total fat mass, kg	12.8±2.0	13.2±1.9	13.4±1.9‡	14.1±2.0*‡
Systolic BP, mm Hg	128±5	129±6	127±5	137±7†§
Diastolic BP, mm Hg	73±7	75±5	76±6	79±5‡
Mean BP, mm Hg	92±6	93±5	94±6	98±7*‡
Heart rate, bpm	65±6	69±5	69±6	72±6
Norepinephrine, pmol/mL	0.99±0.16	1.10±0.22	1.09±0.14‡	1.40±0.10†§

Data are mean±SD; n=160.

**P*<0.05, †*P*<0.01 vs value at entry; ‡*P*<0.05, §*P*<0.01 vs subjects without Gly16 allele (Arg16Arg genotype).

significant weight gain or BP elevation over the 5-year study. Higher levels of plasma norepinephrine at entry were also seen in the groups with the Gly16 or Glu27 alleles. As we have shown in all studies, a heightened SNA (high mean plasma norepinephrine) predicted subsequent weight gain and BP elevation.^{15,16,21} Now we show that the increased SNA is in part determined by the genetic influence of the β_2 -adrenergic receptor systems.

Pathophysiological involvement of genetic abnormalities in the β_2 -adrenergic receptor system in hypertension and obesity are well described.^{5,6,24–26} Among β_2 -adrenergic receptor polymorphisms, Arg16Gly and Gln27Glu are considered the most functionally important.^{5,6,24–26} Gratz et al²⁷ found that young normotensive white men homozygous for the Gly16 allele of the β_2 -adrenoceptor gene had higher BP and lower peripheral vasodilation after infusion of the β -blocker salbutamol. The Gly16 substitution exaggerates agonist-mediated receptor downregulation.^{6,28} Our findings that the Gly16 allele is associated with weight gain and BP elevation associated with higher plasma norepinephrine lev-

els are in accordance with these findings. The subjects who had weight gain-related BP elevation also had higher frequencies of the Gly16 and Glu27 alleles compared with those without BP elevation, suggesting that Gly16/Glu27 is related to obesity-related hypertension. On the other hand, the frequency associations of the Arg16 or Gly16 alleles of the Arg16Gly and the Gln27 or Glu27 alleles of the Gln27Glu with the onset of hypertension and obesity are more controversial.⁶ The Glu27 receptor had been shown to be resistant to downregulation compared with Gln27 but when coexpressed with Arg16.²⁹ We were not able to observe any significant association of the Arg16 and Glu27 alleles with weight gain or BP elevation, probably because of the small sample size of the study.

The β_3 -adrenergic receptor system is important in mediating the stimulation of lipolysis by catecholamines in white adipose cells in humans and in the development of obesity.^{8–10} It is well documented that weight gain leads to BP elevation,^{1,15,16} but there are few investigations about the genetic relations in the β_3 -adrenoceptor such as polymor-

TABLE 4. Characteristics of Subjects According to Genotype of Gln27Glu at Entry and at 5 Years

	Without Glu27 Allele (Gln27Gln)		With Glu27 Allele (Gln27Glu)	
	At Entry	At Year 5	At Entry	At Year 5
Subjects, n	137	137	14	14
Smoker/nonsmoker, n (%)	34/103 (24.8/75.2)	22/115 (16.1/83.9)	3/11 (21.4/78.6)	1/13 (7.1/92.9)
BMI, kg/m ²	22.6±1.7	23.0±2.5	23.5±2.1	24.6±3.0*‡
Waist-to-hip ratio	0.89±0.10	0.92±0.11	0.92±0.11	0.99±0.10*‡
Total fat mass, kg	13.0±1.9	13.4±2.0	13.9±1.3‡	14.9±2.3*§
Systolic BP, mm Hg	127±5	135±5*	132±5	138±6*
Diastolic BP, mm Hg	75±5	76±6	77±6	83±5*§
Mean BP, mm Hg	93±5	94±5	95±5	101±6*§
Heart rate, bpm	67±5	71±6	69±5	70±6
Norepinephrine, pmol/mL	1.03±0.20	1.30±0.18*	1.29±0.14‡	1.42±0.19*‡

Data are mean±SD; n=151.

**P*<0.05, †*P*<0.01 vs value at entry; ‡*P*<0.05, §*P*<0.01 vs subjects without Glu allele (Gln27Gln genotype).

TABLE 5. Characteristics of Subjects According to Genotype of Trp64Arg at Entry and at 5 Years

Genotype	With Trp64 Allele (Trp64Trp+Trp64Arg)		Without Trp64 Allele (Arg64Arg)	
	At Entry	At Year 5	At Entry	At Year 5
Subjects, n	155	155	3	3
Smoker/nonsmoker, n (%)	36/119 (23.2/76.8)	23/132 (14.6/85.4)	1/2 (33.3/66.7)	0/3 (0.0/100.0)
BMI, kg/m ²	23.1±1.7	23.2±2.7	22.8±0.5	24.0±0.6
Waist-to-hip ratio	0.90±0.06	0.93±0.08	0.90±0.09	0.94±0.10
Total fat mass, kg	13.2±1.8	13.9±2.0	13.1±2.0	13.5±2.0
Systolic BP, mm Hg	127±5	134±6†	126±6	128±7
Diastolic BP, mm Hg	75±5	78±5*	75±5	77±6
Mean BP, mm Hg	93±5	97±5†	92±5	94±6
Heart rate, bpm	68±5	71±6*	67±5	68±6
Norepinephrine, pmol/mL	1.06±0.20	1.31±0.14*	1.03±0.25	1.27±0.23

Data are mean±SD; n=158.

* $P<0.05$, † $P<0.01$ vs value at entry.

phisms in Trp64Arg and the association of these polymorphisms with hypertension in obesity.³⁰ Fujisawa et al²³ have shown in a Japanese population that the allele frequency of Arg64 in hypertensive subjects was similar to that in normotensive subjects. Other investigators have reported in a large Japanese cohort (n=3706) that the subjects with the Arg64/Arg64 genotype had a greater BMI and percent fat mass than those with the in Trp64/Trp64 genotype.⁹ Conversely, we did not observe these associations in the genotype of the β_3 -adrenoceptor in relation to weight gain-related BP elevation.

In the present study we used plasma norepinephrine levels as an index of SNA. Tuck,³¹ Grassi and Esler,³² and Rahn et al³³ observed that there are different results in SNA values in hypertensive patients depending on the method of SNA measurement, including regional norepinephrine spillover, muscle sympathetic nerve activity (microneurography), and plasma norepinephrine measurements. Spillover methods are considered the "gold standard" for SNA measurements, but in humans these are difficult and invasive measurements. Plasma norepinephrine levels are more practical for large population studies and represent several different processes (secretion, clearance, and reuptake).^{3,15,16}

It is known that Asian people (Japanese) have a lower definition of obesity than the World Health Organization BMI cutoff point for obesity (≥ 30 kg/m²),^{13,14} which is controlled by genotypes. In a Japanese population, a strong association between visceral fat content and the metabolic syndrome has been reported, as seen even in subjects defined as nonobese by BMI but who were obese by CT.³⁴ In the present study the subjects who had the most significant weight gain and BP elevations also had a greater total body fat mass and waist-to-hip ratio plus higher plasma norepinephrine levels at entry, but BMI was not different between these entry groups. These findings suggest that abdominal obesity might be the link to heightened SNA, which is in part determined genetically by the abnormal β -adrenoceptor polymorphism. Alvarez et al^{35,36} have reported that visceral obesity, but not subcutaneous obesity, is best associated with

increased SNA. Grassi et al³⁷ have also found that central obesity is characterized by greater sympathetic activation and impaired baroreceptor sensitivity than peripherally obese or lean subjects.

In summary, these findings are from the first large cohort-based longitudinal study analyzing the effect of genetic variation in the β_2 - and β_3 -adrenoceptor genes over a fixed time period, showing their strong association with initiation of weight gain and BP elevation. SNA, as seen in plasma norepinephrine accompanying abdominal obesity, may be the major mediator of the β_2 -adrenoceptor gene changes.

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β_2 -Adrenoceptor Polymorphisms Relate to Insulin Resistance and Sympathetic Overactivity as Early Markers of Metabolic Disease in Nonobese, Normotensive Individuals

Kazuko Masuo, Tomohiro Katsuya, Yuxiao Fu, Hiromi Rakugi, Toshio Ogihara, and Michael L. Tuck

Background: The genes responsible for insulin resistance are also candidate genes for insulin resistance-related diseases, such as obesity and hypertension. Functional polymorphisms in the β_2 - and β_3 -adrenergic receptors have been reported to be associated with diabetes, hypertension, and obesity. To clarify the relevance of the β -adrenergic receptor polymorphisms to insulin resistance, we studied their association with polymorphisms of β_2 (Arg16Gly, Gln27Glu) and β_3 (Trp64Arg) adrenoceptor genes.

Methods: We studied 155 young, nonobese Japanese men using the homeostasis model assessment of insulin resistance (HOMA-IR) to divide individuals into insulin-sensitive and insulin-resistant groups. Insulin resistance in the participants was defined as HOMA-IR equal to or greater than the average plus 1 SD of 3.1. There were 69 men who were insulin resistant and 86 men who were insulin sensitive. Body mass index (BMI), blood pressure (BP), plasma glucose, insulin, leptin, norepinephrine (NE) levels, and the polymorphisms of Arg16Gly and Gln27Glu of the β_2 - and Trp64Arg of the β_3 -adrenoceptor polymorphisms were measured in all participants.

Results: The insulin-resistant group had higher frequency of the Gly16 allele of Arg16Gly compared with

the insulin-sensitive group, whereas the frequencies of genotypes or alleles of Gln27Glu and Trp64Arg were similar. The insulin-resistant group had a higher mean HOMA-IR, fasting insulin, NE, and total fat mass compared with levels in the insulin-sensitive group, but the BMI and leptin levels were similar. The subjects carrying the Gly16 allele of the β_2 -adrenoceptor gene had a higher mean HOMA-IR, fasting insulin, NE, body fat mass, and BP than those without the Gly16 allele.

Conclusions: The Gly16 mutation of the β_2 -adrenoceptor gene is associated with increased insulin resistance, adiposity, and BP accompanied by higher plasma NE levels early in the metabolic disease in developing obesity. These findings show an important role of β_2 -adrenoceptor gene polymorphisms in the association of insulin resistance in hypertension and obesity. Am J Hypertens 2005;18:1009–1014 © 2005 American Journal of Hypertension, Ltd.

Key Words: Insulin resistance, sympathetic nerve activity, β_2 - and β_3 -adrenoceptor polymorphisms, blood pressure, and obesity.

Obesity and hypertension are associated with metabolic disturbances such as insulin resistance, hyperinsulinemia, and dyslipidemia.^{1,2} One pathophysiologic significance of early insulin resistance is that insulin has mitogenic properties that can potentiate vascular smooth-muscle growth, promoting structural changes in blood vessels and possibly con-

tributing to atherosclerosis. Thus, insulin resistance may be an important etiologic factor in the cardiovascular risk seen in the development of obesity and hypertension.^{1–3}

One major risk is that human obesity and hypertension have well defined genetic determinants such polymorphisms in the β_2 - and β_3 -adrenergic receptor.^{4–12} We have

Received November 21, 2004. First decision December 29, 2004. Accepted January 12, 2005.

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reported that insulin resistance and hyperinsulinemia are associated with heightened sympathetic nerve activity¹³ and that heightened sympathetic nerve activity, as seen in elevated plasma NE, predicts insulin resistance, subsequent weight gain, and BP elevation.^{14–16} In addition, normotensive and normal-weight individuals who have a positive family history of hypertension and obesity also have heightened sympathetic nerve activity.^{17,18} These findings imply that sympathetic overactivity defined here as high plasma NE levels are associated with genetic determinants on the β -adrenergic receptor that may contribute to insulin resistance. The present study further examines the relationship between polymorphisms of the β -adrenergic receptors and progression in reduced insulin sensitivity in nonobese, normotensive Japanese men.

Methods

Subjects

A cohort of 1121 men working in Osaka, Japan, as part of their biannual medical evaluation were studied. Subjects were excluded who were >50 years of age, overweight (body mass index [BMI] 25 to 30 kg/m²) or obese (BMI >30 kg/m²), had diabetes mellitus (fasting glucose level >100 mg/dL), or hypertension (\geq 160/95 mm Hg). Additional exclusions were subjects who were taking medications for hypertension, hyperlipidemia, hyperuricemia, or other illness. After exclusion, 155 young men who were nonobese (BMI <25 kg/m²) and nonhypertensive (BP <160/95 mm Hg) and who were not using any medications were recruited from the cohort. The subjects were subdivided into an insulin-sensitive group and an insulin-resistant group using the homeostasis model assessment of insulin resistance (HOMA-IR) and a cut-off limit of average + 1 SD (2.2 + 0.9) in participants. Because it is well known that recent alterations in plasma insulin, leptin, and NE levels are altered with weight changes, only those subjects who had steady body weight (weight had not changed significantly (<5%) over the past year) were enrolled in the present study.^{15,16,19}

The protocol was approved by the Ethics Committee of Osaka University Graduate School of Medicine, Japan, and written informed consent was obtained from all of the subjects.

Measurements

After an overnight fast of 12 h, BMI, total body fat mass, BP, heart rate, and venous sampling for blood glucose, plasma norepinephrine (NE), insulin, leptin, and the extraction of genomic DNA from leukocytes were obtained after a 30-min rest period in the supine position. Lipids profiles (total cholesterol, triglyceride, HDL-cholesterol) and uric acid levels were also evaluated. Both BP and heart rate were measured three times in the supine position by an automated sphygmomanometer (TM-2713, A&D Co. Ltd., Tokyo, Japan), which had been standardized against a mercury sphyg-

momanometer. The percentage body fat mass was determined with impedance measurements (BF-102, Tanita, Japan), and total body fat mass (kg) was calculated according to the following formula: [percentage body fat mass (%)/100] \times body weight (kg). Plasma NE was measured by high-performance liquid chromatography with a fluorometric method (intra-assay coefficient of variation [CV] = 2.1%; inter-assay CV = 3.6%; sensitivity = 0.06 to 120 nmol/L). Plasma immunoreactive insulin was measured by standard radioimmunoassay methods (insulin RIABEAD II, Dinabott; intra-assay CV = 1.9%; inter-assay CV = 2.2%; sensitivity = 0.75 to 300 μ U/mL). Plasma leptin was measured by radioimmunoassay (human leptin RIA kit, Linco; intra-assay CV = 5.0%, interassay CV = 4.5%, and sensitivity = 0.03 to 6 nmol/L). The HOMA-IR was defined as the product of fasting plasma insulin (μ U/mL) and glucose (mg/dL) divided by 405.²⁰

Genotyping

Genotyping was performed by the TaqMan assay, as previously described.²¹ Two polymorphisms (arginine/glycine substitution, Arg16Gly, and glutamine/glutamate substitution, Gln27Glu) of the β_2 -adrenoceptors⁶ and one polymorphism (tryptophan/arginine substitution, Trp64Arg) of the β_3 -adrenergic receptor^{11,12} were evaluated. For single-nucleotide polymorphisms of the β_2 -adrenergic receptor gene, the probes and primers were as follows: for Arg16Gly, the probes were CGCATGGCTTCCATTGGGTGC and CGCATGGCTTCTATTGGGTGC, and the primers were GGAACGGCAGCGCCTTCT and CAGGACGATGAGAGACATGACGAT; for Gln27Glu, the probes were CTCGTCCCTTTCCTGCGTGACGT and CTCGTCCCTTTGCTGCGTGACGT, and the primers used in this assay were the same as those used for Arg16Gly. For the Trp64Arg single-nucleotide polymorphism in the β_3 -adrenergic receptors, the probes were TCTCGGAGTCCAGGCGATGGCCA and CTCGGAGTCCGGGCGATGGCC, and the primers were GGAGGCAACCTGCTGGTCAT and CACGAACACGTTGGTCATGGT.

Statistical Analyses

Genotype frequencies and Hardy-Weinberg equilibrium were estimated with χ^2 test. Values are shown as mean \pm SD. Differences among groups were examined by the paired or unpaired *t* test. Multiple regression linear analyses were applied to evaluate the relationship between HOMA-IR as a dependent variable and plasma NE, BMI, total body fat mass, and mean BP (systolic and diastolic BP) as independent variables. Values of *P* < .05 were considered significant.

Results

Prevalence of Insulin Resistance

A total of 69 subjects were insulin resistant and 86 subjects were insulin sensitive as defined by the HOMA-IR. The

insulin-resistant group had a significantly lower frequency of the Arg16/Arg16 genotype ($\chi^2 = 12.38$, $P = .002$) and a higher frequency of the Gly16 allele ($\chi^2 = 5.53$, $P = .019$) in analysis of the β_2 -adrenoceptor gene compared with results in the insulin-sensitive group (Fig. 1). Frequencies of each genotype and allele of Gln27Glu and those of Trp64Arg were similar between the insulin-sensitive and insulin-resistant groups.

Profiles of Insulin-Resistant Subjects

The insulin-resistant group had higher HOMA-IR, fasting plasma insulin, NE, total body fat mass, uric acid, total cholesterol, triglyceride, and lower HDL-cholesterol levels, whereas BMI, BP levels, and leptin levels were similar in both groups (Table 1).

Profiles of the Subjects Carrying the Gly16 Allele of the β_2 -Adrenoceptor

Insulin resistant subjects had a higher frequency of the Gly16 allele of the β_2 -adrenoceptor gene, suggesting the Gly16 allele is related to insulin resistance. Thus, we compared the subjects with and without the Gly16 allele of the β_2 -adrenoceptor gene regardless of the status of insulin sensitivity. The HOMA-IR, fasting plasma insulin, NE, total body fat mass, serum uric acid levels, and systolic, diastolic, and mean BP levels were higher in the subjects with the Gly16 allele (the Arg16/Gly16 + Gly16/Gly16 genotype) compared with values in subjects without the Gly16 allele (the Arg16/Arg16 genotype) of the β_2 -adrenoceptor gene (Table 2). When those subjects were subdivided by insulin sensitivity, only the insulin-resistant group with higher fasting plasma insulin ($P < .05$) and NE ($P < .05$) levels were found in the group with the Gly16 allele (Fig. 2).

Multiple Regression Linear Analyses

When HOMA-IR was used as a dependent variable, plasma NE ($P = .012$), total body fat mass ($P = .016$), and systolic ($P = .034$) and mean BP ($P = .007$) levels were significant determinant variables ($R^2 = 0.379$, $F = 19.96$, $P < .001$) in multiple regression linear analysis.

Discussion

To clarify the relationship of β -adrenoceptors polymorphisms, insulin resistance, and plasma NE levels as an index of the sympathetic nervous system activity, we studied profiles of hormones and relations of polymorphisms of β -adrenoceptor genes over time in healthy individuals. We found that the insulin-resistant subjects had higher frequencies of the Gly16 allele of the β_2 -adrenoceptors, and that the subjects who carried the Gly16 allele had higher levels of fasting insulin (HOMA-IR), plasma NE, and uric acid. In addition, total body fat mass and BP levels were higher in the subjects with the Gly16 allele in nonobese, nonhypertensive men. These findings suggest 1)

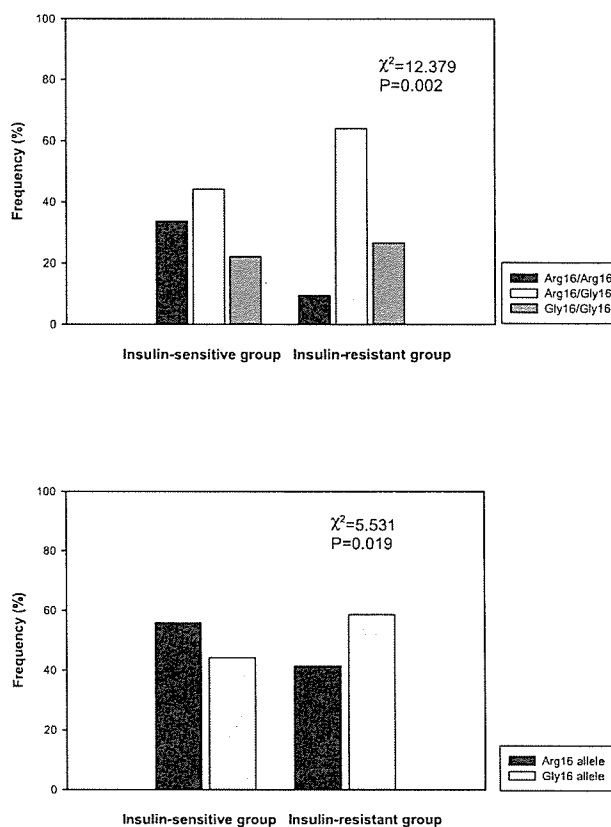


FIG. 1. Frequencies of the genotypes (upper panel) and the allele (lower panel) at Arg16Gly of the β_2 -adrenoceptor gene.

that insulin resistance could in part be determined by the genetic variant of the β_2 -adrenoceptor gene, and 2) that the β_2 -adrenoceptor polymorphism accompanying higher plasma NE levels could increase insulin resistance, adiposity (obesity), and BP elevation.

In the present study, we used plasma NE levels as an index of sympathetic nerve activity. Tuck,²² Grassi and Esler,²³ and Rahn et al²⁴ reported different results in sympathetic nervous system activity in hypertensive patients according to NE measurement methods, muscle sympathetic nerve activity using microneurography methods, plasma NE measurements, and regional spillover method.²⁵ Many investigators recommend the regional spillover method as a gold standard for sympathetic nerve activity, but these are difficult and invasive measurements. Plasma NE levels are much more practical for large populations and represent the result of several different processes such as secretion, clearance, and reuptake, especially in large population studies such as cross-sectional design studies^{13,17} and in repeated measurements in longitudinal studies.¹⁴⁻¹⁶

β -Adrenoceptor Polymorphisms Versus Insulin Resistance

Significant evidence has been provided for a strong physiologic relationship between the β_2 -adrenoceptor and β_3 -adre-

Table 1. Comparisons of values between insulin-sensitive subjects and insulin-resistant subjects

Characteristic	Insulin-Sensitive Subjects	Insulin-Resistant Subjects
Number	86	69
Age (y)	37.0 \pm 6.9	36.8 \pm 7.8
Body mass index (kg/m ²)	21.6 \pm 2.8	22.8 \pm 2.8
Total body fat mass (kg)	14.4 \pm 4.1	16.1 \pm 3.9*
Waist-to-hip circumference ratio	0.90 \pm 0.11	0.92 \pm 0.13
Systolic blood pressure (mm Hg)	127 \pm 12	129 \pm 11
Diastolic blood pressure (mm Hg)	78 \pm 11	79 \pm 12
Mean blood pressure (mm Hg)	94 \pm 10	96 \pm 12
Heart rates (beats/min)	64 \pm 3	65 \pm 4
HOMA-IR	1.7 \pm 0.9	4.2 \pm 0.5†
Plasma insulin (μ U/mL)	8.1 \pm 2.7	17.1 \pm 2.9†
Plasma norepinephrine (pmol/mL)	1.26 \pm 0.29	1.74 \pm 0.38*
Plasma leptin (ng/mL)	3.9 \pm 2.0	4.1 \pm 2.1
Blood glucose (mg/dL)	90.7 \pm 5.8	93.5 \pm 6.0
Total cholesterol (mg/dL)	200 \pm 27	216 \pm 22*
Triglyceride (mg/dL)	117 \pm 35	173 \pm 48‡
HDL-cholesterol (mg/dL)	58 \pm 13	50 \pm 12*
Uric acid (mg/dL)	5.3 \pm 1.4	5.8 \pm 1.2*

HOMA-IR = homeostasis model of insulin resistance.

* $P < .05$, † $P < .001$, ‡ $P < .01$ versus values in the insulin-sensitive subjects.

noceptor as seen in obesity,^{6-9,11,26,27} hypertension,^{6,10} and insulin resistance.^{11,12} Among β_2 - and β_3 -adrenoceptor polymorphisms, amino acid substitutions, Arg16Gly and Gln27Glu of the β_2 -adrenoceptor polymorphism, and Trp64Arg of the β_3 -adrenoceptor polymorphism are also considered functionally important in understanding the genetic relationship among obesity, hypertension, and insulin resistance.

Gratze et al²⁸ found that young, normotensive, white male subjects homozygous for the Gly16 allele of the

β_2 -adrenoceptor gene had higher BP and lower peripheral vasodilation in response to the infusion of the β -blocker salbutamol. The β_2 -adrenoceptor is also expressed in pancreatic β -cells to modulate insulin secretion. Irakashi et al²⁹ suggested that the Arg16Gly variant of the β_2 -adrenoceptor gene has an influence on insulin secretion. In the present study, the subjects with the Gly16 allele of the β_2 -adrenoceptor gene had higher plasma insulin and NE levels, suggesting that the Gly16 allele of the β_2 -adrenoceptor gene is closely linked to insulin-resistant status

Table 2. Comparisons of values between subjects with and without Gly16 allele of the β_2 - adrenoceptor gene

Characteristic	Subjects Without Gly16 Allele Arg16/Arg16	Subjects With Gly16 Allele (Arg16/Gly16 + Gly16/Gly16)
Number	45	110
Age (y)	36.2 \pm 6.9	37.2 \pm 6.5
Body mass index (kg/m ²)	21.6 \pm 2.1	22.4 \pm 2.5
Total body fat mass (kg)	14.6 \pm 3.7	15.5 \pm 3.9*
Waist to hip circumference ratio	0.90 \pm 0.11	0.91 \pm 0.13
Systolic blood pressure (mm Hg)	124 \pm 12	129 \pm 14*
Diastolic blood pressure (mm Hg)	76 \pm 11	80 \pm 12*
Mean blood pressure (mm Hg)	92 \pm 12	96 \pm 8*
Heart rates (beats/min)	63 \pm 4	65 \pm 3
HOMA-IR	2.5 \pm 0.7	3.0 \pm 0.5*
Plasma insulin (μ U/mL)	10.2 \pm 3.7	12.9 \pm 2.2*
Plasma norepinephrine (pmol/mL)	1.28 \pm 0.29	1.57 \pm 0.38*
Plasma leptin (ng/mL)	3.8 \pm 2.0	4.1 \pm 2.1
Blood glucose (mg/dL)	91.0 \pm 5.8	92.3 \pm 6.0
Total cholesterol (mg/dL)	201 \pm 30	210 \pm 27
Triglyceride (mg/dL)	127 \pm 43	148 \pm 50
HDL-cholesterol (mg/dL)	57 \pm 12	53 \pm 13
Uric acid (mg/dL)	5.0 \pm 1.4	5.7 \pm 1.2*

Abbreviation as in Table 1.

* $P < .05$ versus values in the insulin-sensitive subjects.

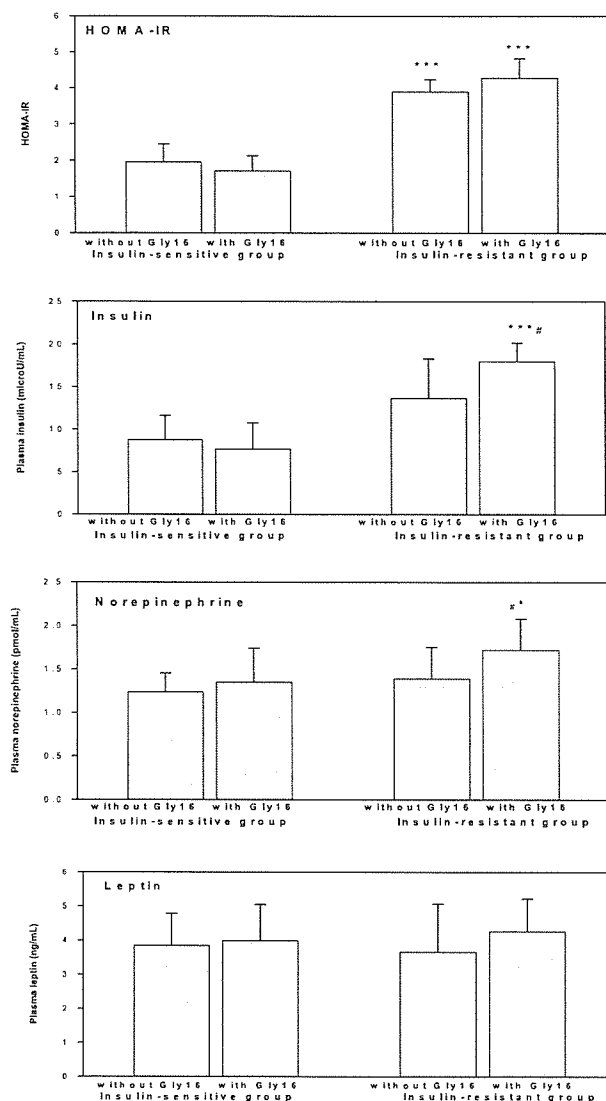


FIG. 2. The homeostasis model assessment of insulin resistance (HOMA-IR) (**top panel**), fasting plasma insulin levels (**second panel from top panel**), supine plasma norepinephrine levels (**second panel from bottom panel**), and plasma leptin levels (**bottom panel**) in the insulin-sensitive group and the insulin-resistant group according to the Gly16 allele of the β_2 -adrenoceptor gene. * $P < .05$, *** $P < .001$ versus values in the insulin-sensitive subjects. # $P < .05$ versus values in the subjects without Gly16 allele (carrying Arg16/Arg16 genotype) of the β_2 -adrenoceptor gene.

associated with heightened sympathetic nerve activity shown as higher plasma NE levels and BP elevation. Thus, the Gly16 allele could lead to heightened sympathetic nerve activity, insulin resistance, and higher BP and adiposity and could predict these developments in nonobese, nonhypertensive individuals.

The Glu27/Glu27 genotype of the β_2 -adrenoceptor gene has a well established association with obesity.⁷ Subjects with Glu27 homozygotes have excess body fat and increased fat cell size compared with Gln homozygotes in a white population and also have abdominal obesity and insulin resistance.²⁶ We did not observe the

association of the polymorphism at Gln27Glu of the β_2 -adrenoceptor gene with insulin resistance, perhaps because of the very low frequency of the Glu27 allele. In a healthy Japanese population, distribution of the Glu27 allele of the β_2 -adrenoceptor gene is different from that in individuals of non-Asian white ethnicity, as previously reported,³⁰ and the frequency of the Glu27 allele of the β_2 -adrenoceptor gene is much lower.

Insulin Resistance Versus Sympathetic Overactivity

The group with the Gly16 allele of the β_2 -adrenoceptor gene had a higher total body fat mass and BP levels, and our results in multiple regression analyses showed close relationships between HOMA-IR, plasma NE, total body fat mass, and mean BP. These findings demonstrate that the Gly16 allele that accompanies insulin resistance and heightened sympathetic nerve activity is associated with relatively greater adiposity and BP elevation. In addition, we have previously shown that insulin resistance is strongly related to heightened sympathetic nerve activity, BP elevation, and increased adiposity.^{13-15,19} The present study was examined in a cross-sectional design. Hence, we could not discern the relations between genotype, BP elevation, and weight gain; however, we have reported in longitudinal studies that higher levels of plasma NE as a phenotype marker of sympathetic nerve activity predicts subsequent BP elevation and weight gain.¹⁴⁻¹⁶ Taken together, our findings suggest the proposal that the adrenergic receptor defects lead to sympathetic nervous system overactivity that might play a role in the development of insulin resistance, hypertension, and obesity. In conclusion, a polymorphism at Arg16Gly of the β_2 -adrenoceptor gene could be linked to insulin resistance and sympathetic nerve overactivity, as in this population of nonobese, nonhypertensive Japanese men.

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Rebound Weight Gain as Associated With High Plasma Norepinephrine Levels That Are Mediated Through Polymorphisms in the β 2-Adrenoceptor

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Background: A successful weight loss program is essential treatment for obesity-related diseases, but it is well known that the majority of individuals do not succeed in weight loss maintenance. The present study evaluates hormonal mechanisms and the relationship of β 2-adrenoceptor polymorphisms involved in individuals who regain weight after initially successful weight loss.

Methods: Overweight Japanese men ($n = 154$) were enrolled in a 24-month weight loss program. Body mass index (BMI), total body fat mass, plasma norepinephrine (NE) and leptin levels, and β 2-adrenoceptor polymorphisms (Arg16Gly, Gln27Glu) were measured every 6 months for the 24-month period. Maintenance of weight loss was defined as significant weight loss ($\geq 10\%$ reduction) from entry weight at 6 months and maintenance of the weight loss for an additional 18 months. Rebound weight gain was defined as significant weight loss at 6 months but subsequent regain of body weight during the next 18 months.

Results: The results showed that 37 subjects maintained weight loss during 24 months, whereas 36 subjects had rebound weight gain. The BMI at entry and calorie intake and physical activity at each period were similar

between the two groups. Subjects who maintained weight loss had at entry a significantly lower fat mass and plasma NE levels compared to those with rebound weight gain. Body fat mass, NE, and leptin levels at entry predicted the degree of change in body weight during the 24-month study period. Subjects with rebound weight gain had a significantly higher frequency of the Gly16 allele for the β 2-adrenoceptor polymorphism compared to subjects who had a 24-month maintenance of weight loss. Subjects carrying the Gly16 allele also had significantly higher plasma NE, leptin, and body fat mass levels and a greater waist-to-hip ratio both at entry and throughout the study.

Conclusions: A high initial degree of body fat mass and high plasma NE levels as determined by the Gly16 allele for the β 2-adrenoceptor polymorphisms predict those individuals who will have rebound weight gain after their initial successful weight loss. Am J Hypertens 2005;18:1508–1516 © 2005 American Journal of Hypertension, Ltd.

Key Words: Rebound weight gain, weight loss resistance, sympathetic nerve activity, leptin, obesity, β 2-adrenoceptor polymorphisms.

Weight loss and maintenance of weight loss are the most effective nonpharmacologic treatments for correction of cardiovascular and metabolic risk factors in obese patients.^{1–7} However, few obese people succeed in sustained weight loss, and long-term results of weight loss programs are disappointing with a substantial

proportion of people regaining most of the weight initially lost.

There is strong evidence suggesting that human obesity has both genetic and environmental determinants.^{8,9} Investigations have reported associations of polymorphisms of the β 2- and β 3-adrenoceptors in obesity,^{10–15} and regulation of thermogenesis is mainly attributed to β 2- and β 3-adrenergic receptor activity. Increased energy expenditure and increased resting metabolic rate are predictive

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Received April 5, 2005. First decision May 4, 2005. Accepted May 12, 2005.

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0895-7061/05/\$30.00

doi:10.1016/j.amjhyper.2005.05.006

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Published by Elsevier Inc.

of weight loss, and the sympathetic nervous system plays a key role in regulating energy balance through stimulation of thermogenesis. Effects on rates of thermogenesis are also influenced by genetic factors. Few studies have taken into account success in maintenance of weight loss, resistance to weight loss, and rebound weight gain as part of hormonal changes associated with changes in body weight or the polymorphisms of the β -adrenoceptor genes that occur with weight change. We examined weight loss in relation to changes in body fat mass, plasma norepinephrine (NE), leptin, and insulin. In addition, we compared polymorphisms of β 2- and β 3-adrenoceptor genes in subjects who maintained weight loss during 24 months to those who regain body weight (rebound weight) in a protocol of a defined, constant dietary intake and exercise program.

Methods

Subjects

The weight loss program enrolled 154 overweight ($25 \text{ kg/m}^2 \leq \text{body mass index [BMI]} < 30 \text{ kg/m}^2$) men, consisting of 89 overweight normotensive men (blood pressure [BP] $< 140/90 \text{ mm Hg}$) and 65 overweight, untreated mildly hypertensive men ($140/90 \text{ mm Hg} \leq \text{BP} < 160/95 \text{ mm Hg}$). None of the subjects had diabetes (fasting blood glucose level $> 100 \text{ mg/dL}$) or other illness including psychological or emotional problems.¹⁶ No subject was taking antihypertensive agents or other medications. Furthermore, no subject had any symptoms of obstructive sleep apnea (ie, breathing pauses every night or almost every night) or extremely loud habitual snoring or sleepiness during the daytime.^{17,18} Only subjects whose body weight had not changed for at least the past 2 years (weight change $< 5\%$) provided in their biannual medical evaluation records were enrolled in the present study.^{4,19} The subjects enrolled in this weight loss program were emotionally stable,¹⁶ and had a similar socioeconomic status. The protocol was approved by the Ethics Committee of Osaka University Graduate School of Medicine, Japan, and written informed consent was obtained from all the subjects.

Study Design

The weight loss program consisted of a low caloric diet (1600 kcal/d, 55% of calories from carbohydrate, 30% from protein, and 15% from fat) and a low sodium diet (7g NaCl per day) and aerobic exercise of more than 1 h daily (eg, walking, jogging, or gym exercise). The subjects attended a 1-h private teaching and counseling session each week for 4 weeks, followed by biweekly 1-h sessions for 23 additional months. All sessions were led by experts in nutrition and exercise counseling. Calorie intake was calculated based on the subjects meal diary, which was assisted by nutritionists. The physical activity was quantified and recorded by the use of step-counters used on a

daily basis. Diet and exercise compliance were monitored according to the subjects' own records every 2 weeks and were recorded at private counseling sessions. Compliance to diet and exercise was considered excellent and consistent based on those records.

Methods

After an overnight fast of 12 h and 30 min rest in the supine position, height, body weight, BMI, percentage total body fat mass, BP, heart rate, and venous blood sampling for measurements of blood glucose, plasma NE, leptin, insulin, and the extraction of genomic DNA from leukocytes were obtained. Samples were taken at entry and at 6, 12, and 24 months during the study. The BP and heart rate were measured more than three times in the supine position by an automated sphygmomanometer (TM-2713, A&D, Tokyo, Japan) using an adjusted cuff size based on arm circumference. Recorded BP levels and heart rates were averaged. The percentage body fat mass was determined by impedance measurements (BF-102, Tanita, Tokyo, Japan). Total body fat mass (in kilograms) was calculated according to the following formula: [percentage body fat mass (%) / 100] \times body weight (kg). Plasma NE was measured after separation by high-performance liquid chromatography using the fluorometric method as previously described in detail,¹⁹ and plasma immunoreactive insulin was measured by a standard radioimmunoassay method as described in detail (insulin RIABEAD II, Dintabott, Tokyo, Japan).¹⁹ Plasma leptin was measured by radioimmunoassay¹⁹ (human leptin RIA kit, Linco, St. Charles, MO, USA). The homeostasis model assessment of insulin resistance (HOMA-IR) was defined as the product of fasting plasma insulin (in microunits per milliliter) and glucose (in milligrams per deciliter) divided by 405.²⁰

Genotyping

Genotyping was performed by the TaqMan assay, as previously detailed (Applied Biosystems, Foster City, CA, USA).²¹ Two polymorphisms (Arg16Gly, Gln27Glu) of the β 2-adrenoceptors^{13,14} and one polymorphism (Trp64Arg) of the β 3-adrenoceptor²² were evaluated. For single-nucleotide polymorphisms (SNPs) in the β 2-adrenoceptor genes, the probes and primers were as follows: for Arg16Gly, the probes were CGCATGGCTTCCATTGGGTGC and CGCATGGCTTCTATTGGGTGC, and the primers were GGAACGGCAGCGCCTTCT and CAGGACGATGAGAGACATGACGAT; and for Gln27Glu, the probes were CTCGTCCCTTTTCCTGCGTGACGT and CTCGTCCCTTTGCTGCGTGACGT (the primers used in this assay were the same as those used for Arg16Gly). For the Trp64Arg SNP in the β 3-adrenoceptor, the probes were TCTCGGAGTCCAGGCGATGCCA and CTCGGAGTCCGGGCGATGGCC, and the primers were GGAGGCAACCTGCTGGTCAT and CACGAACACGTTGGTCATGGT.

Table 1. Characteristics in the four study groups according to responses to weight loss

	Weight Loss Maintenance	Rebound	Slow Weight Loss	Weight Loss Resistance
Subjects (n)	37	36	60	21
Age at entry (yr)	35 ± 6	37 ± 6	37 ± 6	37 ± 8
Height (m)	1.73 ± 0.05	1.74 ± 0.04	1.74 ± 0.05	1.72 ± 0.05
BMI (kg/m ²)				
Entry	27.1 ± 1.9	27.7 ± 1.6	27.3 ± 1.7	27.4 ± 2.0
6 months	22.8 ± 1.4†**	22.8 ± 0.8†**	25.4 ± 2.0‡	26.6 ± 2.2§
12 months	22.6 ± 2.3†**	23.4 ± 2.2*#	24.9 ± 1.9	26.1 ± 2.9‡
18 months	22.4 ± 2.0†‡**	25.1 ± 2.2#	24.1 ± 2.0*#	26.0 ± 2.3 #
24 months	22.1 ± 1.5†§**	26.4 ± 2.1	23.8 ± 1.9*†**	26.1 ± 2.2 #
Total body fat mass (kg)				
Entry	21.5 ± 5.4†‡	25.6 ± 4.9*	25.9 ± 6.1	27.8 ± 4.2‡
6 months	17.8 ± 4.7†‡ #	21.0 ± 3.8*#	22.3 ± 5.2	24.3 ± 4.1‡
12 months	16.5 ± 4.1†‡ #	21.5 ± 4.1#	20.7 ± 4.9#	22.8 ± 3.8#
18 months	15.6 ± 3.8†§**	22.2 ± 4.7 #	18.7 ± 5.1*†**	21.9 ± 4.1 **
24 months	15.2 ± 4.3†§**	22.5 ± 5.0 #	17.8 ± 4.9*†**	21.2 ± 4.7 **
Waist-to-hip ratio				
Entry	1.16 ± 0.10*	1.20 ± 0.11	1.23 ± 0.15	1.23 ± 0.15
6 months	0.98 ± 0.09* #	1.03 ± 0.10* #	1.15 ± 0.14*‡	1.22 ± 0.09‡
12 months	0.95 ± 0.10*‡#	1.05 ± 0.09*#	1.05 ± 0.11*#	1.17 ± 0.13‡
18 months	0.92 ± 0.09†§**	1.15 ± 0.20	1.03 ± 0.13*‡#	1.12 ± 0.11 #
24 months	0.90 ± 0.12†§**	1.12 ± 0.14	0.98 ± 0.12*†**	1.16 ± 0.13 #
Systolic BP (mm Hg)				
Entry	136 ± 12	134 ± 10	137 ± 10	133 ± 12
6 months	135 ± 10	134 ± 9	134 ± 9	134 ± 8
12 months	133 ± 9	136 ± 7	134 ± 8	135 ± 8
18 months	128 ± 10*‡	135 ± 8	132 ± 9	134 ± 6
24 months	128 ± 9#	133 ± 8	130 ± 10#	130 ± 11
Diastolic BP (mm Hg)				
Entry	78 ± 10	77 ± 9	79 ± 9	74 ± 11
6 months	77 ± 9	76 ± 7	76 ± 8	73 ± 7
12 months	76 ± 8	77 ± 6	75 ± 8	73 ± 8
18 months	74 ± 9	77 ± 7	74 ± 9	76 ± 7
24 months	73 ± 8#	76 ± 7	72 ± 10#	72 ± 11
Mean BP (mm Hg)				
Entry	98 ± 12	96 ± 10	98 ± 9	94 ± 14
6 months	97 ± 10	96 ± 7	96 ± 9	94 ± 7
12 months	95 ± 9	97 ± 6	95 ± 8	94 ± 8
18 months	92 ± 10	96 ± 8	94 ± 9	95 ± 6
24 months	92 ± 9#	95 ± 8	91 ± 11#	93 ± 13
Heart rate (beats/min)				
Entry	68 ± 7	70 ± 8	68 ± 8	71 ± 7
6 months	66 ± 6	68 ± 7	67 ± 7	71 ± 6
12 months	65 ± 7	69 ± 7	66 ± 8	69 ± 6
18 months	64 ± 5‡	70 ± 8	66 ± 7	68 ± 7
24 months	62 ± 6‡#	68 ± 7	65 ± 7	67 ± 5
Plasma norepinephrine (pmol/mL)				
Entry	1.53 ± 0.32†‡	1.87 ± 0.37*	2.25 ± 0.31*‡	2.59 ± 0.53‡
6 months	1.31 ± 0.30†¶	1.49 ± 0.41†#	2.01 ± 0.33‡	2.22 ± 0.51§
12 months	1.17 ± 0.31†‡¶#	1.63 ± 0.44*	1.78 ± 0.35#	2.07 ± 0.47‡
18 months	1.11 ± 0.32† #	1.40 ± 0.51*#	1.54 ± 0.31**	2.02 ± 0.46‡ #
24 months	1.09 ± 0.28†‡ **	1.32 ± 0.37*#	1.41 ± 0.37**	1.87 ± 0.48‡ **
Plasma leptin (ng/mL)				
Entry	7.9 ± 2.8*	8.9 ± 2.9*	10.1 ± 3.0‡	11.7 ± 2.7‡
6 months	5.8 ± 2.5†#	6.2 ± 2.4†#	7.8 ± 2.9*	10.2 ± 3.0§
12 months	4.5 ± 1.9† #	5.8 ± 2.3*#	6.8 ± 2.7*#	8.5 ± 2.4‡
18 months	4.0 ± 1.7†‡**	6.1 ± 2.6*#	6.0 ± 2.8*#	8.2 ± 3.0‡ #
24 months	3.7 ± 1.8†‡**	6.7 ± 2.5 #	5.1 ± 1.7*†**	7.1 ± 2.9 #
HOMA-IR				
Entry	2.3 ± 0.5	2.5 ± 0.5	2.5 ± 0.6	2.7 ± 0.6
6 months	2.0 ± 0.3*	2.0 ± 0.4*#	2.3 ± 0.5	2.5 ± 0.5‡
12 months	1.7 ± 0.5	2.0 ± 0.5	2.1 ± 0.4	2.2 ± 0.6
18 months	1.7 ± 0.5*#	2.1 ± 0.6	2.0 ± 0.5#	2.2 ± 0.5
24 months	1.4 ± 0.6*† **	2.1 ± 0.5	1.8 ± 0.5**	2.2 ± 0.4#