in glimepiride-treated subjects; and 77.3±25.5 mg/day in gliclazide-treated subjects with no significant difference between the 2 groups.

Of 33 subjects who completed the study, 22 subjects were treated with sitagliptin and SUs, 6 subjects were treated with sitagliptin and SUs and MET, and 3 subjects were treated with sitagliptin and SUs and TZD; changes in HbA1c in 52 weeks were −4 mmol/mol (95% CI; −6 to −2 mmol/mol) ($p<0.05$), −6 mmol/mol (95% CI; −10 to −2 mmol/mol) ($p<0.05$), and −3 mmol/mol (95% CI; −0.5 to −0 mmol/mol) ($p<0.05$), respectively (◉ **Table 2**). However, there was no significant difference among the 3 groups.

Change in body weight, BMI, and frequency of hypoglycemia

Body weight in final subjects at baseline was 64.2±9.5 kg, and was decreased to 63.5±8.7 kg at 52nd week. Change in body weight in 52 weeks was −0.71 kg (95% CI; −1.42 to −0.004 kg) ($p<0.05$) (◉ **Table 3**). BMI at baseline was 24.8±3.6 kg/m^2, and decreased to 24.5±3.4 kg/m^2 at 52nd week. Change in BMI in 52 weeks was −0.27 kg/m^2 (95% CI; −0.54 to 0.004 kg/m^2) ($p>0.05$). Frequency of hypoglycemia at baseline was 1.21±1.05 times/month, and was significantly decreased to 0.06±0.24 times/month at 52nd week ($p<0.001$). Change in frequency in hypoglycemia in 52 weeks was −1.21 times/months (95% CI; −1.5 to −0.80 times/month) ($p<0.05$) (◉ **Table 3**). During the study, no severe hypoglycemia was noted. During the study, no other adverse events were observed after replacement of basal insulin with sitagliptin.

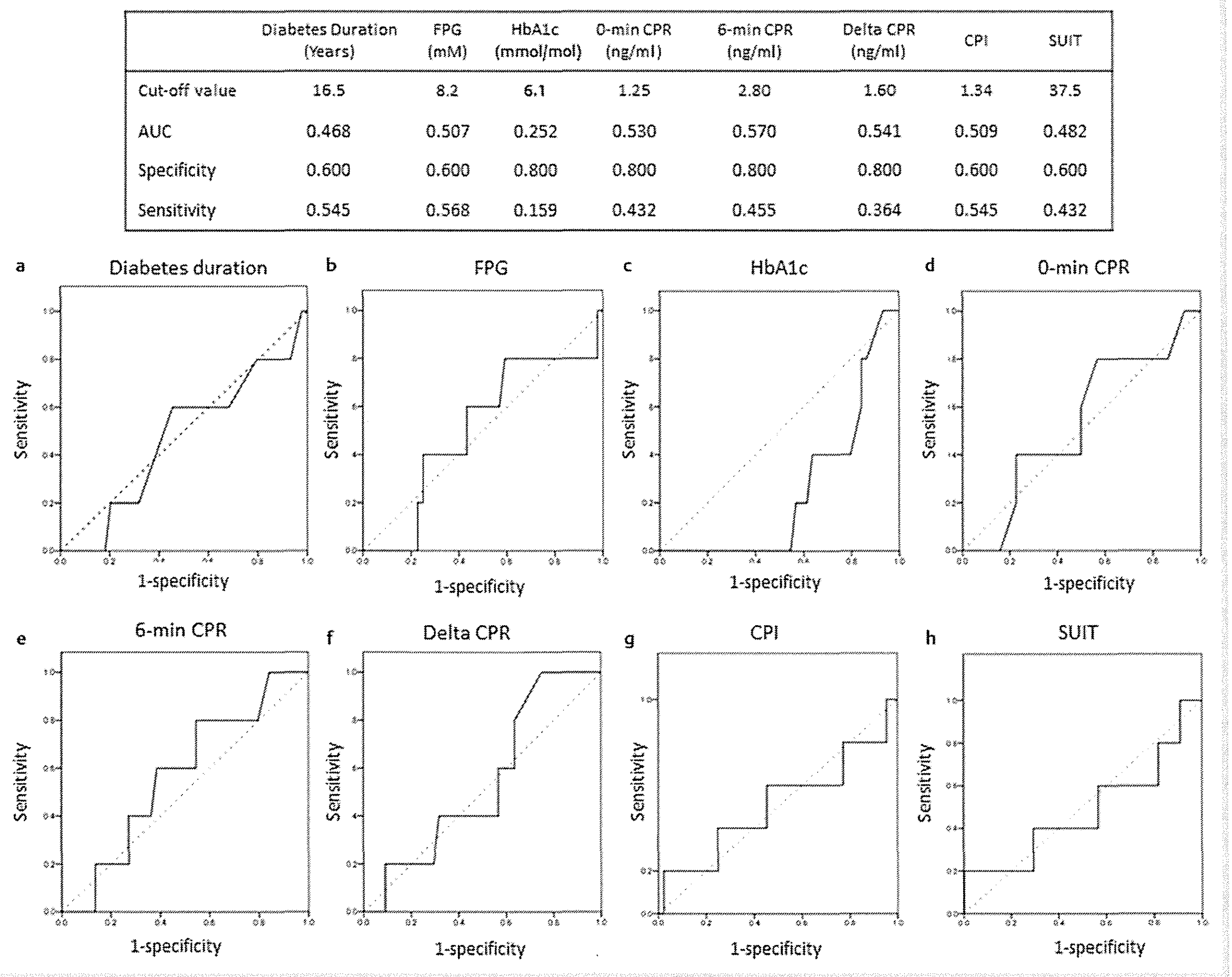
Differences in HbA1c findings in 8-week in the final and dropped subjects

Sixteen of 49 subjects recruited dropped out after 8 weeks due to increased HbA1c level. The remaining 33 subjects completed the study. HbA1c level at baseline (0-week) in final subjects was 61±8 mmol/mol, and was significantly decreased to

Table 3 Changes in weight, BMI, and frequency in hypoglycemia.

	Weight (kg)	BMI (kg/m^2)	Hypoglycemia (times/month)
0-week	64.2±9.5	24.8±3.6	1.21±1.05
52nd week	63.5±8.7	24.5±3.4	0.06±0.24***
Change	−0.71*	−0.27	−1.21*
(95% CI)	(−1.42 to −0.004)	(−0.54 to 0.004)	(−1.5 to −0.80)

*p<0.05, ***p<0.001



	Diabetes Duration (Years)	FPG (mM)	HbA1c (mmol/mol)	0-min CPR (ng/ml)	6-min CPR (ng/ml)	Delta CPR (ng/ml)	CPI	SUIT
Cut-off value	16.5	8.2	6.1	1.25	2.80	1.60	1.34	37.5
AUC	0.468	0.507	0.252	0.530	0.570	0.541	0.509	0.482
Specificity	0.600	0.600	0.800	0.800	0.800	0.800	0.600	0.600
Sensitivity	0.545	0.568	0.159	0.432	0.455	0.364	0.545	0.432

Fig. 1 Cutoff values and receiver-operator characteristic curves of **a** diabetes duration, **b** fasting plasma glucose, **c** HbA1c, **d** 0-min CPR, **e** 6-min CPR, **f** delta CPR, **g** CPI, and **h** SUIT at baseline. CPR: C-peptide reaction; CPI: C-peptide index; SUIT: the secretory unit of islet in transplantation.

Table 4 Changes in HbA1c and background of final and dropped subjects.

	Final subjects	Dropped subjects		Final subjects	Dropped subjects
	33	16		33	16
0 Wk HbA1c (mmol/mol)	61 ± 7	69 ± 10	**Original dosage of SUs (mg)**	Glimepiride 1.58 ± 0.93 Gliclazide 36.2 ± 10.2	Glimepiride 2.70 ± 2.05 Gliclazide 38.2 ± 14.1
8 Wk HbA1c (mmol/mol)	58 ± 7***	73 ± 10**	**Basal insulin (Units)**	14.8 ± 9.3	15.2 ± 6.4
Delta HbA1c (mmol/mol) (95 % CI)	−4* (−5 to −2)	7* (0.3 to 11)	**FPG (mM)**	7.4 ± 1.5	8.9 ± 2.9*
Age (years)	69.8 ± 10.7	70.5 ± 9.3	**HbA1c (mmol/mol)**	61 ± 7	69 ± 10**
Male (%)	66.7	56.3	**Glucagon test** 0-min CPR (ng/ml)	1.95 ± 1.25	1.37 ± 0.64*
Diabetes duration (years)	12.1 ± 6.6	18.7 ± 9.5*	6-min CPR (ng/ml)	3.81 ± 2.13	2.42 ± 1.21*
Weight (kg)	64.2 ± 9.5	58.4 ± 11.5	Delta CPR (ng/ml)	1.98 ± 1.35	1.16 ± 0.69*
BMI (kg/m^2)	24.8 ± 3.6	23.4 ± 4.0	**CPI**	1.35 ± 0.68	0.92 ± 0.51*
			SUIT	42.7 ± 23.0	23.1 ± 10.6**

*$p<0.05$, **$p<0.01$, ***$p<0.001$

58±7 mmol/mol at 8th week ($p<0.001$) (◎ **Table 4**). Change in HbA1c was −4 mmol/mol (95 % CI; −5 to −2 mmol/mol) ($p<0.05$). On the other hand, HbA1c level at baseline (0-week) in dropped subjects was significantly higher than that in final subjects ($p<0.05$), and was significantly increased from 69±9 to 73±11 mmol/mol in 8 weeks ($p<0.01$). Change in HbA1c was +7 mmol/mol (95 % CI; 0.3 to 11 mmol/mol) ($p<0.05$).

Differences in clinical factors in final and dropped subjects

There were no differences in age, sex, dosage of SUs, or dosage of basal insulin in final and dropped subjects (◎ **Table 4**). Body weight and BMI also were not significantly different ($p=0.065$ and $p=0.2432$, respectively). On the other hand, diabetes duration in dropped subjects was longer than that in final subjects (12.1±6.6 vs. 18.7±9.5 years, $p<0.05$). FPG and HbA1c also were higher in dropped subjects than in final subjects (FPG; 7.4±1.5 vs. 8.9±2.9 mM, $p<0.05$) (HbA1c; 61±7 vs. 69±9 mmol/mol, $p<0.01$).

Insulin secretion capacity was significantly higher in final subjects than that in dropped subjects (◎ **Table 4**) ($p<0.05$). In final subjects, CPR level at 0-min, 6-min, and delta CPR (6-min CPR to 0-min CPR) were 1.95±1.25 ng/ml, 3.81±2.13 ng/ml, and 1.98±1.35 ng/ml, respectively. In dropped subjects, CPR level at 0-min, 6-min, and delta CPR were 1.37±0.64 ng/ml, 2.42±1.21 ng/ml, and 1.16±0.69 ng/ml, respectively. CPI and SUIT index also were significantly higher in final subjects than those in dropped subjects. CPI at baseline in final subjects was 1.35±0.68, while that in dropped subjects was 0.92±0.51 ($p<0.05$). SUIT at baseline was 42.7±23.0 in final subjects, and 23.1±10.6 in dropped subjects ($p<0.01$). We examined cutoff values of diabetes duration, FPG, HbA1c, 0-min CPR, 6-min CPR, delta-CPR, CPI, and SUIT by analyzing ROC curves; they were 16.5 years, 8.2 mM, 62 mmol/mol, 1.25 ng/ml, 2.80 ng/ml, 1.60 ng/ml, 1.34, and 37.5, respectively (◎ **Fig. 1**).This indicates that with longer diabetes duration, insulin secretion capacity becomes lower and the consequent poorer glycemic control makes switching BOT-treated patients from basal insulin to sitagliptin unsafe.

Correlation between efficacy of sitagliptin on glycemic control and insulin secretion capacity, CPI, and SUIT

We examined whether or not insulin secretion capacity, CPI, or SUIT at baseline predicted the efficacy of replacing basal insulin with sitagliptin on glycemic control (◎ **Fig. 2**). There was a correlation between change in HbA1c at 8th week and 0-min CPR ($r=-0.281$), 6-min CPR ($r=-0.326$), and delta CPR ($r=-0.290$), assessed by glucagon loading test at baseline (◎ **Fig. 2a, b, c**) ($p<0.05$). In addition, CPI ($r=-0.360$) or SUIT ($r=-0.306$) at baseline was correlated with change in HbA1c at 8th week (◎ **Fig. 2d, e**) ($p<0.05$). The value of 0-min CPR, 6-min CPR, delta CPR, CPI, and SUIT at which the HbA1c level was not increased by replacement of basal insulin by sitagliptin were calculated to be 1.64 ng/ml, 3.36 ng/ml, 1.71 ng/ml, 1.19, and 36.4, respectively, by Pearson's product-moment correlation test (◎ **Table 5**). The value of 0-min CPR, 6-min CPR, delta CPR, CPI, and SUIT at which the HbA1c level was decreased by 0.5 % in 8 weeks were calculated to be 1.86 ng/ml, 3.83 ng/ml, 1.98 ng/ml, 1.36, and 41.3, respectively. Other clinical characteristics of the patients such as disease duration and body weight were not significantly correlated with efficacy of replacing basal insulin with sitagliptin on glycemic control (data not shown).

Discussion

▼

We show here that basal insulin can be switched to sitagliptin with good effects in type 2 diabetes patients treated with BOT. With this treatment, the HbA1c level decreased from 61±7 to 57±7 mmol/mol in 52-week ($p<0.01$). The change in HbA1c in 52 weeks was −4 mmol/mol (95 % CI; −5 to −4 mmol/mol) ($p<0.05$). The efficacy of switching to sitagliptin from basal insulin was correlated with insulin secretion capacity, CPI, and SUIT; CPI being most correlated marker in the present study. The average CPI in final subjects was 1.35±0.68 ng/ml, while that of dropped subjects was 0.92±0.51 ng/ml. Pearson's product-moment correlation test revealed that HbA1c was improved by switching from basal insulin to sitagliptin if CPI was equal to or higher than 1.19 (◎ **Fig. 2d** and ◎ **Table 5**). Similarly, basal insulin could be switched to sitagliptin if SUIT was equal to or larger than 36.4 (◎ **Fig. 2e** and ◎ **Table 5**). In the dropped subjects, diabetes duration was longer, FPG and HbA1c were worse, 0-min CPR, 6-min CPR, delta-CPR, CPI, and SUIT were lower compared to those in final subjects (◎ **Table 4**). Cutoff values were 16.5 years, 8.2 mM, 62 mmol/mol, 1.25 ng/ml, 2.80 ng/ml, 1.60 ng/ml, 1.34, and 37.5, respectively (◎ **Fig. 1**). This suggests that the efficacy of switching from basal insulin to sitagliptin, when

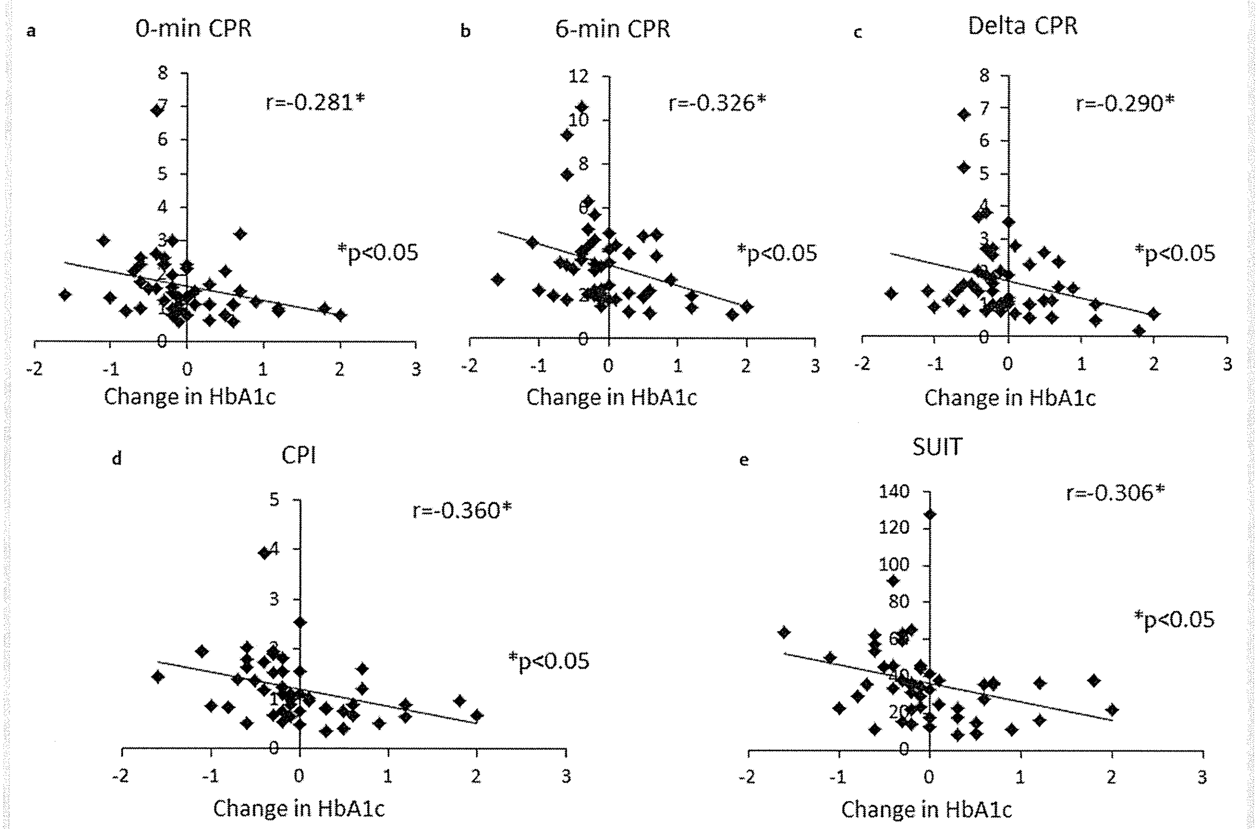


Fig. 2 Relationship between changes in HbA1c in 8 weeks and results of glucagon loading test, CPI, and SUIT at baseline. Changes in HbA1c in 8 weeks and 0-min CPR **a**, 6-min CPR **b**, delta CPR **c**, CPI **d**, and SUIT index **e** at baseline. CPR: C-peptide reaction; CPI: C-peptide index; SUIT: the secretory unit of islet in transplantation. *$p < 0.05$.

Table 5 Correlation between change in HbA1c and insulin secretion capacity.

Change in HbA1c (mmol)	0-Minute CPR (ng/ml)	6-Minute CPR (ng/ml)	Delta CPR (ng/ml)	CPI	SUIT
0.0	1.64	3.36	1.71	1.19	36.4
−5	1.86	3.83	1.98	1.36	41.3

combined with SUs, is dependent on basal glycemic control and the insulin secretion capacity. Baseline HbA1c of dropped subjects was higher than that of the final subjects. A higher dosage of basal insulin was required to reach target HbA1c level in dropped subjects compared to that in final subjects because of lower insulin secretion capacity. Thus, if baseline HbA1c level were reduced by increasing the dosage of basal insulin, it would be difficult to replace basal insulin with sitagliptin.

Replacement of basal insulin by sitagliptin resulted in a reduction in body weight and hypoglycemia. Body weight was reduced by 0.71 kg (95% CI; −1.41 to −0.004 kg) ($p < 0.05$). Frequency of hypoglycemia was decreased from 1.21±1.05 to 0.06±0.24 times/month ($p < 0.001$). Since sitagliptin is known to be body weight neutral [21,22], discontinuation of basal insulin might contribute to body weight reduction. The combination of basal insulin and SUs often induces mild hypoglycemia by which patients feel a sense of hunger and eat between-meal snacks. This sometimes induces weight gain and poor glycemic control in BOT-treated patients. On the other hand, combination therapy with sitagliptin and low dosage SUs (less than or equal to 2 mg/day glimepiride or 40 mg/day gliclazide) was body weight neutral or led to a decrease in BMI [14]. In the current study, hypoglycemia seldom occurred, and BMI was significantly decreased by 0.38 kg/m^2 (95% CI −0.72 to −0.04 kg/m^2) [14]. Switching from basal insulin to sitagliptin also reduced the frequency of hypoglycemia. Although energy intake was not evaluated between baseline and 52-week in the present study, patients who had previously experienced frequent hypoglycemia reported to their physicians that the number of between-meal snacks in 52 weeks was fewer than at baseline. Thus, excess energy intake may be reduced after switching from basal insulin to sitagliptin to account for some of the body weight reduction and improvement in HbA1c. Another reason for improvement in the HbA1c level may be the reduced postprandial glucose level by the combination therapy with sitagliptin and SUs compared to that by BOT.

The combination therapy of glimepiride and sitagliptin was more effective for HbA1c reduction than that of gliclazide and sitagliptin. Recently, it was reported that cAMP sensor Epac2 is a direct target of several sulfonylureas [23]. Tolbutamide, glibenclimide, and glimepiride bound Epac2 and enhanced glucose-stimulated insulin secretion. However, gliclazide did not bind Epac2. Because Epac2 also mediates the potentiation of insulin secretion by cAMP increased by endogenous incretin, the combination therapy of glimepiride and sitagliptin enhances more insulin secretion through activation of Epac2. This might be a potential mechanism why the combination therapy of glimepiride and sitagliptin was more effective for glycemic control than that of gliclazide and sitagliptin.

Generally, insulin secretion capacity of Japanese is as half as that of Caucasian [16–18]. Therefore, more than 60% of Japanese type 2 diabetes patients are treated with SUs [24]. DPP-4 inhibitor now is one of the most popular OADs, and more than 2 million patients were treated with DPP-4 inhibitors in Japan. Based on pathophysiology of Japanese patients and the mechanism of incretin effect, the combination therapy with SUs and DPP-4 inhibitors seems to be most effective for glycemic control compared to that with other OADs and DPP-4 inhibitors. On the other hand, the main pathophysiology of Caucasian type 2 diabetes is insulin resistance compared to that of Japanese type 2 diabetes [25,26]. Dosage of basal insulin in BOT in Caucasian patients is greater than that in Japanese patients. For example, in 4-T study, the mean dosage of basal insulin was 86 U (1.03 U/kg) [8], while 8.5 U (0.15 U/kg) in Japanese type 2 diabetes [10], and 15 U (0.24 U/kg) in our study. Therefore, it is not sure if basal insulin could be replaced with DPP-4 inhibitors even in subjects treated with high dosage of basal insulin. However, there is still a possibility that in Caucasian subjects whose BMI is less than 25 kg/m^2 and CPI is over 1.3, basal insulin could be replaced with DPP-4 inhibitors. Or, if the combination therapy with high dosage of MET and DPP-4 inhibitors is more effective for glycemic control compared to other combinations in Caucasian type 2 diabetes, basal insulin with MET could be replaced with DPP-4 inhibitors and metformin.

During the course of the disease, type 2 diabetes patients are treated with several OHAs [27,28]. However, if the HbA1c level does not reach less than 53 mmol/mol, insulin treatment is considered the next step [1,2]. BOT is often selected for outpatients because once daily injection is acceptable and the glycemic control is superior, with fewer hypoglycemic episodes and less weight gain compared to biphasic insulin [8]. In Japan, the commonly used SUs are combined with basal insulin in BOT [10]. One of the biggest problems of combination therapy with basal insulin and SUs is the high level of postprandial blood glucose while fasting blood glucose is within normal range. An increase in dosage of SUs or basal insulin does not resolve this problem, and sometimes leads to increased hypoglycemia. However, our results show that better glycemic control and lower frequency of hypoglycemia is obtained when switching from basal insulin to sitagliptin in subjects with sufficiently preserved insulin secretion capacity.

The advantages of discontinuation of basal insulin are 1) patients become free from daily injections; 2) they do not need to regularly perform self-monitoring of blood glucose (SMBG); and 3) oral therapy costs less than insulin therapy.

In summary, basal insulin in BOT can be switched to sitagliptin if CPI and/or SUIT are equal to or higher than 1.19 or 36.4, respectively. On the other hand, sitagliptin can be added to insulin therapy if insulin secretion capacity is not sufficient for switching to sitagliptin. However, the effectiveness of combination therapy with basal insulin and sitagliptin on glycemic control in type 2 patients with CPI and/or SUIT less than 1.19 or 36.4, respectively, is unknown. Further studies are required to determine the optimum insulin secretion capacities for switching BOT therapy to sitagliptin combined with SUs or combination therapy with sitagliptin and basal insulin or GLP-1 receptor analogues.

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Conflict of Interest

None of the authors have any conflicts of interest to declare.

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ORIGINAL ARTICLE

Clinical and functional characterization of the Pro1198Leu *ABCC8* gene mutation associated with permanent neonatal diabetes mellitus

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ABSTRACT

Aims/Introduction: The adenosine triphosphate (ATP)-sensitive potassium (K_{ATP}) channel is a key component of insulin secretion in pancreatic β-cells. Activating mutations in *ABCC8* encoding for the sulfonylurea receptor subunit of the K_{ATP} channel have been associated with the development of neonatal diabetes mellitus (NDM). The aim was to investigate clinical and functional characterization of the Pro1198Leu *ABCC8* gene mutation associated with permanent NDM (PNDM).

Materials and Methods: The coding regions and conserved splice sites of *KCNJ11*, *ABCC8* and *INS* were screened for mutations in a 12-year-old girl diagnosed with PNDM. The functional property of the mutant channel identified was examined with patch-clamp experiments in COS-1 cells. We also investigated the difference of effectiveness between two groups of oral sulfonylureas *in vitro* and in the patient.

Results: We identified a heterozygous missense mutation (c.3593 C>T, Pro1198Leu) in *ABCC8*. The mutated residue (P1198) is located within a putative binding site of sulfonylureas, such as tolbutamide or gliclazide. In patch-clamp experiments, the mutant channel was less ATP sensitive than the wild type. Furthermore, the sensitivity to tolbutamide was also reduced in the mutant channel. In addition to the tolbutamide/gliclazide binding site, glibenclamide is thought to also bind to another site. Glibenclamide was more effective than other sulfonylureas *in vitro* and in the patient. The treatment of the patient was finally able to be switched from insulin injection to oral glibenclamide.

Conclusions: We identified the Pro1198Leu *ABCC8* mutation in a PNDM patient, and clarified the functional and clinical characterization. The present findings provide new information for understanding PNDM. (J Diabetes Invest, doi: 10.1111/jdi.12049, 2013)

KEY WORDS: ***ABCC8*, Neonatal diabetes, Sulfonylurea receptor**

INTRODUCTION

Neonatal diabetes mellitus (NDM) is a specific form of diabetes[1]. It has been defined as diabetes with onset before 6 months-of-age and autoantibody negative for type 1 diabetes in general. NDM is classified into two categories clinically. One is transient NDM (TNDM), in which diabetes develops within the first few weeks of life and resolves by a few months of age, although it might frequently relapse in adolescence or young adulthood. The other is permanent NDM (PNDM), in which diabetes does not remit and the patients usually require insulin treatment for life. Approximately 50% of NDM is transient and 50% is permanent[2]. The majority (~70%) of cases of TNDM have abnormalities in the imprinted region of chromosome 6q24, such as paternal uniparental isodisomy, paternally inherited duplication and maternal methylation defects, leading to overexpression of paternally expressed genes[3]. The adenosine triphosphate (ATP)-sensitive potassium (K_{ATP}) channel is a key component of insulin secretion in pancreatic β-cells. The channel is comprised of two proteins, an inwardly rectifying potassium ion pore-forming subunit (Kir6.2; encoded by *KCNJ11*) and a high-affinity β-cell sulfonylurea receptor (SUR1; encoded by *ABCC8*)[4]. Activating mutations in *KCNJ11* and *ABCC8* account for 12% and 13% of cases of TNDM, respectively[5]. They also account for 31% and 10% of cases of PNDM, respectively[6]. Furthermore, 12% of PNDM is caused by mutations in the insulin (*INS*) gene itself[6]. It has also been reported that a few cases of PNDM are attributed to genetic abnormalities in other genes, such as *GCK*, *FOXP3*, *EIF2AK3*, *PDX1*, *PTF1A*, *GLIS3*, *NEUROD1* and *HNF1B*, which are important to pancreatic β-cell function and development[1].

The K_{ATP} channel plays a key role in glucose-dependent insulin secretion from pancreatic β-cells. After entry of glucose into

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the β-cells, glucose is metabolized and ATP is produced. The elevated intracellular ATP levels cause closure of K_{ATP} channels on the cell surface, which then depolarize the cell membrane leading to opening of the voltage-dependent calcium channels. The resultant influx of calcium triggers a cascade of events that result in the secretion of insulin. Overactive mutant channels as a result of activating mutations in *KCNJ11* or *ABCC8*, therefore, hyperpolarize the cell membrane, reduce calcium influx and decrease insulin secretion. Sulfonylureas bind to the SUR1 subunit of the K_{ATP} channel, and close the channel in an ATP-independent manner. It has been reported that oral sulfonylurea administration increases insulin secretion and improves metabolic control in patients with PNDM as a result of activating mutations in *KCNJ11* and *ABCC8*[7,8]. In the present study, we investigated genetic abnormalities in a patient with PNDM, and found the Pro1198Leu mutation in *ABCC8*. We examined the functional property of a mutant channel with the patch-clamp experiments, and the clinical response to oral sulfonylurea administration.

MATERIALS AND METHODS

Mutation Screening

The proband is a 12-year-old girl. She was born after 38 weeks of an uneventful pregnancy with a birthweight of 2778 g (just under the 50th percentile). At 28 weeks-of-age, she presented with severe hyperglycemia (blood glucose 915 mg/dL, glycated hemoglobin [HbA_{1c}] 12.8%) with ketoacidosis. The HbA_{1c} value was estimated as a National Glycohemoglobin Standardization Program (NGSP) equivalent value calculated by the formula $HbA_{1c} = HbA_{1c}$ (Japan Diabetes Society [JDS]) + 0.5%, considering the relational expression of HbA_{1c} (JDS) measured by the previous Japanese standard substance and measurement methods, and HbA_{1c} (NGSP)[9]. Fasting serum C-peptide level was undetectable (<0.5 ng/mL) at first, but it was recovered to 0.9 ng/mL after 2 months of treatment with insulin. NDM is defined as diabetes with onset before 6 months-of-age in general. As her HbA_{1c} at the time of diagnosis was notably high, it could be speculated that her plasma glucose had been elevated before 6 months-of-age. Her medical record of bodyweight also suggested that failure to thrive had started from 5 months-of-age. No neurological abnormality was observed, and anti-glutamic acid decarboxylase (GAD) antibody was undetectable. Abdominal ultrasound examination at the age of 12 years showed a normally-developed pancreas. She had been treated with insulin from the onset of diabetes. The pedigree of the family is shown in Figure 1.

After obtaining written informed consent, genomic DNA was isolated from peripheral blood leukocytes. The coding regions and conserved splice sites of *KCNJ11, ABCC8* and *INS* were amplified from genomic DNA by polymerase chain reaction using specific primers (Supporting Information Table S1). The products were sequenced using Dye Terminator chemistry on an ABI 3100 (Applied Biosystems, Warrington, UK). The study protocol was approved by the institutional review board.

Functional Analysis of Mutant K_{ATP} Channel

The mammalian expression plasmids containing the whole coding region of the human Kir6.2 and SUR1 have been described previously[4,10]. We generated the expression plasmid of SUR1

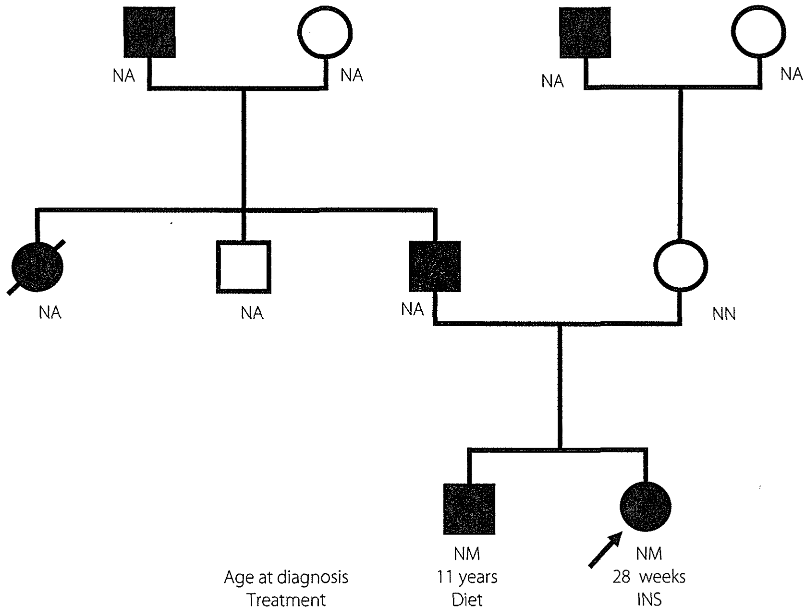

Figure 1 | Pedigree of the family. The allele status is indicated under the symbols. Directly below the genotype is the age of diagnosis of diabetes and treatment. INS, insulin; NA, not available for testing; NM, one normal and one mutated allele; NN, two normal alleles; OHA, oral hypoglycemic agent.

containing P1198L with QuickChange™ site-directed mutagenesis system (Stratagene, La Jolla, CA, USA). The presence of P1198L and the absence of other mutations were confirmed by sequencing the whole insert.

COS-1 cells were plated on 35-mm dishes containing cover slips. The cells were then transiently transfected with wild-type or mutated human SUR1 cDNA (1.5 μg per dish) plus human Kir6.2 (1.5 μg per dish) using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA). Recordings were made 24–72 h after transfection. The ATP sensitivity of the wild-type and mutant channels were determined basically as described previously[4,10] with a patch-clamp amplifier, Axopatch 200B (Axon Instruments, Foster City, CA, USA). Sulfonylurea sensitivity was assessed as the ratio between the amplitudes of the K_{ATP} channel currents before and after tolbutamide or glibenclamide application. Data were analyzed with pCLAMP (version 9.0; Axon Instruments), XLfit (CTC Laboratory System Corporation, Tokyo, Japan) and in-house software. Unpaired Student's *t*-test was used to test for statistical significances, and the results were expressed as mean ± SE.

RESULTS

Mutation Screening

We identified a heterozygous missense mutation in *ABCC8*. The mutation results in the substitution of leucine for proline at residue 1,198 in exon 29 (c.3593 C>T, p.P1198L, GenBank NM_000352). It was not found in the databases, such as dbSNP (http://www.ncbi.nlm.nih.gov/snp/) or 1,000 genome project (http://browser.1000genomes.org/index.html), and also in 150 unrelated Japanese subjects. The mutated residue is located within the short cytosolic loop that links transmembrane domains 15 and 16. The proline (P1198) is conserved across a range of species, from mammals (human and rat) to zebrafish, and is also found at a similar position in human SUR2. The *in silico* prediction programs, SIFT (http://sift.jcvi.org/) and PolyPhen-2 (http://genetics.bwh.harvard.edu/pph2/index.shtml), both predicted that the substitution would affect protein function. No mutations associated with diabetes were found in *KCNJ11* and *INS*.

Functional Analysis of Mutant K_{ATP} Channel

We tested the sensitivity of ATP to block the wild-type and the mutant K_{ATP} channels in inside-out membrane patches (Figure 2a). The concentration of ATP required to half-maximally inhibit the channel (IC_{50}) increased ≈ sevenfold from 23.4 ± 2.5 μmol/L for wild-type channels to 164.7 ± 19.3 μmol/L for mutant channels. This result shows that the mutant channel is less ATP sensitive than the wild type.

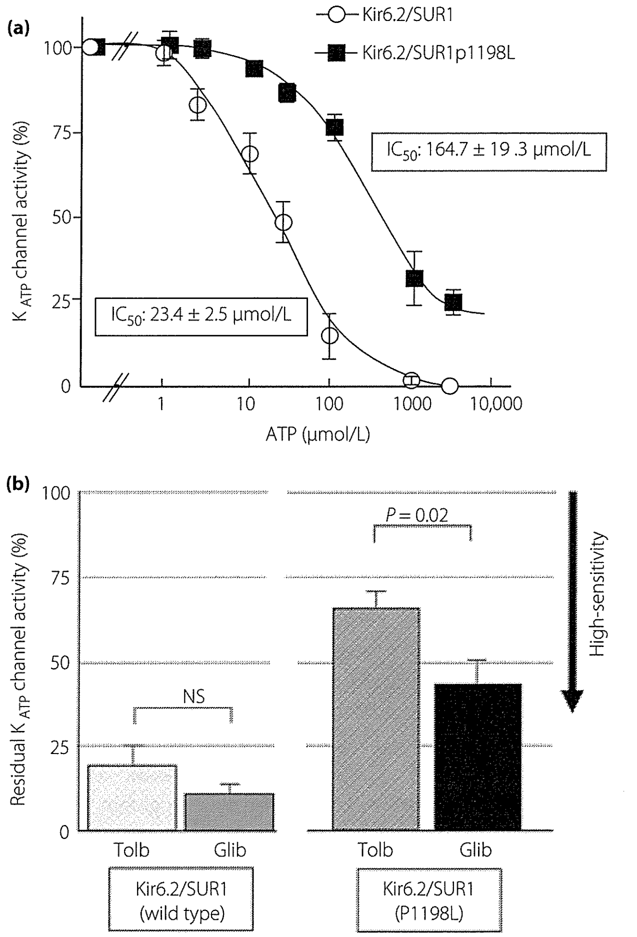

Figure 2 | (a) Adenosine triphosphate (ATP) sensitivity of wild-type and mutant ATP-sensitive potassium (K_{ATP}) channels. The dose-dependent inhibitory effects of ATP on the activities of the wild-type (Kir6.2/SUR1) and mutant (Kir6.2/SUR1P1198L) K_{ATP} channels are shown. Five experiments were carried out for each type of channel. The channel conductance of the mutant channel in a ATP-free condition was similar to that of the wild-type channel (73.1 ± 0.57 vs 72.9 ± 0.52 picosiemens (pS), $P = 0.765$). (b) Sulfonylurea sensitivity of the wild-type (Kir6.2/SUR1) or the mutant (Kir6.2/SUR1P1198L) K_{ATP} channels. Residual K_{ATP} channel activities were determined by the ratio between the amplitudes of K_{ATP} channel currents before and after 100 μmol/L tolbutamide (Tolb) or 30 nmol/L glibenclamide (Glib) applications. Data are mean ± standard error from seven independent experiments. IC_{50}, the concentration of adenosine triphosphate at which the inhibition is half of the maximal.

We next tested the response to sulfonylureas for the wild-type and the mutant K_{ATP} channels in inside-out membrane patches in nucleotide-free condition (Figure 2b). A total of 100 μmol/L tolbutamide inhibited the current by 65.6 ± 4.8% for the mutant channel, whereas 19.3 ± 5.2% for the wild type. In contrast, 30 nmol/L glibenclamide inhibited the current by 44.5 ± 6.5% for the mutant channel, whereas 10.8 ± 2.7% for the wild type. The residual current in the presence of glibenclamide for the mutant channel was significantly smaller than that of tolbutamide ($P = 0.02$). These results show that the sensitivity to sulfonylureas is reduced in the mutant channel and glibenclamide is more effective than tolbutamide.

Clinical Effectiveness of Oral Sulfonylurea Therapy

After identification of an *ABCC8* gene mutation, the patient's treatment was switched from insulin injection (40 units a day)

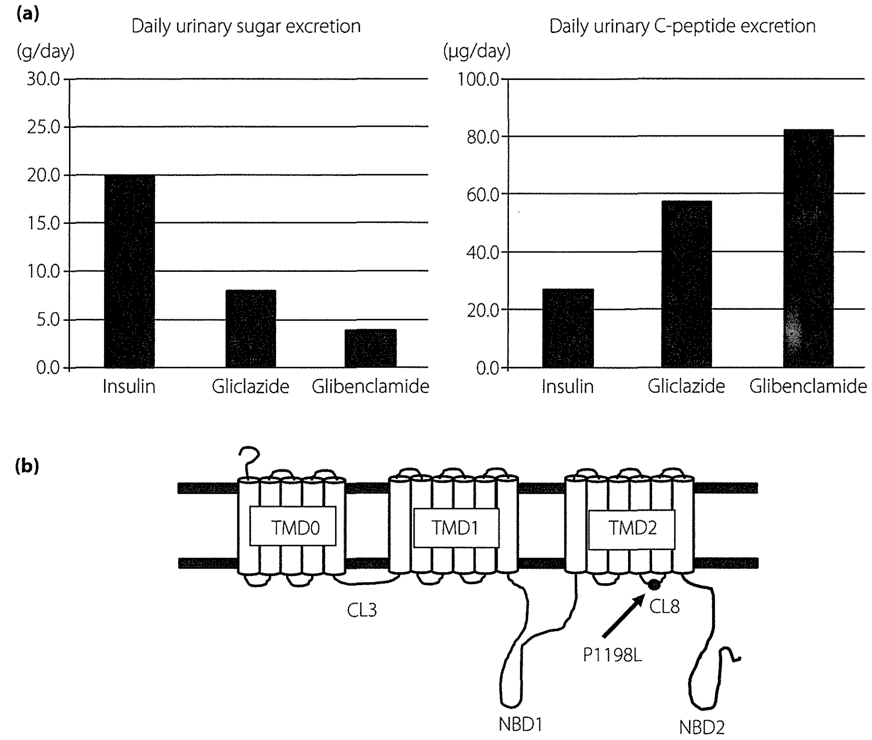

Figure 3 | (a) Daily urinary sugar excretion and daily urinary C-peptide excretion at insulin injection, high-dose gliclazide (a daily dose of 160 mg) or low-dose glibenclamide (a daily dose of 0.625 mg, which is 0.017 mg/kg/day) administration in the patient. (b) Schematic representation of the sulfonylurea receptor and the location of P1198L mutation (arrowed) identified in the patient. CL, cytosolic loop; NBD, nucleotide-binding domain; TMD, transmembrane domain.

to oral sulfonylureas under intensive monitoring in the hospital. Daily urinary C-peptide excretion, which was 27.8 μg/day before initiating sulfonylureas, increased to 58.1 μg/day at high-dose gliclazide (a daily dose of 160 mg) alone. Furthermore, daily urinary C-peptide excretion was further increased to 83 μg/day at low-dose glibenclamide (a daily dose of 0.625 mg, which is 0.017 mg/kg/day; Figure 3a). Simultaneously, daily urinary sugar excretion was decreased in inverse proportion to urinary C-peptide excretion (20.0, 8.0 and 4.0 g/day, respectively). Thus, oral glibenclamide treatment was selected for the patient's therapy and insulin injection was completely discontinued. Her blood glucose level was finally controlled with 0.17 mg/kg/day of glibenclamide.

DISCUSSION

In the present study, we identified the Pro1198Leu mutation in a patient with PNDM. The mutation was not found in the databases, such as dbSNP or 1,000 genome project, and also in 150 unrelated Japanese subjects. Furthermore, two *in silico* prediction programs, SIFT and PolyPhen-2, predicted that the mutation would affect protein function. We further confirmed that the mutant channel was less ATP sensitive than the wild type with a patch-clamp experiment. The degree of ATP insensitivity was comparable with that in a previous report for PNDM as a result of activating mutations in *ABCC8*[11]. These findings suggest that the P1198L mutation is strongly associated with the development of PNDM in the patient. Furthermore, it has only recently been reported from Turkey that the same mutation was identified in a girl with NDM[12]. In that report, the patient presented with severe hyperglycemia with ketoacidosis at 1 month-of-age and was initially treated with insulin. After genetic diagnosis, her treatment was successfully converted from insulin to glibenclamide (0.2 mg/kg/day). In addition, no neurological abnormality and no family history of diabetes were observed in the patient. These clinical characteristics were similar to the present case, except there was no family history of diabetes. In contrast, *in vitro* functional analysis of the mutation was not carried out in the report.

The mutated residue P1198 is located within the eighth cytosolic loop (CL8) that links transmembrane domains 15 and 16 in the SUR1 (Figure 3b). This loop has been reported to be a binding site of tolbutamide[13], and our functional analysis also showed that the sensitivity to tolbutamide was reduced in the mutant channel. Based on the drug structure, gliclazide is also thought to bind to the CL8. In contrast, in addition to the CL8, glibenclamide is able to bind to another site in the SUR1, which is located within the third cytosolic loop (CL3)[14]. This could explain the reason why glibenclamide was more effective both in patch-clamp experiments and in the patient.

In the family of the patient, her elder brother carried the P1198L mutation in the heterozygous state, whereas her mother did not (Figure 1). This suggests a possibility that her father might have the same mutation. The elder brother was diagnosed with diabetes at 11 years-of-age on medical examination at his school, but his diabetes was very mild and has been treated with diet alone. Furthermore, the proband's father, paternal aunt and paternal grandfather have diabetes. However, there is little information on these members, because her parents have divorced and members of her father's family did not agree to cooperate in the present study. The phenotypic variability of diabetes within families has been reported in some families with *ABCC8* gene mutations[8,15]. The precise reason for the variability is currently unknown. It might be explained by the influence of unknown other genetic and/or epigenetic factors.

Many patients with PNDM caused by *ABCC8* or *KCNJ11* gene mutations have been successfully treated with sulfonylureas[7,8]. In the present study, the treatment of our patient was also able to be switched from insulin injection to oral sulfonylurea therapy. In contrast, response to sulfonylureas has not been seen in PNDM caused by other gene mutations, such as *INS*[1]. This suggests that genetic diagnosis can provide clinical benefits to the patients with PNDM. It has been reported that genetic testing for *KCNJ11* and *ABCC8* in all children diagnosed before 6 months-of-age results not only in improved quality of life, but also in cost savings[16]. However, a large number of patients with PNDM have still been misdiagnosed as a very early onset form of type 1 diabetes and treated with insulin. The genetic diagnosis of PNDM will take on a growing importance in clinical practice.

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SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article:

Table S1 | Primer sequences for amplification of *ABCC8* gene

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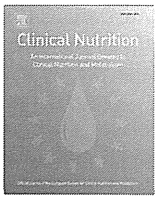

Original article

A new equation to estimate basal energy expenditure of patients with diabetes☆

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SUMMARY

Background & aims: Predictive equations for basal energy expenditure (BEE) derived from Caucasians tend to overestimate BEE in non-Caucasians. The aim of this study was to develop a more suitable method to estimate BEE in Japanese patients with diabetes using indices readily measured in clinical practice.

Methods: BEE was measured by indirect calorimetry under a strict basal condition in 68 Japanese patients with type 1 or type 2 diabetes. The best fitting equation was investigated by multiple regression analysis using of age, sex, and anthropometric indices. The resultant new equation was tested in a separate group of 60 Japanese patients with type 1 or type 2 diabetes, and the accuracy compared with existing equations.

Results: The best-fit equation was BEE [kcal/day] = 10 × (body weight)[kg] − 3 × (age)[y] + 125 (if male) + 750. Adjusted coefficient of determination was 81.0%. Root mean squared errors and accurate prediction in the validation set were 103 kcal/day and 78% for the new equation; 184 and 50 for Harris-Benedict; 209 and 38 for Oxford; 205 and 42 for Liu; and 140 and 63 for Ganpule.

Conclusions: This new equation is simpler and estimates BEE more accurately in Japanese patients with diabetes than the presently used equations do.

1. Introduction

Diet is the most fundamental and initial treatment for all patients with diabetes, and poor dietary management alone predicts poor subsequent glycemic control.[1] Estimation of daily energy expenditure for each patient is necessary for effective individualized diabetic meal planning. Resting energy expenditure (REE) or basal energy expenditure (BEE) is defined as the energy expended to maintain minimal metabolic activities, and is the main component of total daily energy expenditure. To estimate daily energy expenditure, REE or BEE is multiplied by a number specific to the various daily activities.

In healthy subjects, 65–90% of inter-individual variation in REE is explained by fat-free mass (FFM).[2] In patients with diabetes, FFM is also the main factor in REE and BEE,[3-5] and there is no difference in FFM-adjusted REE between mildly hyperglycemic patients and controls.[6] In clinical practice, BEE or FFM are not usually available. Equations factoring body weight, height, age and sex are widely used for clinical estimation of the daily energy requirement of patients with diabetes.[7] However, there has been little investigation of the comparative validity of these equations.

The existing predictive equations derived from Caucasians are unevenly applied to non-Caucasians, tending to overestimate energy expenditure.[8–11] This accords with the recent finding from the basal metabolic rate database that BEE is higher in Caucasians than in non-Caucasians.[12] However, REE is similar in Asians and Caucasians after adjustment for FFM, and BEE in Indians and

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☆ A part of this study was presented in abstract form at the annual meeting of American Diabetes Association, New Orleans, Louisiana, 5–9 June 2009.

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Australians is similar after adjustment for FFM and fat mass.[13,14] To date, there are few equations to estimate energy expenditure specifically in Asian populations.[10,15]

Differences in the measurement technique of REE can cause biases.[12] In most studies evaluating energy expenditure, REE has been used rather than BEE. However, REE is defined less rigorously than BEE and is influenced by physical and psychological stress and ambient and body temperature.[16–18] Since BEE is measured early in the morning before the subject begins any physical activity and at least 10 h after ingestion of any food, drink, or nicotine, it remains remarkably constant on a daily basis.[16,18]

In the present study, by measuring BEE under strict conditions, we developed a new equation for estimation of BEE in Japanese patients with diabetes for use in a clinical setting.

2. Patients, materials and methods

2.1. Patients

Japanese patients with type 1 or type 2 diabetes admitted to the Department of Diabetes and Clinical Nutrition, Kyoto University Hospital, Kyoto, Japan for diabetes self-management education during the period of December 2007 through September 2009 were recruited for derivation study. Written, informed consent was obtained from all participants. During hospital stay, the participants had a prescribed diet with or without medications including oral hypoglycemic agents and insulin according to the treatment guide for diabetes of the Japan Diabetes Society.[19] Their physical activity was not restricted, but they did not engage in vigorous exercise. Participants were screened by medical history, physical examination, and laboratory testing to assure the absence of hepatic, pulmonary, thyroid, cardiac and renal dysfunction, macroalbuminuria, inflammatory diseases, and malignant tumors. Those who took steroids or beta blockers or had physical disabilities were excluded. The study protocol was approved by Kyoto University Graduate School and Faculty of Medicine, Ethics Committee.

2.2. Indirect calorimetry

Basal energy expenditure (BEE) was measured in the morning under glycemic control with prescribed diet (29.1 ± 2.5 kcal/kg of standard body weight per day consisting of 52% carbohydrate, 20% protein, and 28% fat in energy component) and with medications when needed. Standard body weight (kg) was calculated by multiplying 22 (kg/m^2) by square of height (m). Whole-body oxygen consumption (VO_2) and carbon dioxide production (VCO_2) was measured for more than 10 min with indirect calorimetry (AE300S, Minato Medical Science, Osaka, Japan) by one investigator (KI) at the bedside of each patient under the strict condition described previously.[5,16,17] Briefly, an afebrile patient in a post-absorptive state after an overnight fast (14 h) with $<$180 mg/dL capillary plasma glucose remained in a supine position after waking on the bed in the ward without smoking or taking caffeine, and the measurements were performed at room temperature between 22 °C and 27 °C. After discarding the initial 5 min of recording, we took 5-min of data, in accord with the steady state definition,[17] during which the coefficient of variation for VO_2 per minute and VCO_2 per minute was achieved $\leq$10%, and applied them to the Weir formula with 24-h urinary urea nitrogen.[20]

2.3. Anthropometry and body composition

Height was measured on the day of admission. Body weight, skinfold thickness, and waist circumference were measured immediately after the measurement of BEE by one investigator (KI). Triceps-skinfold thickness (TSF) and mid-upper arm circumference (MAC) were measured in the non-dominant arm with the elbow bent at 90°. The physical markers were measured at least twice, and their respective mean values expressed according to Japanese standard method.[21] Arm muscle circumference (AMC) and arm muscle area (AMA) were calculated; AMC [cm] $=$ MAC [cm] $- \pi \times$ TSF [mm]/10, AMA [cm^2] $=$ (AMC [cm])$^2 / 4\pi$. Waist circumference was measured at the mid-point between the lowest rib and the iliac crest in a standing position at the end of gentle expiration keeping the measuring tape horizontal and just fitted to the skin. Hip circumference was measured at the widest part of the hip while standing. FFM and fat mass were measured by dual energy X-ray absorptiometry scanner (Discovery, Hologic, Bedford, MA, USA) within 3 days before and after measurement of BEE.

2.4. Other measurements

Glycated hemoglobin was measured by use of HPLC (ADAMS™ A1C HA8180, Arcray, Kyoto, Japan) and expressed as a National Glycohemoglobin Standardization Program (NGSP) equivalent value [%] calculated by the formula HbA1c [%] $=$ HbA1c [Japan Diabetes Society (JDS)] [%] $+$ 0.4 [%], which considers the relational expression of HbA1c (JDS) measured by the previous Japanese standard substance and measurement methods and HbA1c (NGSP).[22] Capillary glucose before each meal was measured by glucose meter (One Touch Ultra™, Johnson & Johnson, New Brunswick, NJ, USA) and expressed as capillary plasma glucose (PG). As a parameter of glycemic control, mean preprandial PG for three consecutive days before the measurement of BEE and fasting PG (FPG) just before the measurement of BEE are shown.

2.5. Testing the new equation

A separate data set of Japanese patients with type 1 or type 2 diabetes admitted to the same department for the same purpose during the period of June 2005 through December 2007 was drawn from the medical records for validation study. Inclusion/exclusion criteria and dietary condition during hospital stay were similar to that of the derivation sample.

Whole-body VO_2 and VCO_2 was measured after an overnight fast (14–16 h) for more than 15 min with the same calorimetry by one investigator (MI) on the same condition. Each patient was conveyed from their ward to the examination room by a healthcare staff member in a wheel chair and they rested in bed in a supine position for 30 min before the measurement of BEE. BEE was calculated from VO_2 and VCO_2 by use of Elwyn formula (BEE [kcal/day] $= 3.581 \times VO_2$ [L/day] $+ 1.448 \times VCO_2$ [L/day] $- 32.4$).[16] Body weight was measured on the day of calorimetry.

The protocol of this validation study was also approved by Kyoto University Graduate School and Faculty of Medicine, Ethics Committee.

2.6. Statistical analysis

Numerical data are summarized as means ± SDs. Categorical data were treated as dummy variables.

We first explored good estimators for FFM and fat mass in anthropometric indices, such as body weight, height, TSF, AMA, waist circumference and hip circumference, because FFM and fat mass are known as two major estimators of BEE. Correlations between these variables were evaluated by Pearson's correlation analysis. Multiple linear regression analysis was then performed to evaluate the contribution of anthropometric indices, age, and sex to FFM and fat mass. Next, a best-fit equation to estimate BEE from anthropometric indices, age, and sex was explored by multiple linear regression analysis with consideration of estimators of FFM and fat mass.

For testing the validity of our new equation and comparing it with existing prediction equations, we calculated measures of accuracy. The mean percentage difference between BEE estimated and measured (bias) was considered systematic error. The root mean squared error (RMSE) was considered to reflect each individual's error range unrelated to whether it was over or under estimation. The proportion of patients with BEE estimated within ±10% of BEE measured was considered another measure of accuracy.[23]

Data were analyzed by use of Stata 11.0 (Stata Corporation, College Station, TX, USA). Statistical significance was set at $P < 0.05$ (2-tailed).

3. Results

Data were obtained and analyzed in 68 patients, of which 7 had type 1 diabetes and 61 had type 2 diabetes. Mean glycated hemoglobin (HbA1c) on admission was as high as 10.5%, but mean fasting plasma glucose just before the measurement of BEE (FPG) was as low as 113.7 mg/dL due to the treatments during hospital stay (Table 1). Additional characteristics of patients in the derivation set and the results of measurement are shown in Table 1.

Body weight had the highest correlation with FFM ($r = 0.90$), followed by arm muscle area (AMA), height and hip circumference ($r = 0.84$, 0.75 and 0.73, respectively) (Table 2). Waist circumference had the highest correlation with fat mass ($r = 0.91$), followed by hip circumference, triceps-skinfold thickness (TSF) and body weight ($r = 0.79$, 0.78 and 0.75, respectively).

Table 1
Characteristics of patients (derivation set).

	All	Male	Female
No. of patients	68	39	29
Type of diabetes (type1/type2) (n)	7/61	4/35	3/26
Age (years)	59.8 ± 11.2 (range 19–78)	58.3 ± 10.3	61.8 ± 12.2
Height (cm)	161.3 ± 9.5	167.6 ± 6.0	152.9 ± 6.3
Body weight (kg)	62.8 ± 14.7 (range 34.6–113.6)	67.3 ± 16.0	56.7 ± 10.2
BMI (kg/m^2)	24.0 ± 4.7	23.9 ± 5.3	24.2 ± 3.8
FFM (kg)	47.7 ± 10.6	53.4 ± 9.4	39.9 ± 6.5
Fat mass (kg)	16.0 ± 7.0	14.8 ± 8.0	17.8 ± 4.9
TSF (mm)	15.9 ± 7.8	13.1 ± 6.5	19.8 ± 7.8
AMA (cm^2)	44.6 ± 10.2	48.9 ± 9.7	38.8 ± 7.9
Waist (cm)	86.5 ± 12.4	86.2 ± 14.0	86.9 ± 10.3
Hip (cm)	91.3 ± 7.8	92.4 ± 8.5	89.8 ± 6.7
BEE (kcal/day)	1290 ± 217	1395 ± 210	1149 ± 130
FPG (mg/dL)	113.7 ± 25.8	113.3 ± 25.5	114.3 ± 26.6
PPPG (mg/dL)	143.5 ± 35.9	146.5 ± 39.7	139.3 ± 30.3
HbA1c (%)	10.5 ± 2.5	10.3 ± 2.4	10.8 ± 2.7
Duration of diabetes (years)	9.3 ± 7.8	10.9 ± 8.9	7.1 ± 5.5
Treatment			
Diet (kcal/SBW/day)	29.1 ± 2.5	28.9 ± 2.1	29.3 ± 3.0
Medications			
Ins only (n)	34	21	13
Ins + Met (n)	10	4	6
Ins + SU (n)	3	2	1
Ins + SU + Met (n)	1	0	1
SU (n)	8	5	3
SU + Met (n)	5	2	3
Met only (n)	4	3	1
None (n)	3	2	1

Data are means ± SD. BMI, body mass index; FFM, fat-free mass; TSF, triceps-skinfold thickness; AMA, arm muscle area; Waist, waist circumference; Hip, hip circumference; BEE, basal energy expenditure; FPG, fasting plasma glucose just before the measurement of BEE; PPPG, mean preprandial plasma glucose for three consecutive days before the measurement of BEE; HbA1c, glycated hemoglobin; SBW, standard body weight; Ins, insulin; SU, sulfonylurea; Met, metformin.

Table 2
Correlations between FFM, fat mass and anthropometric indices.

	FFM	FM	Ht	Wt	TSF	AMA	Waist	Hip
FFM	1.00	–	–	–	–	–	–	–
FM	0.38†	1.00		–	–	–	–	–
Ht	0.75‡	−0.12	1.00	–	–	–	–	–
Wt	0.90‡	0.75‡	0.49‡	1.00	–	–	–	–
TSF	0.13	0.78‡	−0.30*	0.46‡	1.00	–	–	–
AMA	0.84‡	0.48†	0.50‡	0.83‡	0.07	1.00	–	–
Waist	0.56‡	0.91‡	0.02	0.83‡	0.70‡	0.60‡	1.00	–
Hip	0.73‡	0.79‡	0.28*	0.90‡	0.50‡	0.73‡	0.83‡	1.00

Pearson's correlation coefficients ($n = 68$):*$p < 0.05$; †$p < 0.01$; ‡$p < 0.001$. FFM, fat-free mass; Ht, height; Wt, weight; TSF, triceps-skinfold thickness; AMA, arm muscle area; Waist, waist circumference; Hip, hip circumference.

In regression analysis for FFM, we selected body weight, AMA, height and hip circumference as potent estimators together with other plausible estimators, age and sex. As both AMA and hip circumference were strongly correlated with body weight and AMA was also strongly correlated with hip circumference, to analyze these three variables separately, we used three sets of independent variables, (body weight, height, age and sex), (AMA, height, age and sex), and (hip circumference, height, age and sex). The regressions revealed that all four variables were significant estimators for FFM in the first analysis (model 1 in Table 3), that AMA and height were significant in the second analysis (model 2) and that hip circumference, height and sex were significant in the third analysis (model 3). The first four variables accounted for 95% of variation in FFM, the second two variables 84%, and the third three variables 87%. For fat mass, we selected another three sets of independent variables, (waist circumference, age and sex), (hip circumference, TSF, age and sex) and (body weight, TSF, age and sex) because waist circumference had a strong correlation with hip circumference, TSF and body weight, and hip circumference also had a strong correlation with body weight. In the first analysis, only waist circumference and sex were significant estimators for fat mass, accounting for 86% of fat mass (model 4). In the second analysis, hip circumference, TSF and age were significant, accounting for 84% of fat mass (model 5). In the third analysis, body weight, TSF, age and sex were significant, accounting for 87% of fat mass (model 6).

We performed regression analysis to determine BEE with the most influential estimators (FFM and fat mass) and plausible additional estimators (age and sex), which together explained 81% of the variation (model 7 in Table 3). We then performed backward stepwise estimation, using three sets of variables, (significant variables in model 1 and 6; body weight, height, TSF, age and sex), (significant variables in model 2 and 4 plus age; AMA, height, waist, sex and age), and (significant variables in model 3 and 5; hip circumference, height, TSF, age and sex). The best fitting regression for BEE consisted of body weight, age and sex in the first analysis (model 8), height, waist, age and sex in the second analysis (model 9), and hip circumference, height, TSF and sex in the third analysis (model 10). The adjusted coefficient of determination in model 8 was 81%, which was larger than the 73% in model 9 and the 77% in model 10. The detailed results of model 8 are shown in Table 4.

We then simplified the resultant equation of model 8 to make it easy to use in clinical practice.

$$\mathrm{BEE} = 10 \times \text{body weight} - 3 \times \text{age} + 125(\text{if male}) + 750.$$

$$[\mathrm{BEE}\ (\text{kcal/day}),\ \text{body weight (kg)},\ \text{age (year)}]$$

The bias of this equation in the derivation set was – 1.2 ± 6.4%; RMSE was 94 kcal/day; accurate estimation was 91%.

Table 3
Results of multiple regressions for FFM, FM and BEE.

	Adj. R^2		Model
$\text{FFM} = -26.9 + 0.5 \times \text{Wt} + 0.3 \times \text{Ht} - 0.1 \times \text{Age} + 3.9 \times \text{Sex}$[a]	0.95		1
$\text{FFM} = -60.8 + 0.6 \times \text{AMA} + 0.5 \times \text{Ht}$[b]	0.84		2
$\text{FFM} = -102.8 + 0.8 \times \text{Hip} + 0.5 \times \text{Ht} + 4.5 \times \text{Sex}$[c]	0.87		3
$\text{FM} = -26.3 + 0.5 \times \text{Waist} - 2.6 \times \text{Sex}$[c]	0.86		4
$\text{FM} = -45.4 + 0.5 \times \text{Hip} + 0.4 \times \text{TSF} + 0.1 \times \text{Age}$[d]	0.84		5
$\text{FM} = -14.3 + 0.4 \times \text{Wt} + 0.2 \times \text{TSF} + 0.1 \times \text{Age} - 5.1 \times \text{Sex}$	0.87		6
$\text{BEE} = 691.6 + 11.6 \times \text{FFM} + 8.9 \times \text{FM} - 2.6 \times \text{Age} + 106.7 \times \text{Sex}$	0.81		7
$\text{BEE} = 748.4 + 10.4 \times \text{Wt} - 3.0 \times \text{Age} + 125.4 \times \text{Sex}$[e]	0.81	Model (1 + 6)	8
$\text{BEE} = -332.3 + 6.1 \times \text{Ht} + 9.5 \times \text{Waist} - 4.6 \times \text{Age} + 147.1 \times \text{Sex}$[f]	0.73	Model (2 + 4)	9
$\text{BEE} = -1139.3 + 13.8 \times \text{Hip} + 6.1 \times \text{Ht} + 5.6 \times \text{TSF} + 157.9 \times \text{Sex}$[c]	0.77	Model (3 + 5)	10

FFM, fat-free mass (kg); FM, fat mass (kg); BEE, basal energy expenditure (kcal/day); Wt, body weight (kg); Ht, height (cm); AMA, arm muscle area (cm^2); Hip, hip circumference (cm); Waist, waist circumference (cm); TSF, triceps-skinfold thickness (mm); Adj. R^2, adjusted coefficient of determination.

[a] Male = 1, female = 0.

[b] Age and sex were not significant determinants when added to this model.

[c] Age was not a significant determinant when added to this model.

[d] Sex was not a significant determinant when added to this model.

[e] Height and TSF were not significant determinants when added to this model.

[f] AMA was not a significant determinant when added to this model.

We then tested this new equation in a separate validation data set comparing it with existing equations (Table 5). Characteristics of patients in the validation set are shown in Table 6. The ratio of patients with type 1 and 2 diabetes was almost the same as in the derivation set. Mean age was similar to that in the derivation set, but there were more obese people in the validation set. FPG and PPPG, which represent the glycemic levels around the time of measurement of BEE, were higher, but HbA1c on admission was lower than that in the derivation set. Mean duration of diabetes was similar to that in the derivation set. Prescribed diet was almost the same as in the derivation set, but treatment with insulin was more common in the derivation set. The bias of the new equation was 4.8 ± 7.7%, RMSE was 103 kcal/day, and the percent of patients estimated within ±10% of measured value was 78%. The new equation had better validity than Harris and Benedict equation, Oxford equation, or the Liu equation and Ganpule equation (Table 7).

4. Discussion

We report a new equation to estimate BEE in Japanese patients with diabetes with higher accuracy compared to existing equations. As in other BEE estimation equations, the main estimator was FFM and additional estimators were fat mass, age and sex.[2–4,24] Stepwise estimation analysis of the estimators of FFM and fat mass in the present study revealed that no other indices improved fitting of the equation for BEE except body weight, age and sex. Although anthropometric indices are good estimators for body composition and they improve predictability of certain equations for BEE,[25,26] they were not as effective as body weight in the present study. This accords with the finding that the standard error of the estimate of REE prediction by weight, height, sex and age was well within the range of the standard error of estimates from other FFM-derived prediction equation.[27] Since ethnic difference in BEE is derived from differences in body composition,[13] an ethnicity-specific constant term could more precisely estimates BEE,[4,12] but an ethnicity-specific coefficient of anthropometry is also valid.

Table 4
Detailed result of model 8.

Dependent variable BEE[a]	Coef.[b]	95% CI[c]		Std. coef.[d]	$P > t$	Adj. R^{2}[e]
Independent variables						
Intercept	748.4	562.6	934.1		<0.001	0.810
Wt (kg)	10.4	8.6	12.1	0.70	<0.001	
Age (year)	−3.0	−5.2	−0.9	−0.16	0.007	
Sex (male = 1, female = 0)	125.4	75.6	175.1	0.29	<0.001	

[a] BEE, basal energy expenditure (kcal/day).

[b] Coef., partial regression coefficient.

[c] CI, confidence interval.

[d] Std. coef., standardized coefficient.

[e] Adj. R^2, adjusted coefficient of determination.

We compared our new equation with existing equations such as Harris and Benedict, Oxford, Liu, and Ganpule because the Harris and Benedict equation is widely known in clinical practice in Japan, the Oxford equation was recently developed from a large number of subjects including many ethnicities, and the Liu equation and Ganpule equations were derived from Chinese and Japanese subjects, respectively.[7,10,12,15] The validation analysis revealed better validity of the new equation in Japanese patients with diabetes than any of the other equations.

BEE was measured under strictly controlled conditions in the present study. In addition, we confirmed the FPG of the patients to be < 180 mg/dL just before the measurement of BEE, since BEE is unaffected by the glucose level when its value is < 180 mg/dL.[5,6] As the mean FPG of patients in the derivation set was improved to 114 mg/dl just before the measurement of BEE due to the prescribed diet and medications during hospital stay, in contrast to the poor mean FPG level as high as 170 mg/dl just after admission, clinical application of this equation to patients with stable glycemic control is recommended.

Table 5
Equations to estimate BEE.[a]

	Formula	Reference
New equation	$10\ W - 3\ A + 125\ (\text{if male}) + 750$[b,c]	
Harris and Benedict (1919)	Male: $13.75\ W + 5.00\ H - 6.76\ A + 66.47$[d] Female: $9.56W + 1.85\ H - 4.68\ A + 655.10$	7
Oxford (2005)	Male: 18–30 years; $16.0\ W + 545$ 30–60 years; $14.2\ W + 593$ 60 + years; $13.5\ W + 514$ Female: 18–30 years; $13.1\ W + 558$ 30–60 years; $9.74\ W + 694$ 60 + years; $10.1\ W + 569$	12
Liu (1995)	$13.88\ W + 4.16\ H - 3.43\ A - 112.40\ (\text{if female}) + 54.34$	10
Ganpule (2007)	$(48.1\ W + 23.4\ H - 13.8\ A - 547.3(\text{if female}) - 423.5)/4.186$	15

[a] BEE, basal energy expenditure (kcal/day).

[b] W, weight (kg).

[c] A, age (year).

[d] H, height (cm).

Table 6
Characteristics of patients (validation set).

	All	Male	Female
No. of patients	60	36	24
Type of diabetes (type1/type2) (n)	6/54	3/33	3/21
Age (years)	58.9 ± 13.3 (range 21–82)	55.8 ± 13.5	63.6 ± 11.8
Body weight (kg)	66.9 ± 18.2 (range 41.1–138.0)	70.0 ± 19.2	62.2 ± 15.8
BMI (kg/m^2)	25.7 ± 6.7	24.6 ± 6.2	27.5 ± 7.2
BEE (kcal/day)	1260 ± 219	1342 ± 225	1137 ± 141
FPG (mg/dL)	132.1 ± 20.8	130.8 ± 20.5	133.9 ± 21.6
PPPG (mg/dL)	157.6 ± 32.3	156.7 ± 34.8	159.0 ± 28.9
HbA1c (%)	9.3 ± 1.5	9.5 ± 1.8	9.0 ± 1.1
Duration of diabetes (years)	10.0 ± 8.8	9.3 ± 8.4	11.0 ± 9.5
Treatment			
Diet (kcal/SBW/day)	29.4 ± 2.8	29.4 ± 3.0	29.4 ± 2.5
Medications			
Ins only (n)	28	15	13
Ins + Met (n)	2	1	1
Ins + SU (n)	2	2	0
SU (n)	13	9	4
SU + Met (n)	4	4	0
Met only (n)	3	1	2
None (n)	8	4	4

Data are means ± SD. BMI, body mass index; BEE, basal energy expenditure; FPG, fasting plasma glucose just before the measurement of BEE; PPPG, mean preprandial plasma glucose for three consecutive days before the measurement of BEE; HbA1c, glycated hemoglobin; SBW, standard body weight; Ins, insulin; SU, sulfonylurea; Met, metformin.

There are potential weaknesses of the present study. First, only a small number of patients with type 1 diabetes was included. However, no difference in the value of BEE between patients with type 1 and type 2 diabetes has been described to date. In type 1 diabetes, the elevated energy expenditure is observed only during insulin deprivation, and it returns to normal level by insulin treatment.[28] In type 2 diabetes, there is no difference in FFM-adjusted REE between mildly hyperglycemic patients and controls.[6] Thus, when they are under treatment, BEE in both type 1 and type 2 diabetes patients can be assumed comparable to that in healthy people. In addition, our validation data set has more background in common with the derivation set than the general population of Japanese patients with diabetes. We also did not measure BEE of healthy Japanese for comparison. It remains to be established whether or not the difference in BEE between Japanese patients with diabetes and healthy Japanese is insignificant when FPG of patients are <180 mg/dL.

Table 7
Evaluation of equations in validation set.

Equation	Estimated BEE per body[a]	Estimated BEE per kg Wt[b]	Bias[c]	RMSE[d]	Accurate estimation[e]
New equation	1317 ± 227	20.2 ± 2.3	4.8 ± 7.7	103	78
Harris and Benedict	1388 ± 309	21.1 ± 2.2	9.8 ± 9.4	184	50
Oxford	1420 ± 309	21.6 ± 2.3	12.3 ± 9.5	209	38
Liu	1407 ± 321	21.3 ± 2.1	11.1 ± 10.9	205	42
Ganpule	1323 ± 295	20.1 ± 2.4	4.5 ± 10.5	140	63

n = 60. Data are means ± SD.

[a] Estimated BEE per body, mean basal energy expenditure estimated per body (kcal/day).

[b] Estimated BEE per kg Wt, mean basal energy expenditure estimated per kg body weight (kcal/kg/day).

[c] Bias, mean percentage error between estimated and measured BEE ((BEE estimated − BEE measured)/BEE measured) (%).

[d] RMSE, root mean squared error (kcal/day).

[e] Accurate estimation, percent of the patients estimated by each equation within ±10% of measured value (%).

The values estimated from the proposed equation in the present study are well matched to the reference values for Japanese BEE (Dietary reference intakes) reported in healthy Japanese as values per body weight among different groups for age and sex.[29] In addition, when mean BEE values were calculated by the proposed equation from mean body weight and age reported in other studies including healthy Japanese and Chinese, estimated BEE values were in good agreement with measured values.[10,15,30]

We report a new equation using parameters readily available in clinical practice to estimate BEE of patients with diabetes in an Asian population. Further studies are required to in a wide range of populations to determine its usefulness in Asian clinical settings.

Statement of authorship

The authors' responsibilities were as follows: KI, SF, MG, and TK designed research; KI, CY, AH, MI, KN and KS conducted research; KI, MG, and SF analyzed data; KI and SF wrote the paper; and NI supervised research. All authors read and approved the final manuscript.

Conflict of interest

None of the authors had any conflict of interest.

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ORIGINAL ARTICLE

Reduction of Reactive Oxygen Species Ameliorates Metabolism-Secretion Coupling in Islets of Diabetic GK Rats by Suppressing Lactate Overproduction

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We previously demonstrated that impaired glucose-induced insulin secretion (IS) and ATP elevation in islets of Goto-Kakizaki (GK) rats, a nonobese model of diabetes, were significantly restored by 30–60-min suppression of endogenous reactive oxygen species (ROS) overproduction. In this study, we investigated the effect of a longer (12 h) suppression of ROS on metabolism-secretion coupling in β-cells by exposure to tempol, a superoxide (O_2^-) dismutase mimic, plus ebselen, a glutathione peroxidase mimic (TE treatment). In GK islets, both H_2O_2 and O_2^- were sufficiently reduced and glucose-induced IS and ATP elevation were improved by TE treatment. Glucose oxidation, an indicator of Krebs cycle velocity, also was improved by TE treatment at high glucose, whereas glucokinase activity, which determines glycolytic velocity, was not affected. Lactate production was markedly increased in GK islets, and TE treatment reduced lactate production and protein expression of lactate dehydrogenase and hypoxia-inducible factor 1α (HIF1α). These results indicate that the Warburg-like effect, which is characteristic of aerobic metabolism in cancer cells by which lactate is overproduced with reduced linking to mitochondria metabolism, plays an important role in impaired metabolism-secretion coupling in diabetic β-cells and suggest that ROS reduction can improve mitochondrial metabolism by suppressing lactate overproduction through the inhibition of HIF1α stabilization. ***Diabetes* 62:1996–2003, 2013**

In pancreatic β-cells, intracellular glucose metabolism regulates the exocytosis of insulin granules according to metabolism-secretion coupling in which ATP production in mitochondria plays an essential role (1). The reduction of mitochondrial ATP production causes the impairment of glucose-induced IS in various conditions (2).

Reactive oxygen species (ROS) such as superoxide (O_2^-) and hydrogen peroxide (H_2O_2) are normal byproducts of glucose metabolism, including glycolysis and mitochondrial oxidative phosphorylation (3). In pancreatic β-cells, ROS production via nonmitochondrial and mitochondrial pathways has been proposed. In the mitochondrial pathway, ROS is generated in the electron transport chain associated with the mitochondrial membrane potential (4). However, in pathophysiological conditions, NADPH oxidase, an important nonmitochondrial ROS source, may play an important role in ROS generation in β-cells (5). Antioxidant capacity in β-cells is very low because of weak expression of antioxidant enzymes such as catalase, glutathione peroxidase (GPx), and O_2^- dismutase (SOD) in pancreatic islets compared with that in various other tissues (6,7), which suggests vulnerability of β-cells to ROS. Gene expression profiling in islets revealed that SOD, which metabolizes O_2^- to H_2O_2, was 30–40% and GPx, which metabolizes H_2O_2 to H_2O, was 15% of that in liver. Moreover, catalase was not detectable in islets (7).

In β-cells, ROS is one of the most important factors that impair metabolism-secretion coupling (1). Exposure to exogenous H_2O_2, the most abundant ROS, reduces glucose-induced IS by impairing mitochondrial metabolism in β-cells (8). We have proposed that endogenous overproduction of ROS that involves the activation of Src, a nonreceptor tyrosine kinase, plays an important role in impaired metabolism-secretion coupling in islets of diabetic Goto-Kakizaki (GK) rats (9–11). The suppression of the overproduction of ROS for 30–60 min by exposure to ROS scavengers and by suppression of Src activity restores impaired glucose-induced IS and ATP elevation in GK rat islets (9,10). However, the effect of reducing the overproduction of ROS for a longer duration on impaired metabolism-secretion coupling in diabetic β-cells remains unknown.

In the current study, we investigated the effects of 12-h suppression of endogenous ROS production on impaired metabolism-secretion coupling in β-cells by exposing cell-permeable antioxidant enzyme mimics, including tempol, an SOD mimic (12), and ebselen, a GPx mimic (13), which are commonly used in the field of diabetology without cytotoxic effects (14,15). Our results indicate that 12-h suppression of ROS improves metabolism-secretion coupling by a mechanism different from that involved in improvement by ROS reduction for 30–60 min.

RESEARCH DESIGN AND METHODS

Materials. Ebselen was purchased from Calbiochem (La Jolla, CA). HEPES, KCl, EGTA, glucose, NaCl, $NaHCO_3$, $HClO_4$, Na_2CO_3, H_2O_2, BSA, and the substrates used in ATP production, except glycerol phosphate, were purchased from Nacalai (Kyoto, Japan). [U-^{14}C]-glucose was obtained from GE Healthcare (Uppsala, Sweden). Lactate dehydrogenase (EC 1.1.1.27) and Dowex 1 × 8 anion exchange resin (formate) (50–100 mesh) were obtained from Wako (Osaka, Japan). Hypoxia-inducible factor 1α (HIF1α) inhibitor (3-[2-(4-adamantan-1-yl-phenoxy)-acetylamino]-4-hydroxybenzoic acid methyl ester) was obtained from Merck Millipore (Darmstadt, Germany). All other reagents were obtained from Sigma-Aldrich (St. Louis, MO).

Animals. Male Wistar and GK rats were obtained from Shimizu (Kyoto, Japan). All experiments were carried out with rats 7–10 weeks of age. The body weight

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of GK rats used in the experiments was similar to that of Wistar rats (means ± SE; Wistar, 231 ± 3, vs. GK, 217 ± 3 g, not significant). The nonfasting plasma glucose of GK rats was higher compared with that of Wistar rats (means ± SE; Wistar, 5.72 ± 0.12, vs. GK, 11.57 ± 0.58 mmol/L, $P < 0.01$). The animals were maintained and used in accordance with the guidelines of the animal care committee of Kyoto University.

Islet isolation and culture. Pancreatic islets were isolated from Wistar and GK rats by collagenase digestion as described previously (16). Isolated islets were washed with Krebs-Ringer bicarbonate buffer (KRBB) containing 2.8 mmol/L glucose and cultured for 12 h in RPMI-1640 medium containing 10% FCS and 5.5 mmol/L glucose without or with 10 mmol/L tempol, 10 μmol/L ebselen, or combination of tempol and ebselen (TE treatment) at 37°C in humidified air containing 5% CO_2. Insulin content of GK islets was similar to that of Wistar islets (means ± SE; Wistar, 20.0 ± 2.2, vs. GK, 23.0 ± 2.6 ng/islet, not significant).

Measurement of O_2^- and H_2O_2 generations. O_2^- and the H_2O_2 production were measured at the end of the 12-h culture in conditions described above. O_2^- generation was detected by nitroblue tetrazolium (NBT) assay (17) using KRBB supplemented with 0.2% BSA (fraction V) and 10 mmol/L HEPES adjusted to pH 7.4 (KRBB medium). Groups of 100 islets were batch incubated in tubes containing 0.5 mL KRBB medium supplemented with 5.5 mmol/L glucose with 0.2% (weight/volume) NBT at 37°C for 30 min. After the islets were centrifuged (1,000 rpm for 2 min at 4°C), the supernatant was removed and formazan-NBT (NBT reduced) was dissolved in 100 μL 50% (volume/volume) acetic acid by sonication (5-s pulse, five times). The sonicate was briefly centrifuged, and the absorbance of the supernatant was measured at 560 nm using a spectrofluorometer (Shimadzu RF-5000, Kyoto, Japan). H_2O_2 release from islets was measured according to the method previously described (18). In brief, islets were cultured for 12 h in various conditions as described above. Groups of 150 islets were batch incubated for 60 min in KRBB medium containing 5.5 mmol/L glucose with 0.1 mg/mL horseradish peroxidase (type II) and 0.44 mmol/L homovanillic acid. After the islets were centrifuged (1,000 rpm for 2 min at 4°C), the supernatant was removed. Fluorescence of the supernatant was measured at excitation and emission of 315 and 425 nm, respectively, using a spectrofluorometer (Shimadzu RF-5000). Standard curves were produced using samples containing known amounts of H_2O_2 without islets.

Measurement of insulin release, ATP contents, and glucose oxidation. Insulin release from islets was monitored using batch incubation as described previously (16). ATP content in islets was determined as previously described (9). ATP contents were measured using ENLITEN luciferin-luciferase solution (Promega, Madison, WI) by luminometer (GloMax 20/20n; Promega). Glucose oxidation was carried out using the previously described method (19).

Intraperitoneal glucose tolerance tests. After GK rats were divided into two groups, one group received intraperitoneal injection of tempol (50 mg/kg) and ebselen (10 mg/kg) twice (12 and 6 h before intraperitoneal glucose tolerance tests [ip-GTTs]) during a 15-h fast (TE); the other group was treated similarly with vehicle alone. After these treatments, ip-GTTs (1 g/kg body weight) were performed. Plasma glucose and plasma insulin levels were measured in samples taken at the indicated times. Plasma glucose levels were determined by the glucose oxidase method. Plasma insulin levels were determined using an enzyme immunoassay (Shibayagi, Gunma, Japan).

Immunoblot analysis. The preparations for whole-islet lysate and for the mitochondrial fraction were described previously (20,21). Western blotting was performed as previously described (20) with the following antibodies: mouse monoclonal anti–complex I (39 kDa subunit), anti–complex III (core II),

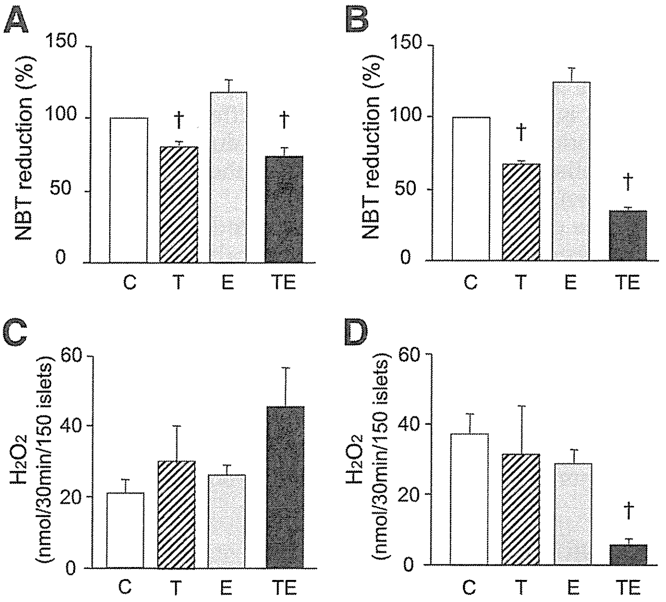

FIG. 1. Effects of antioxidant enzyme mimics on ROS production in Wistar (*A* and *C*) and GK (*B* and *D*) islets. Islets were isolated and cultured without (control [C]; white bars) or with 10 mmol/L tempol (T; hatched bars), 10 μmol/L ebselen (E; gray bars), or T plus E (TE; black bars). O_2^- generation (*A* and *B*) was determined by measuring the reduction of NBT using 100 islets, and data were shown as fold increase relative to control. H_2O_2 generation (*C* and *D*) was determined by measuring the peroxidation of homovanillic acid included in the reaction mixtures as a substrate using 150 islets. Data are shown as means ± SE of three different experiments. †$P < 0.01$ vs. control.

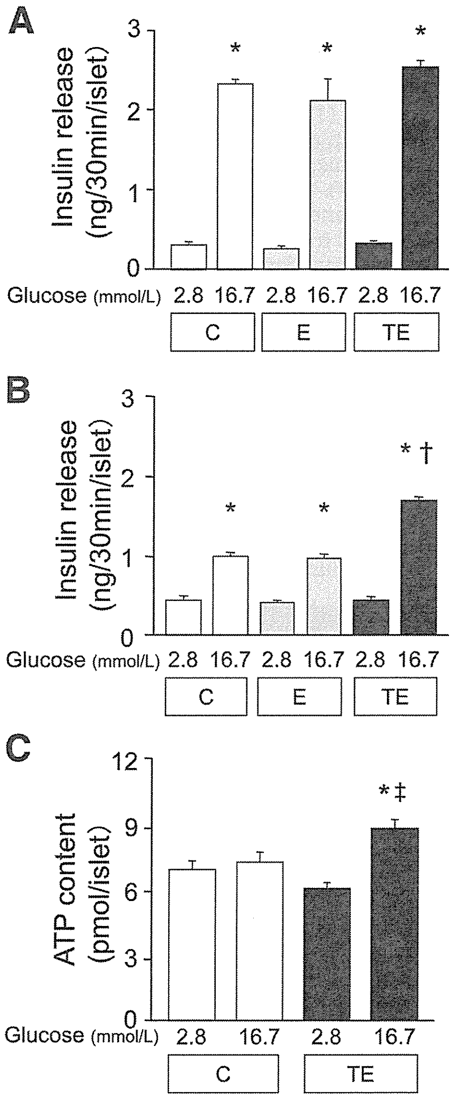

FIG. 2. Effects of antioxidant enzyme mimics on IS (*A* and *B*) and ATP contents (*C*). Islets were cultured without (control [C]) or with ebselen (E; gray bars) and tempol plus ebselen (TE; black bars) for 12 h. After cultured islets were washed and preincubated with 2.8 mmol/L glucose for 30 min, islets were incubated for 30 min at 2.8 and 16.7 mmol/L glucose, and released insulin was measured. Insulin release from Wistar islets (*A*) and in GK islets (*B*) is shown. After cultured GK islets were washed and preincubated with 2.8 mmol/L glucose for 30 min, islets were incubated for 30 min at 2.8 and 16.7 mmol/L glucose, and ATP contents in GK islets were measured (*C*). Data are expressed as the mean ± SE of 25 (*A* and *B*) or 20 (*C*) determinations from three (*A* and *C*) and four (*B*) experiments. *$P < 0.01$ vs. corresponding 2.8 mmol/L glucose; †$P < 0.01$ vs. 16.7 mmol/L glucose in control; ‡$P < 0.05$ vs. 16.7 mmol/L glucose in control.

anti–complex IV (subunit I), and anti–complex V (subunit α) of the mitochondrial respiratory chain (1:1,000) from Invitrogen (Carlsbad, CA), mouse anti–β-actin (1:5,000) from Sigma-Aldrich, rabbit polyclonal anti–LDH-A (1:1,000) from Cell Signaling (Danvers, MA), rabbit anti–PDK-1 (1:1,000) and rabbit anti-HIF1α (1:250) from Abcam (Paris, France), rabbit anti-UCP2 (1:200) from Chemicom (Temecula, CA), mouse anti–hsp-60 (1:5,000) from BD Biosciences (Franklin Lakes, NJ), rabbit anti–PK-M2 (1:2,500) from Novus Biological, LLC (Littleton, CO), and horseradish peroxidase–conjugated anti-rabbit and -mouse antibody (1:5,000) from GE Healthcare. Proteins were detected using an enhanced chemiluminescence system (GE Healthcare). Protein density was quantified by densitometric analysis using Multi Gauge software (Fujifilm, Tokyo, Japan).

Measurements of enzyme activities. After islets were cultured with or without TE for 12 h, whole-islet homogenates and mitochondrial fractions from cultured islets were obtained. Glucokinase and hexokinase activities were determined using whole-islet homogenates by NADH formation in an enzyme reaction as previously described (22). The activity of mitochondrial glycerol phosphate dehydrogenase (mGPDH) in whole-islet homogenates of Wistar and GK rats was measured by the reduction of 2-*p*-iodo-3-*p*-nitro-5-phenyltetrezolium to indoformazan as previously described (23). The activity of mGPDH in the mitochondrial fraction from GK islets was measured by the method based on the generation of ^{3}HOH from L-[2-^{3}H]glycerol-3-phosphate (24). In brief, after mitochondrial fractions were incubated at 37°C for 30 min with 2.5 mCi/mmol L-[2-^{3}H] glycerol-3-phosphate and the reaction was stopped by the addition of antimycin A, the mixture was immediately applied to a column of Dowex 1-X8 (formate), which was washed with 0.5 mL water. The radioactivity of the column effluent was measured by a liquid scintillation counter.

Measurement of mitochondrial ATP production. The mitochondrial fraction from islets and measurement of ATP production were performed as previously described (21).

Measurement of lactate production. Lactate production was measured as previously described (25). In brief, after preincubation, groups of 20 islets were batch incubated in KRBB medium containing 2.8 and 16.7 mmol/L glucose for 60 min at 37°C. The supernatant (200 μL) was mixed with 0.5 mL of 0.5 mol/L glycine/0.4 mol/L hydrazine buffer (pH 9.0) containing 2.4 mmol/L NAD and 7.2 units/mL lactate dehydrogenase, and was incubated for 30 min at 37°C. The fluorescence of NADH was then measured at an excitation of 340 nm and emission of 450 nm. Standard curves were produced from samples containing known amounts of lactate.

Statistical analysis. The data are expressed as means ± SE. Statistical significance was determined by unpaired Student *t* test. $P < 0.05$ was considered significant.

RESULTS

O_2^- and H_2O_2 production during culture with antioxidant mimics. Tempol, an SOD mimic, decreased O_2^- production in Wistar (Fig. 1*A*) and GK islets (Fig. 1*B*) but had no effect on H_2O_2 production in either of the islets (Fig. 1*C* and *D*). Ebselen, a GPx mimic, had no reducing effect on O_2^- and H_2O_2 production in either of the islets (Fig. 1). Cotreatment with TE reduced O_2^- production by 27.0% but had no effect on H_2O_2 production in Wistar islets (Fig. 1*A* and *C*). On the other hand, in GK islets, TE treatment prominently reduced O_2^- and H_2O_2 production by 65.0 and 84.6%, respectively (Fig. 1*B* and *D*). Taken together, these findings indicate that TE treatment is effective in reducing oxidative stress in GK islets.

Effect of TE treatment on IS. The effect of antioxidant mimics on β-cell function was investigated. In the presence of 16.7 mmol/L glucose, insulin secretion (IS) from GK islets was reduced compared with that from control Wistar rats (GK, 1.01 ± 0.06, vs. Wistar, 2.32 ± 0.11 ng/30 min/islet, $P < 0.01$). Although TE treatment had no effect on IS from Wistar islets (Fig. 2*A*), it restored high glucose–induced IS (Fig. 2*B*) and ATP content (Fig. 2*C*) in GK islets. We demonstrated previously that impaired glucose-induced IS in GK islets was significantly restored by acute exposure to PP2, a Src inhibitor (9). To examine the involvement of Src inhibition in the improvement of glucose-induced IS after TE treatment, TE-treated GK islets were incubated for 30 min with or without 10 μmol/L PP2 in the presence of 16.7 mmol/L glucose. In TE-treated GK islets, 30-min exposure to PP2 prominently enhanced IS at high glucose (control, 1.71 ± 0.07, vs. PP2, 4.06 ± 0.22 ng/30 min/islet, $P < 0.01$), which implies involvement of an independent mechanism of Src inhibition in the improvement of glucose-induced IS by chronic TE treatment.

To investigate the effects of TE treatment on β-cell function in vivo, a GTT was assessed after intraperitoneal TE administration (Table 1). In GK rats, TE treatment decreased the glucose level at 15 and 30 min and increased insulin levels at 30 min after glucose loading. Studies using isolated islets from GK rats after TE treatment in vivo revealed that high glucose–induced IS was increased by TE treatment (Table 2).

Effect of TE treatment on expression of UCP2 and mitochondrial respiratory chain proteins. Immunoblot analysis showed that TE treatment had no effect on protein levels of UCP2 in protein extracts of the islet mitochondrial fraction (Supplementary Fig. 1*A*) and on those of complex I, III, IV, and V of the mitochondrial respiratory chain in lysates of whole islets (Supplementary Fig. 1*B*) in both GK and Wistar islets.

Effect of TE treatment on glucose metabolism. TE treatment had no effect on glucokinase and hexokinase activities, which determines the velocity of glycolysis in β-cells (26), in GK and Wistar islets (Table 3). By TE treatment, glucose oxidation at high glucose, an indicator of Krebs cycle velocity, was not affected in Wistar islets, whereas it was significantly increased in GK islets (control, 25.4 ± 4.1, vs. TE, 55.8 ± 12.2 pmol/islet/90 min, $P < 0.05$) (Fig. 3).

Effect of TE treatment on ATP production and on activity of mGPDH. ATP production by mitochondria from control and TE-treated islets of Wistar and GK rats was measured in the presence of various substrates and inhibitors (Table 4), including succinate (electron transfer at complex I by NADH generation in the Krebs cycle and at complex II directly), succinate with rotenone (electron

TABLE 1
Ip-GTT in GK rats treated with TE in vivo

		Minute				
		0	15	30	60	120
Glucose (mg/dL)	Control	145 ± 4	475 ± 6	423 ± 11	340 ± 14	184 ± 7
	TE	144 ± 11	330 ± 41†	359 ± 28*	330 ± 24	200 ± 13
Insulin (pg/mL)	Control	164 ± 70	ND	172 ± 50	ND	205 ± 75
	TE	205 ± 32	ND	400 ± 101*	ND	209 ± 46

After the intraperitoneal injection of 50 mg/kg tempol plus 10 mg/kg ebselen (TE) or vehicle alone (control) twice during a 15-h fast in GK rats, GTT with intraperitoneal injection of glucose (1 g/kg body weight) was performed and plasma glucose and insulin levels were measured. Data are means ± SE of seven independent experiments. ND, not determined. *$P < 0.05$ vs. corresponding control TE. †$P < 0.01$ vs. corresponding control without TE.

TABLE 2
Insulin secretion from isolated islets in GK rats treated with tempol plus ebselen in vivo

	2.8 mmol/L glucose	16.7 mmol/L glucose
Control (ng/30 min/islet)	0.40 ± 0.04	0.84 ± 0.06
TE (ng/30 min/islet)	0.49 ± 0.04	1.42 ± 0.13*

After the intraperitoneal injection of 50 mg/kg tempol plus 10 mg/kg ebselen (TE) or vehicle alone (control) twice during a 15-h fast in GK rats, islets were isolated and IS in the presence of 2.8 and 16.7 mmol/L glucose was measured. Data are means ± SE of nine determinations. $^*P < 0.01$ vs. corresponding control without TE.

transfer at complex II and inhibition of electron transfer through NADH at complex I), glutamate plus malate (electron transfer mainly at complex I by NADH generation derived from reaction via glutamate dehydrogenase), pyruvate plus malate (electron transfer mainly at complex I by NADH generation derived from reaction via pyruvate dehydrogenase), ascorbate plus N,N,N′,N′-tetramethyl-p-phenylenediamine (TMPD) (electron transfer at complex IV directly), and glycerol-3-phosphate (G3P) (electron transfer at complex II by $FADH_2$ generation derived from reaction via mGPDH). Control and TE-treated mitochondria showed similar rates of ATP production for all substrates tested, except for G3P. TE treatment promotes the rate of mitochondrial ATP production in the presence of G3P in Wistar and GK islets 3.3- and 2.2-fold, respectively. In the measurement of activity of mGPDH using whole islet homogenates, the value in GK islets was lower compared with that of Wistar islets, and enhancement of the activity by TE treatment was not significant in either Wistar or GK islets (Table 3). However, in the measurement of activity of mGPDH using intact mitochondria, TE treatment increased mGPDH activity in GK mitochondria (Table 3).

Lactate production and protein expression of lactate dehydrogenase and HIF1α. Lactate production in GK islets was significantly higher compared with that in Wistar islets at both basal and stimulated levels of glucose (at 2.8 mmol/L glucose: Wistar, 1.32 ± 0.15, vs. GK, 8.15 ± 1.36, $P < 0.01$; at 16.7 mmol/L glucose: Wistar, 3.09 ± 0.33, vs. GK, 14.08 ± 1.68, $P < 0.01$) (Fig. 4*A*). TE treatment suppressed lactate production at both basal and stimulated levels of glucose in both Wistar and GK islets; the most prominent reduction in these conditions was at 16.7 mmol/L glucose in GK islets (control, 14.08 ± 1.68, vs. TE, 5.71 ± 0.79, $P < 0.01$). Protein expression levels of HIF1α, a potential upstream regulator of lactate dehydrogenase (LDH), in INS-1 cells were gradually increased over 12 h in the presence of 200 μmol/L $CoCl_2$, a chemical inducer of HIF1α (27) (Supplementary Fig. 2). TE treatment time-dependently suppressed HIF1α levels in GK islets, and the reduction was significant after 9-h TE treatment (~30% reduction at 9 h; ~50% reduction at 12 h) (Fig. 4*B*). Protein expression levels of HIF1α and HIF1α downstream targets, including LDH-A and pyruvate dehydrogenase-1 (PDK-1), were examined 12 h after TE treatment. In GK islets, TE treatment significantly decreased HIF1α, LDH-A, and M2-PK expression (HIF1α, ~50% reduction; LDH-A, ~30% reduction; M2-PK, ~30% reduction) but did not affect PDK-1 expression (Fig. 4*C* and Supplementary Fig. 3).

Effect of HIF1α inhibitor on IS and lactate production in GK islets. IS in the presence of 16.7 mmol/L glucose from GK islets was enhanced by HIF1α inhibitor treatment (control, 1.34 ± 0.07, vs. HIF1α inhibitor, 1.77 ± 0.09 ng/30 min/islet, $P < 0.01$). Lactate production in the presence of 2.8 and 16.7 mmol/L glucose was reduced by HIF1α inhibitor treatment (2.8 mmol/L glucose: control, 12.44 ± 1.12, vs. HIF1α inhibitor, 9.46 ± 0.89 pmol/islet, $P < 0.01$; 16.7 mmol/L glucose: control, 15.39 ± 1.02, vs. HIF1α inhibitor, 12.42 ± 1.40 pmol/islet, $P < 0.01$) (Fig. 5).

DISCUSSION

The current study demonstrates that combination treatment by tempol, an SOD mimic, and ebselen, a GPx mimic (TE treatment), efficiently suppressed both H_2O_2 and O_2^- production in GK islets. Moreover, impaired glucose-induced IS and ATP elevation in GK islets were significantly improved by TE treatment but were not improved by tempol or ebselen alone. These results are compatible with previous studies in which coexpression of the antioxidant enzymes in a β-cell line was more efficient than expression of either single enzyme in reducing ROS production and oxidative injury (7,28,29).

We then examined the precise mechanisms of the improvement in glucose-induced ATP elevation in GK islets by TE treatment. UCP2 decreases mitochondrial ATP production by reducing mitochondrial hyperpolarization derived from an increase in mitochondrial proton conductance. UCP2 negatively regulates metabolism-secretion

TABLE 3
Effect of TE treatment on glucokinase, hexokinase, and mitochondrial G3P dehydrogenase activities

Experimental conditions		Wistar rat	GK rat
Hexokinase (whole islet extracts) (pmol/islet/h)	Control	21.58 ± 3.23	131.46 ± 23.62
	TE	21.63 ± 3.18	138.19 ± 35.97
Glucokinase (whole islet extracts) (pmol/islet/h)	Control	22.79 ± 8.21	52.71 ± 8.82
	TE	22.90 ± 6.53	42.41 ± 8.96
mGPDH (whole islet extracts) (nmol/mg protein/min)	Control	9.90 ± 0.34	6.76 ± 0.32*
	TE	10.60 ± 0.75	7.37 ± 0.14
mGPDH (mitochondrial fraction) (nmol/mg mitochondrial protein/min)	Control	ND	65.77 ± 1.61
	TE	ND	75.41 ± 2.34†

After islets were cultured with or without TE for 12 h, extract from whole islets and mitochondrial fractions were obtained. Data are given as the mean ± SE from five experiments for glucokinase and hexokinase, six experiments for mGPDH using whole-islet extracts, and three experiments for mGPDH using the mitochondrial fraction. ND, not determined. $^*P < 0.05$ vs. Wistar control without TE. $^†P < 0.05$ vs. control without TE.