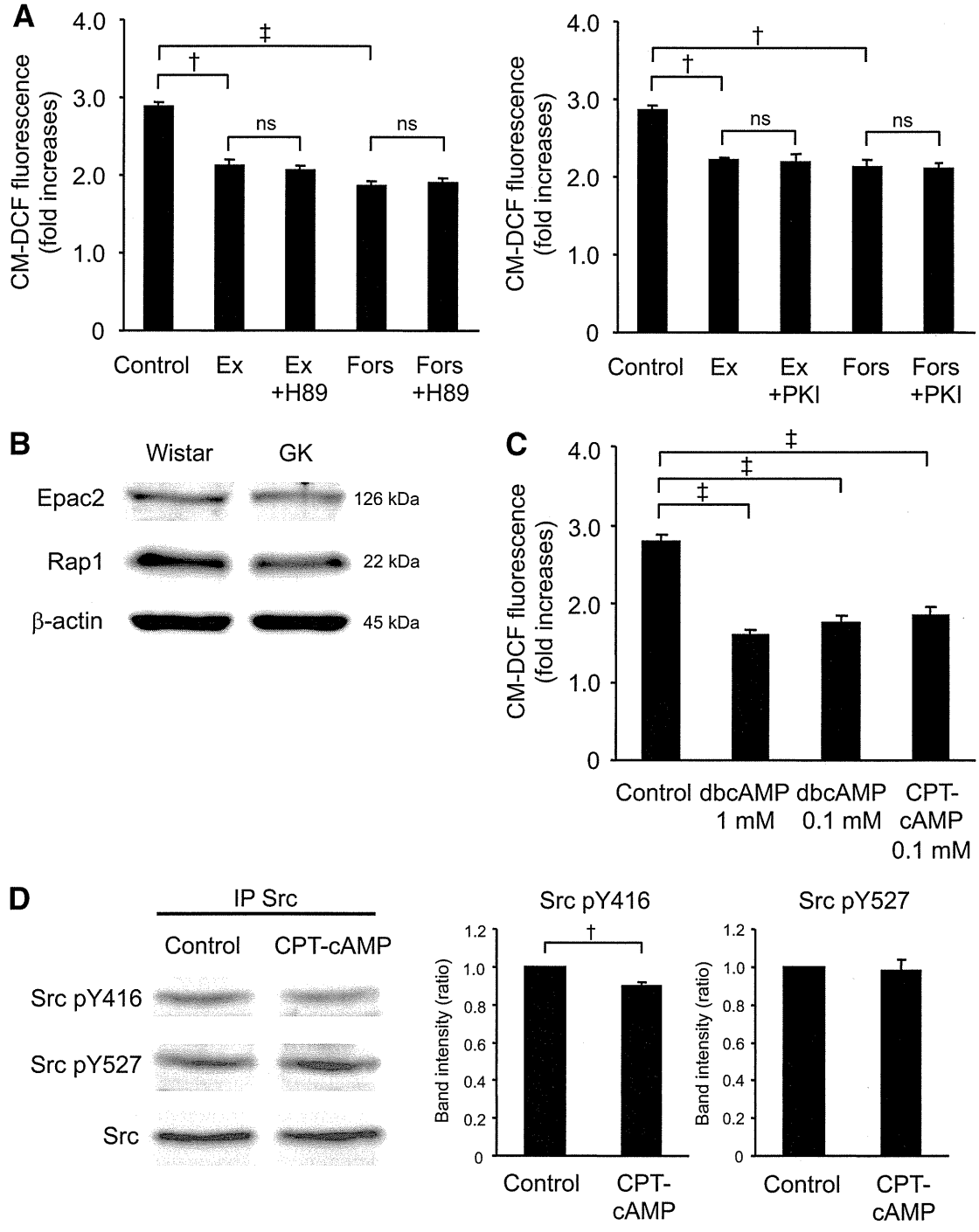

FIG. 5. The effects of exendin-4 are dependent not on PKA but on Epac. *A*: **Effects of H-89 or PKI on the decrease in high-glucose–induced ROS production by exendin-4 or forskolin at 60 min in GK islet cells. After preincubation in the presence of 2.8 mmol/l glucose and 10 μmol/l CM-H_2DCFDA for 20 min, dispersed islet cells were incubated in the presence of 16.7 mmol/l glucose with or without 100 nmol/l exendin-4 or 10 μmol/l forskolin with or without 10 μmol/l H-89 or 10 μmol/l PKI for 60 min. Fluorescence is represented as fold increases against the value at time zero. Data are expressed as means ± SE (n = 3). †P < 0.01; ‡P < 0.001.** *B*: **Expression of Epac2 and Rap1 in Wistar and GK islets. Fresh islets were lysated and subjected to immunoblot analyses. Blots (50 μg of protein) were probed with anti-Epac2 or anti-Rap1. The same blots were stripped and reprobed with anti–β-actin, respectively. Representative blot panels of three independent experiments are shown.** *C*: **Effects of cAMP analogs on high-glucose–induced ROS production at 60 min in GK islet cells. Data are expressed as means ± SE (n = 3–4). ‡P < 0.001.** *D*: **Epac-specific cAMP analog suppresses Src activity at high glucose in GK islets. After preincubation in the presence of 2.8 mmol/l glucose for 30 min, islets were incubated in the presence of 16.7 mmol/l glucose with or without 0.1 mmol/l 8CPT-2Me-cAMP for 8 min. Islet lysates (~2 mg of protein) were immunoprecipitated with anti-Src antibody and subjected to immunoblot analyses. Blots were probed with anti–phospho-Src (Tyr^{416}), anti–phospho-Src (Tyr^{527}), or anti-Src by stripping and reprobing of the same blots. Intensities of the bands were quantified with densitometric imager. The bar graphs are expressed relative to control value corrected by Src level (means ± SE). †P < 0.01. Representative blot panels of four independent experiments are shown.**

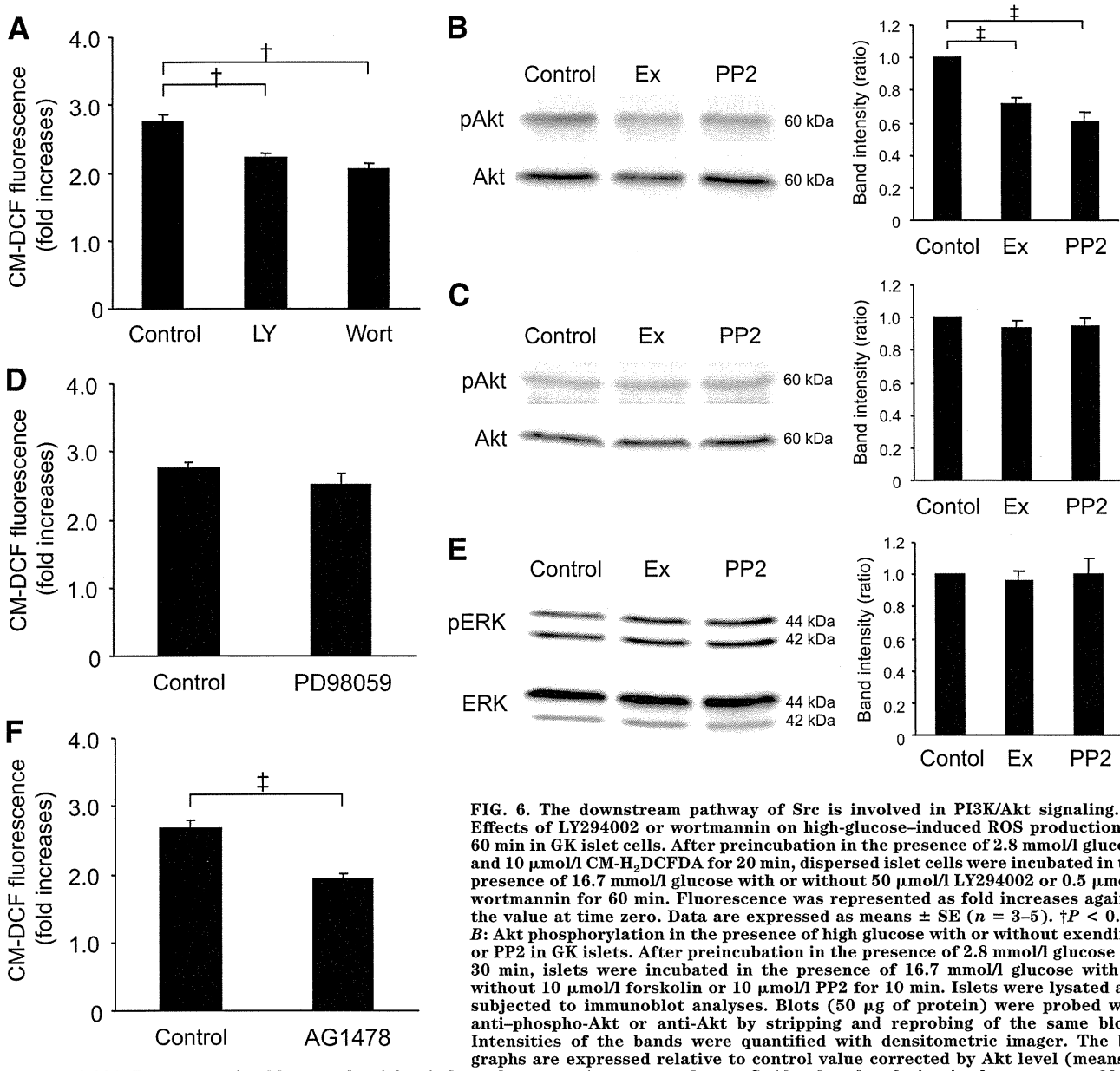

FIG. 6. The downstream pathway of Src is involved in PI3K/Akt signaling. *A*: Effects of LY294002 or wortmannin on high-glucose–induced ROS production at 60 min in GK islet cells. After preincubation in the presence of 2.8 mmol/l glucose and 10 μmol/l CM-H_2DCFDA for 20 min, dispersed islet cells were incubated in the presence of 16.7 mmol/l glucose with or without 50 μmol/l LY294002 or 0.5 μmol/l wortmannin for 60 min. Fluorescence was represented as fold increases against the value at time zero. Data are expressed as means ± SE (n = 3–5). †P < 0.01. *B*: Akt phosphorylation in the presence of high glucose with or without exendin-4 or PP2 in GK islets. After preincubation in the presence of 2.8 mmol/l glucose for 30 min, islets were incubated in the presence of 16.7 mmol/l glucose with or without 10 μmol/l forskolin or 10 μmol/l PP2 for 10 min. Islets were lysated and subjected to immunoblot analyses. Blots (50 μg of protein) were probed with anti–phospho-Akt or anti-Akt by stripping and reprobing of the same blots. Intensities of the bands were quantified with densitometric imager. The bar graphs are expressed relative to control value corrected by Akt level (means ± SE). ‡P < 0.001. Representative blot panels of five independent experiments are shown. *C*: Akt phosphorylation in the presence of high glucose with or without exendin-4 or PP2 in Wistar islets. Representative blot panels of three independent experiments are shown. *D*: Effects of PD98059 on high-glucose–induced ROS production at 60 min in GK islet cells. Data are expressed as means ± SE (n = 4). *E*: ERK phosphorylation in the presence of high glucose with or without exendin-4 or PP2 in GK islets. Blots (50 μg of protein) were probed with anti–phospho-ERK or anti-ERK by stripping and reprobing of the same blots. The bar graphs are expressed relative to control value corrected by ERK level (means ± SE). Representative blot panels of three independent experiments are shown. *F*: Effects of AG1478 on high-glucose–induced ROS production at 60 min in GK islet cells. Data are expressed as means ± SE (n = 5). ‡P < 0.001.

does not affect the phenotype in mice, contrary to neural tube defects and embryonic lethality in homozygous deficient mice (31). Moreover, the localization of Csk in the cytosol before recruitment to the membrane for Src regulation dose not differ in Wistar and GK islets (supplementary Fig. 4). Thus, the lower expression level of Csk found in our results is not likely to play a role in the Src activation in GK islets. Activation of Src as well as elevated endogenous ROS production at high glucose in GK islets was clearly suppressed by exendin-4, which did not affect Src phosphorylation or ROS production in Wistar islets. Thus, the GLP-1 signal might well suppress activation of Src and excessive ROS production under diabetic conditions in addition to other beneficial long-term effects on β-cells.

GLP-1 induces elevation of intracellular cAMP levels and subsequent activation of PKA after binding to the GLP-1 receptor. In the present study, the effect of GLP-1 signaling, which suppresses Src activation and ROS production, was found to be independent of PKA. Epac is a PKA-independent cAMP sensor; Epac2 is expressed mainly in neuroendocrine cells including pancreatic β-cells. Epac2 regulates exocytosis of insulin granules in β-cells by mobilizing intracellular Ca^{2+} and interacting granule-associated proteins (14,15). Although the relationship between Epac and Src is not well known, a recent

report (32) has shown that cAMP protects against hepatocyte apoptosis Epac dependently through Src and PI3K/Akt activation. Further evaluation of the role of cAMP in regulation of Src and PI3K/Akt signaling is required.

In the present study, we have shown that one of these Src signals, the PI3K/Akt signal, regulates ROS production. Furthermore, GLP-1 induces β-cell proliferation through PI3K signaling via Src and EGFR transactivation (33). Our finding that the EGFR kinase inhibitor decreases ROS production suggests that EGFR transactivation may be involved in the ROS-reducing effect of exendin-4 via Src. Under normal conditions, GPCR stimulation generally activates Src toward EGFR transactivation, frequently followed by PI3K activation (25). The present study reveals that Src and PI3K activities are upregulated in islets under diabetic conditions, which are suppressed by the GLP-1 signal. Many studies in oncology have shown that several growth factors including EGF and platelet-derived growth factor induce ROS through PI3K activation (34–36). Thus, EGFR transactivation/PI3K signaling should be activated under pathophysiologically disordered conditions. In the various states between normal and diabetic conditions, the ameliorative effects of the GLP-1 signal may differ (37). Further elucidation of these signals in the pathophysiology of diabetes should be helpful in future development of therapeutic strategies.

Previous studies have shown that the antioxidant capacity in β-cells is very low because of weak expression of antioxidant enzymes in pancreatic islets compared with that in various other tissues (38). The superoxide anion is converted by superoxide dismutase (SOD) into hydrogen peroxide that is eventually removed by glutathione peroxidase (Gpx). The expression level of MnSOD, which is localized in mitochondria, was significantly lower in GK islets than in Wistar islets, and that of of Gpx was similar in Wistar and GK islets (supplementaty Fig. 5*A*). However, an enzymatic assay revealed that MnSOD activity in GK islets was similar to that in Wistar islets and that it was not affected by exendin-4 or PP2 (supplementary Fig. 5*B* and *C*). These results indicate that regulation of MnSOD activity does not play a role in the suppressive effects of ROS production by exendin-4.

One of the important sites of ROS generation in β-cells is the mitochondrial electron transport chain, in which ROS generation increases according to the hyperpolarization of mitochondrial inner membrane derived from accelerated glucose metabolism (39). However, in pathophysiological conditions, NADPH oxidase may play an important role in ROS generation in β-cells. Chronic exposure to proinflammatory cytokines and abundant nutrients including glucose and palmitate augments the expression of a phagocyte-like NADPH oxidase in β-cells (40). Moreover, the expression of NADPH oxidase is increased in islets of diabetic Otsuka Long Evans Tokushima Fatty rats (41). Because Src is involved in regulation of NADPH oxidase activity (42), further examination to elucidate the site of ROS generation related to Src activation in β-cells is needed. On the other hand, previous reports have shown that ROS itself regulates Src activity (43,44) in addition to Src activity regulation of ROS production (45). To clarify this mutual causal relationship between Src and ROS, we examined ROS production in GK islets expressing Src-KN, which was found to cause a distinct decrease in high-glucose–induced ROS production. This finding demonstrates that Src activity regulates ROS production and does not contradict the possibility of a feedback regulation mechanism of ROS on Src activity (45).

The high-glucose–induced increase in ATP production is impaired in GK rats (6,46) as well as in patients with type 2 diabetes (47). In addition, islets in GK rats and human type 2 diabetes are oxidatively stressed (48–50). In the present study, exendin-4 was able to recover this impaired increase in ATP production by high glucose in GK islets as well as to decrease excessive ROS production. Thus, GLP-1 signaling may improve β-cell function in the diabetic state not only because it enhances Ca^{2+} efficacy of the exocytotic system of insulin granules but also because it improves impaired metabolism-secretion coupling. GLP-1 receptor agonists are widely used in treatment of type 2 diabetes for their ability to improve glucose intolerance. Their clinical beneficial effect seems to be provided not only by their insulinotropic action but also by their reduction of β-cell apoptosis and induction of β-cell proliferation (16–18). Further elucidation of endogenous ROS regulation by GLP-1 may help to clarify the mechanism of the various beneficial effects of these agents.

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E.M. researched data, contributed to the discussion, wrote the manuscript, and reviewed/edited the manuscript. S.F. contributed to the discussion, wrote the manuscript, and reviewed/edited the manuscript. H.S., C.O., R.K., Y.S., M.S., and Y.N. researched data. M.O. contributed to the discussion and reviewed/edited the manuscript. N.I. contributed to the discussion and reviewed/edited the manuscript.

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The effect of gastric inhibitory polypeptide on intestinal glucose absorption and intestinal motility in mice

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ABSTRACT

Gastric inhibitory polypeptide (GIP) is released from the small intestine upon meal ingestion and increases insulin secretion from pancreatic β cells. Although the GIP receptor is known to be expressed in small intestine, the effects of GIP in small intestine are not fully understood. This study was designed to clarify the effect of GIP on intestinal glucose absorption and intestinal motility. Intestinal glucose absorption *in vivo* was measured by single-pass perfusion method. Incorporation of [^{14}C]-glucose into everted jejunal rings *in vitro* was used to evaluate the effect of GIP on sodium-glucose co-transporter (SGLT). Motility of small intestine was measured by intestinal transit after oral administration of a non-absorbed marker. Intraperitoneal administration of GIP inhibited glucose absorption in wild-type mice in a concentration-dependent manner, showing maximum decrease at the dosage of 50 nmol/kg body weight. In glucagon-like-peptide-1 (GLP-1) receptor-deficient mice, GIP inhibited glucose absorption as in wild-type mice. *In vitro* examination of [^{14}C]-glucose uptake revealed that 100 nM GIP did not change SGLT-dependent glucose uptake in wild-type mice. After intraperitoneal administration of GIP (50 nmol/kg body weight), small intestinal transit was inhibited to 40% in both wild-type and GLP-1 receptor-deficient mice. Furthermore, a somatostatin receptor antagonist, cyclosomatostatin, reduced the inhibitory effect of GIP on both intestinal transit and glucose absorption in wild-type mice. These results demonstrate that exogenous GIP inhibits intestinal glucose absorption by reducing intestinal motility through a somatostatin-mediated pathway rather than through a GLP-1-mediated pathway.

1. Introduction

Gastric inhibitory polypeptide (GIP), also called glucose-dependent insulinotropic polypeptide, is an incretin of 42-amino-acid polypeptide synthesized by K cells of the duodenum and small intestine [1]. We previously generated GIP receptor-deficient mice (GIPR$^{-/-}$ mice) and showed that GIPR$^{-/-}$ mice have higher blood glucose levels as well as impaired initial insulin response after oral glucose load [2]. Thus, early insulin secretion stimulated by GIP plays an important role in glucose tolerance after oral glucose load.

While GIP receptor mRNA was reported to be present in rat gut [3], the role of the GIP receptor in the gut has not been fully clarified. In this *in vivo* study, we investigated the effect of exogenous GIP on intestinal glucose absorption in mice using the intestinal perfusion method. We investigated the effect of exogenous GIP on SGLT-dependent glucose uptake *in vitro* by using the everted jejunal ring method. Because intestinal motility and absorption are positively related [4,5], we investigated the effect of exogenous GIP on gastrointestinal motility by non-absorbed marker method. Since SST secretion has been reported to be stimulated by GIP and to prolong intestinal motility, we also investigated the involvement of SST in the inhibitory effect of exogenous GIP on both intestinal transit and intestinal glucose absorption by using somatostatin receptor antagonist. Our results demonstrate that exogenous GIP inhibits intestinal glucose absorption by reducing intestinal motility through a somatostatin-mediated pathway rather than through a GLP-1-mediated pathway.

Abbreviations: GIP, Gastric inhibitory polypeptide; GLP-1, glucagon-like-peptide-1; SST, somatostatin; SGLT, sodium-glucose co-transporter; CSS, cyclosomatostatin.

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2. Materials and methods

2.1. Animals

Male C57/BL6J mice weighing 25–30 g (8–14 weeks old) were housed in a temperature (25 ± 2 °C)- and moisture (50%)-controlled room with a 12 h light/dark cycle (6:00 AM/6:00 PM). The mice were fed standard mouse chow (Oriental Yeast, Osaka) and tap water *ad libitium*, and used as wild-type mice.

Generation of GIPR$^{-/-}$ mice and GLP-1 receptor-deficient mice (GLP-1R$^{-/-}$ mice) was described previously [2,6]. GLP-1R$^{-/-}$ mice were kindly provided by Dr. Daniel J. Drucker [6]. Age-matched male GIPR$^{-/-}$ and GLP-1R$^{-/-}$ mice were used in the experiments. The Animal Care Committee of Kyoto University Graduate School of Medicine approved animal care and procedures.

2.2. Materials

Synthetic human GIP was purchased from Peptide Institute (Osaka, Japan). The somatostatin receptor antagonist, cyclo(7-aminoheptanoyl-PHE-D-TRP-LYS-THR(BZL)) (cyclosomatostatin (CSS)) and somatostatin 28 (SST) were from Sigma Chemical Co. (St. Louis, MO). All other chemicals were of reagent grade.

2.3. Perfusion experiment

Single-pass perfusion method [7] was used to measure the effect of exogenous GIP or SST on intestinal glucose absorption using C57/BL6J mice. Preperfusion was done for a 45 min equilibration period and the samples were discarded. Three 15 min samples were then collected. GIP or SST was administered intraperitoneally at 60 min after starting the preperfusion according to the protocol (Fig. 1A). The change of absorption was calculated as the glucose concentration of the first sample collected (Period 1) minus the glucose concentration of the last sample collected (Period 2), and expressed as per centimeter perfused bowel. Negative values indicate an inhibitory effect on absorption; positive values indicate an increased effect on absorption.

2.4. Glucose uptake in jejunum in vitro

Incorporation of D-glucose into everted jejunal rings was determined as described previously [8]. SGLT-dependent glucose uptake for 15 min was determined as the glucose uptake in the absence of phlorizin minus the glucose uptake in the presence of phlorizin.

2.5. Small intestinal transit after intraperitoneal administration of GIP

Transit through the stomach and small intestine was measured by administering a non-absorbed marker containing 10% charcoal suspension in 5% gum Arabic, as previously described [9]. The mice were given 0.2 ml of the suspension by gavage through a straight blunt-ended feeding needle. GIP (50 nmol/kg body weight) or SST (75 nmol/kg body weight) or vehicle (saline) was administered intraperitoneally 15 min prior to the administration of the non-absorbed marker. CSS (1 μg/kg body weight), or vehicle (saline) was intraperitoneally administered 10 min prior to GIP administration.

2.6. Plasma GIP and SST assays

Blood was collected from the tail vein before the intraperitoneal administration of GIP (50 nmol/kg body weight) and collected again 20 min after the administration. ELISA assay kit was used according to the manufacture's instruction for the determination of plasma total GIP concentration (Linco Research, St. Charles, MO) and SST concentration (Phoenix Pharmaceuticals INC., Belmont, CA), respectively.

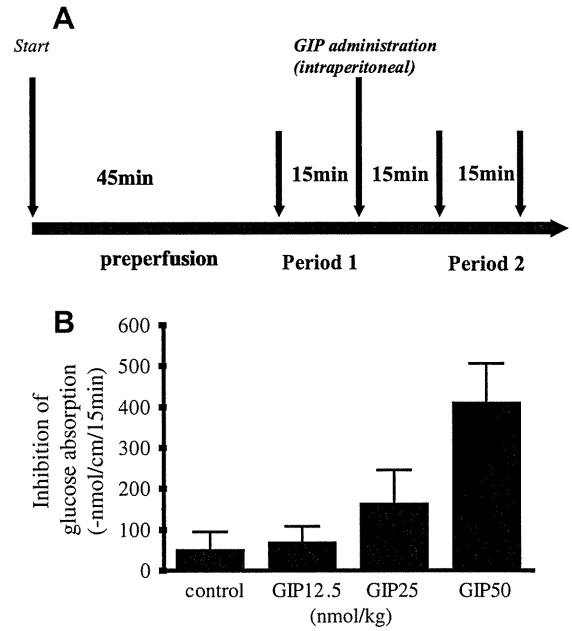

Fig. 1. (A) Diagram showing the sampling protocol of intestinal perfusion. The flow rate of the perfusion fluid was 2 ml/15 min. Perfusion began with an equilibration period of 45 min, which samples were discarded. The samples of Period 1 and Period 2 were then collected. GIP was administered intraperitoneally 60 min after the beginning of preperfusion. The change of absorption was calculated as the glucose concentration of the first samples collected (Period 1) minus the glucose concentration of the last samples collected (Period 2), and expressed as per centimeter perfused bowel. (B) Concentration-dependence of inhibition of glucose absorption by GIP in wild-type mice. Data are shown as means with SEM ($n = 6$ for each group, $P < 0.05$ by ANOVA).

2.7. Analysis

The results are given as mean ± standard error (SEM, n = number of mice). Statistical significance was determined using paired and unpaired Student's t-test and analysis of variance (ANOVA). $P < 0.05$ was considered significant.

3. Results

3.1. Perfusion experiment

Inhibition of glucose absorption was calculated by change in glucose concentration in effluent perfusate in wild-type mice (Fig. 1A). Spontaneous inhibition of glucose absorption of 49 ± 44 nmol/cm/15 min is shown in saline-administered controls (Fig. 1B). Inhibition of glucose absorption was enhanced to 67 ± 40, 163 ± 84, and 409 ± 96 nmol/cm/15 min when the amount of intraperitoneally-administered GIP was increased to 12.5, 25, and 50 nmol/kg body weight, respectively.

3.2. Glucose uptake by jejunum in vitro

We investigated glucose uptake by the jejunum *in vitro* using everted jejunal rings. In the presence of 100 nM GIP in the incubation medium, glucose uptake into jejunal rings in wild-type mice was similar to that in the presence of vehicle (control: 4.2 ± 0.9 μmol/g weight; GIP: 3.5 ± 0.9, P = NS; Fig. 2A). Additionally, glucose uptake into jejunal rings in GIPR$^{-/-}$ mice was similar

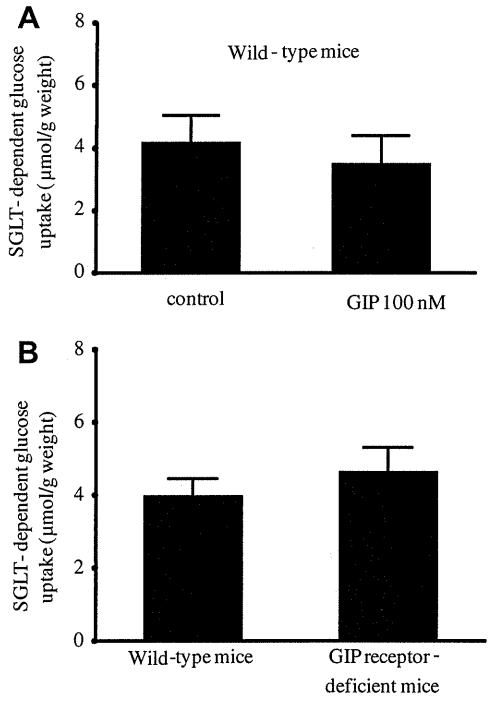

Fig. 2. Glucose uptake in the jejunum. (A) Glucose uptake in the jejunum in wild-type mice in the absence and in the presence of 100 nM GIP. (B) Glucose uptake in the jejunum in wild-type and GIPR$^{-/-}$ mice. SGLT-dependent glucose uptake was determined as the glucose uptake in the absence of 1 mM phlorizin minus the glucose uptake in the presence of 1 mM phlorizin. Data are shown as means with SEM ($n = 8$ for each group).

to that in wild-type mice (wild-type mice: 4.0 ± 0.5 μmol/g weight; GIPR$^{-/-}$ mice 4.6 ± 0.7, P = NS; Fig. 2B).

3.3. Small intestinal transit after intraperitoneal administration of GIP

Intestinal transit rate was measured by the length of small intestine traversed by the charcoal suspension. In wild-type mice, the intestinal transit rate in GIP-administered mice was significantly less than that in saline-administered control (45 ± 8% vs. 68 ± 4%, $P < 0.01$; Fig. 3A). On the other hand, in GIPR$^{-/-}$ mice, the intestinal transit rate was similar to that in saline-administered control and GIP-administered mice (65 ± 3% vs. 63 ± 4%; Fig. 3B).

3.4. Perfusion and intestinal transit in GLP-1 receptor-deficient mice

To determine whether GIP affects intestinal glucose absorption through GLP-1 signaling, inhibition of glucose absorption by GIP was measured in GLP-1R$^{-/-}$ mice. Inhibition of glucose absorption in GLP-1R$^{-/-}$ mice was 44 ± 100 nmol/cm/15 min in saline-administered control mice and 426 ± 104 nmol/cm/15 min in GIP-administered mice (50 nmol/kg body weight, $P < 0.05$, Fig. 3C). Thus, GIP significantly inhibited glucose absorption in GLP-1R$^{-/-}$ mice.

The intestinal transit rate was also evaluated in GLP-1R$^{-/-}$ mice, and was 59 ± 13% in saline-administered control and 42 ± 7% in GIP-administered mice, respectively. Thus, GIP significantly inhibited the intestinal transit rate in GLP-1R$^{-/-}$ mice ($P < 0.01$, Fig. 3D). Consequently, the genetic disruption of GLP-1 receptor did not affect GIP action on intestinal glucose absorption and intestinal transit.

3.5. Involvement of SST in the action of GIP

To determine whether the inhibitory effect of GIP on intestinal transit is due to release of SST, a somatostatin receptor antagonist, CSS (1 μg/kg body weight), was intraperitoneally administered 10 min prior to GIP administration in wild-type mice (Fig. 4A). In the presence of CSS, the intestinal transit rate in GIP-administered wild-type mice was significantly higher than that in the absence of CSS (60 ± 3% vs. 45 ± 8%; $P < 0.01$). Accordingly, CSS reduced the inhibitory effect of GIP on intestinal transit. Moreover, intraperitoneally-administered SST itself significantly inhibited the intestinal transit rate in wild-type mice compared to control (SST: 37 ± 5% vs. control: 68 ± 4%, $P \leqslant 0.01$).

In a perfusion experiment, to confirm that the inhibitory effect of GIP on intestinal glucose absorption is attributable to release of SST, CSS (1 μg/kg body weight) was intraperitoneally administered 10 min prior to GIP administration in wild-type mice (Fig. 4B). In

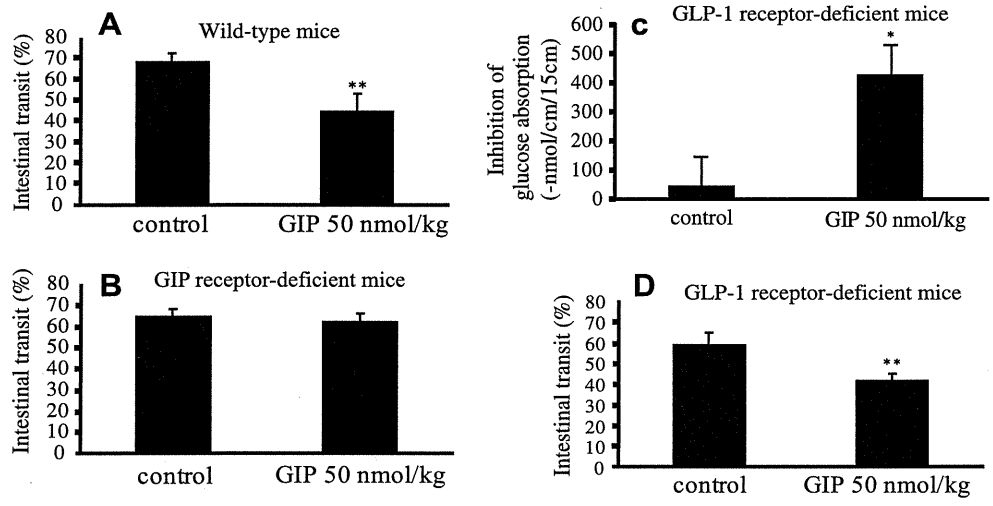

Fig. 3. Intestinal transit after oral administration of non-absorbed marker (10% charcoal suspension in 5% gum Arabic) in wild-type (A) and GIPR$^{-/-}$ (B) mice. Twenty minutes after administration of non-absorbed marker by gavage, the animals were killed and the entire gastrointestinal transit tract was removed. GIP (50 nmol/kg body weight) or saline was administered intraperitoneally 15 min prior to the administration of non-absorbed marker. Data are shown as means with SEM ($n = 6$ for each group). Statistical significance was determined using Student's t-test. $^{**}P < 0.01$ compared with control. (C) Inhibition of glucose absorption in GLP-1R$^{-/-}$ mice with or without intraperitoneal GIP administration as indicated in the legends of Fig 1. (D) Intestinal transit after oral administration of non-absorbed marker in GLP-1R$^{-/-}$ mice with or without intraperitoneal GIP administration as indicated in the legends of Fig 3A. Data are shown as means with SEM ($n = 6$ for each group). Statistical significance was determined using Student's t-test. $^{*}P < 0.05$ compared with control.

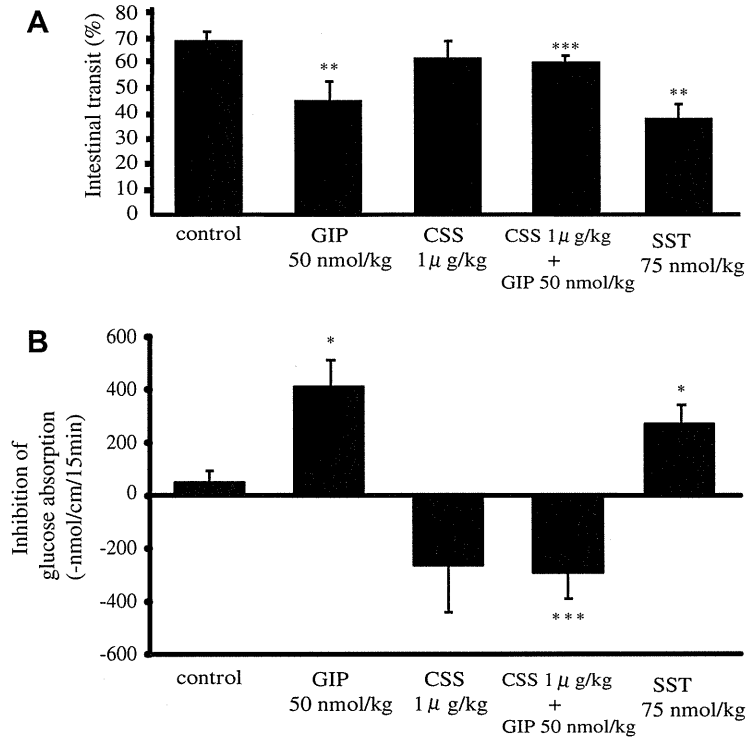

Fig. 4. (A) Intestinal transit after oral administration of non-absorbed marker in wild-type mice with or without pretreatment of CSS. The rate of transit was determined as indicated in the legend of Fig 3A. GIP or SST or saline was administered intraperitoneally 15 min prior to the administration of non-absorbed marker. CSS or saline was intraperitoneally administered 10 min prior to GIP administration. Data are shown as means with SEM ($n = 6$ for each group). Statistical significance was determined using Student's t-test. $^{**}P < 0.01$ compared with control. $^{***}P < 0.01$ compared with GIP alone administered mice. (B) Inhibition of glucose absorption by GIP in wild-type mice with or without pretreatment of CSS, and inhibition of glucose absorption by SST. CSS or saline was intraperitoneally administered 10 min prior to GIP administration. Data are shown as means with SEM ($n = 6$ for each group). Statistical significance was determined using Student's t-test. $^{*}P < 0.05$ compared with control. $^{***}P < 0.01$ compared with GIP alone administered mice.

the presence of CSS, the inhibition of glucose absorption in GIP-administered wild-type mice was significantly lower than that in the absence of CSS (410 ± 96 nmol/cm/15 min vs. −290 ± 99 nmol/cm/15 min; $P < 0.01$). Accordingly, CSS reduced the inhibitory effect of GIP on intestinal glucose absorption. Furthermore, inhibition of glucose absorption in wild-type mice was 49 ± 44 nmol/cm/15 min in saline-administered control mice and 278 ± 63 nmol/cm/15 min in SST-administered mice (75 nmol/kg body weight, $P < 0.05$).

In an experiment of glucose uptake in everted jejunal ring, 100 nM SST did not alter glucose uptake compared to control (control: 4.2 ± 0.9 μmol/g weight; SST: 4.2 ± 0.4, $n = 8$; P = NS).

3.6. Measurement of plasma GIP and SST levels

The plasma levels of total GIP and SST in mice were significantly enhanced 20 min after the intraperitoneal GIP-administration at a dosage of 50 nmol/kg body weight compared to the respective basal levels (GIP: 58 ± 5 pg/ml vs. 3400 ± 257 pg/ml, $n = 8$; $P < 0.01$; SST: 9.9 ± 0.5 ng/ml vs.11.9 ± 0.3 ng/ml, $n = 8$; $P < 0.05$).

4. Discussion

We investigated the inhibitory effect of exogenous GIP on glucose absorption in small intestine. GIP has been known as an important insulinotropic hormone released from duodenal K cells. However, there have been few reports on the effects of GIP on intestinal glucose absorption. In this study, GIP was found to inhibit glucose absorption in a concentration-dependent manner by the perfusion method.

Glucose absorption includes two steps in enterocytes, permeation through brush-border membrane and subsequently through basolateral membrane. Glucose and galactose cross the brush-border membrane by means of SGLT-1, which is a rate-limiting step of glucose absorption [10]. Recent *in vitro* study by Singh et al. found that exogenous GIP stimulates SGLT-dependent glucose absorption by using an Ussing chamber experiment [11]. In the experiment, intestine was fixed between two chambers, and short-circuit-current representing SGLT activity was measured. However, in our experiments using everted jejunal rings, which is another method to measure SGLT-dependent glucose absorption *in vitro*, the lack of effect of exogenous GIP on SGLT-dependent glucose uptake was shown, and genetic disruption of the GIP receptor was found not to affect SGLT-dependent glucose absorption. The reason why our results and theirs are different is unknown, but may be attributable to difference in method.

It is generally accepted that there is a positive relationship between intestinal motility and absorption [4,5]. It has been shown that increased intestinal motility, besides enhancing the functional surface area, facilitates diffusion of glucose to the transporters of the brush-border membrane by altering the unstirred water layer [12,13]. We investigated the effect of GIP on motility of small intestine by evaluating intestinal transit. In this study, GIP was found to inhibit intestinal transit compared to control in wild-type but not in $GIPR^{-/-}$ mice. Thus, the inhibitory effect of GIP on glucose absorption may be attributable, in part, to inhibition of intestinal motility.

GLP-1, another incretin hormone, is secreted from L cells found predominantly in ileal mucosa, and is known to be part of the "ileal brake" that acts as an inhibitor of upper gastrointestinal motility

[14]. In this study, GIP was found to inhibit intestinal transit in GLP-1R$^{-/-}$ mice as well as in wild-type mice, indicating that the inhibitory action of GIP on gastrointestinal transit is not mediated by GLP-1. Furthermore, glucose absorption was found to be inhibited significantly by GIP in GLP-1R$^{-/-}$ mice as well as in wild-type mice, suggesting that the primary mechanism of the inhibition of intestinal glucose absorption by GIP most likely does not involve the GLP-1-mediated pathway.

Recently, Miki et al. reported that GLP-1 inhibited gut motility while GIP did not [15]. In this study, however, GIP was found to inhibit intestinal transit. The inconsistency could be due to their use of a non-absorbed marker containing a high concentration (as much as 50%) of glucose to evaluate gut motility, whereas we used a non-absorbed marker without glucose. Intraduodenal infusion of hyperosmolar solution was reported to increase duodenal motility, which is mediated by activation of osmoreceptors in duodenum [16]. In our preliminary experiment on small intestinal transit using 10% charcoal suspension in 5% gum Arabic with 50% glucose, the intestinal transit rate was significantly greater than that when using glucose-free solution (88 ± 8% vs. 68 ± 4%, $P < 0.05$, unpublished data). Therefore, intestinal transit might be enhanced by the high concentration of glucose itself in the suspension, which could conceal a GIP-evoked inhibitory effect on intestinal transit. However, limitations of this study must be considered. While GIP was found to inhibit intestinal transit under the conditions of this study, the effect of GIP on intestinal transit may differ among the constituents of the food or nutrient. Further investigations are required.

Regarding the GIP dosage applied in the *in vivo* experiments, low GIP dosage has been used when applied by the route of continuous intravenous administration; GIP (0.25 nmol/kg body weight) was reported to stimulate insulin secretion by intravenous administration in rat [17] and (GIP 4 pmol/kg body weight/min) in human [18]. However, high GIP dosage has been used when applied by the other routes of administration than intravenous administration. Indeed, one group has reported that subcutaneous pre-administration of 100 μg GIP (approximately 800 nmol/kg body weight) lowered glucose excursion in oral glucose tolerance test in mice [15] and another group has reported that intraperitoneal administration of [D-Ala^2]GIP (48 nmol/kg body weight/day), a DPP4-resistant analogue, lowered glucose excursion in intraperitoneal glucose tolerance test in mice [19]. In this study, we applied GIP intraperitoneally at a dosage of 50 nmol/kg body weight to demonstrate the pharmacological effects of GIP on intestinal transit and glucose absorption, which dosage is comparable to those used in the latter reports.

Regarding the mechanism of inhibition of intestinal transit by GIP, SST secretion has been reported to be stimulated by GIP [20–22] and to prolong intestinal transit [23,24]. The SST receptor has five isoforms (sst1-5) and all five receptors have been shown to be expressed in gastrointestinal tract, with high levels of sst2 receptor in intestine [25]. The sst2 receptors in intestine have been shown not to be expressed on enterocytes or muscle cells, but on myenteric and submucosal plexuses and on neuroendocrine cells in epithelium [26] and also on interstitial cells of Cajal in deep muscular plexus [27]. Thus, the mechanisms by which exogenous GIP inhibits intestinal motility through two SST-mediated pathways may be as follows. In the first, exogenous GIP binds to the GIP receptors on the cell surface membrane in SST-containing enteric neurons and/or in mucosal endocrine cells of D cells in gastrointestinal tract and/or in pancreatic islets, resulting in the release of SST. Subsequently, the released SST acts as a neurotransmitter and binds to sst2 receptors expressed on other neurons in myenteric plexus, parts of which nerve fibers are distributed to muscular cells, permitting inhibition of intestinal motility. In this pathway, the local SST concentration in interneural synaptic space may be increased prominently. In an alternate pathway, SST secreted from D cells flows into systemic circulation through submucosal vessels to reach the neurons in myenteric plexus. Indeed, in this study, intraperitoneally-administered GIP induced a small but significant increase in plasma SST levels, suggesting involvement of the latter pathway.

In our experiment of intestinal perfusion, GIP was found to inhibit intestinal glucose absorption primarily by reducing intestinal motility. On the other hand, the tissue of everted intestinal ring is set inside-out and distended far from the physiological condition, and thus incapable of reflecting general intestinal motility. Thus, the lack of GIP action on glucose uptake in the tissues of everted intestinal ring in this study may be expected.

Several studies have found that the inhibitory effect of SST on intestinal glucose absorption may be attributable to either the effect of SST on the splanchnic hemodynamics [28] or a direct effect of SST on enterocytes [29]. However, consistent with this study, another study has found that SST delays intestinal glucose absorption by its inhibitory effect on intestinal motility [24]. SST exerts its inhibitory effect on intestinal glucose absorption by several mechanisms; our results indicate that the inhibitory effect of SST is mediated, at least in part, by alteration of intestinal motility.

In this study, the somatostatin receptor antagonist CSS was found to reduce the inhibitory effect of GIP on intestinal transit, suggesting that GIP stimulates SST release. In addition, we show that SST itself inhibits intestinal transit and glucose absorption in perfused intestine. Consistently, a recent study has reported that SST inhibits intestinal glucose absorption [29]. Considered together with previous reports, we conclude that exogenous GIP inhibits intestinal transit and glucose absorption indirectly through a somatostatin-mediated pathway.

One of the physiological roles of GIP is known to be facilitation of nutrient uptake into adipose tissue and bone. In this study, exogenous GIP was found to inhibit intestinal glucose absorption by reducing intestinal motility. Since this observation was obtained by the action of a supraphysiological level of plasma GIP, it is unclear whether or not the action is associated with already known physiological actions of GIP. In the point of delay of intestinal carbohydrate absorption, however, the biological action of GIP found in this study appears to be similar to that of medical medicine α-glucosidase inhibitor, which does not influence the regulation of energy accumulation in adipose tissue or bone.

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GCKR mutations in Japanese families with clustered type 2 diabetes

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ABSTRACT

Objective: The aim was to investigate the genetic background of familial clustering of type 2 diabetes.
Subjects and methods: We recruited Japanese families with a 3-generation history of diabetes. Genome-wide linkage analysis was performed assuming an autosomal dominant model. Genes in the linkage region were computationally prioritized using Endeavour. We sequenced the candidate genes, and the frequencies of detected nucleotide changes were then examined in normoglycemic controls.
Results: To exclude known genetic factors, we sequenced 6 maturity onset diabetes of the young (MODY) genes in 10 familial cases. Because we detected a MODY3 mutation *HNF1A* R583G in one case, we excluded this case from further investigation. Linkage analysis revealed a significant linkage region on 2p25-22 (LOD score = 3.47) for 4 families. The 23.6-Mb linkage region contained 106 genes. Those genes were scored by computational prioritization. Eleven genes, i.e., top 10% of 106 genes, were selected and considered primary candidates. Considering their functions, we eliminated 3 well characterized genes and finally sequenced 8 genes. *GCKR* ranked highly in the computational prioritization. Mutations (minor allele frequency less than 1%) in exons and the promoter of *GCKR* were found in index cases of the families (3 of 18 alleles) more frequently than in controls (0 of 36 alleles, P = 0.033). In one pedigree with 9 affected members, the mutation *GCKR* g.6859C>G was concordant with affection status. No mutation in other 7 genes that ranked highly in the prioritization was concordant with affection status in families.
Conclusions: We propose that *GCKR* is a susceptibility gene in Japanese families with clustered diabetes. The family based approach seems to be complementary with a large population study.

1. Introduction

The national survey in 2007 reported that 8.9 million people suffer from diabetes in Japan [1]. Most of these have type 2 diabetes, and the number of such patients has increased continuously. Both genetic and environmental factors play important roles in the pathogenesis of type 2 diabetes [2].

To elucidate the genetic factors underlying the pathogenesis of type 2 diabetes in the Japanese population, several genome-wide linkage analyses in Japanese sib-pairs have been performed [3–5]. Linkage to 11p13–p12 is consistently implicated in these studies [5]. Recent successes with genome-wide association analyses in the Japanese population have revealed a susceptibility variant in *KCNQ1* located at 11p15.5 [6,7], a locus not far from the region suggested in linkage analyses. The association of susceptibility loci including *TCF7L2*, *CDKAL1*, *CDKN2A/B*, *IGF2BP2*, *SLC30A8*, and *HHEX* with diabetes has been established in Caucasian populations and replicated in the Japanese population [8]. However, the loci identified in association studies have uniformly small effect sizes, and can explain only a small portion of the genetic background of diabetes in the Japanese population. Approaches other than sib-pair linkage analyses and association analyses may therefore be required to elucidate a greater aspect of the genetic background of type 2 diabetes.

In the present study, we used a family-based approach, because high degrees of familial clustering can raise the relative risk and provide better insight to novel loci of larger effect size [9]. Familial clustering of diabetes is well known, the typical example being MODY [10]. On the other hand, in most families in Japan, familial clustering cannot be attributed to mutations of the 6 known MODY genes [10], and genetic predisposition in such families has not been ascertained.

We recruited families having a 3-generation history of diabetes and performed genome-wide linkage analysis. We selected candidate genes in the linked chromosomal region and searched for rare and

Abbreviations: GAD, glutamic acid decarboxylase; GCKR, glucokinase regulator; HLOD, heterogeneity logarithm of the odds; HNF4α, Hepatocyte Nuclear Factor 4α; LOD, logarithm of the odds; MAF, minor allele frequency; MODY, maturity onset diabetes of the young; RFLP, restriction fragment length polymorphism; SNP, single nucleotide polymorphism.

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common nucleotide changes in the genes in familial cases and unaffected controls.

2. Material and methods

2.1. Families and additional index cases

We recruited patients from collaborating hospitals in Japan who had diabetes with a 3-generation family history, which is suggestive of autosomal dominant mode of inheritance [11]. If ≥2 family members with diabetes were alive and donated DNA, the families were regarded as suitable subjects for the present study. Families including members with positive GAD (glutamic acid decarboxylase) antibody were excluded from the study. Four families met these criteria and were included in the linkage analysis (Fig. 1). Affected status of the participants was determined in two ways. First, if participants had been diagnosed with diabetes and treated with oral hypoglycemic agents or insulin injection, they were regarded as affected. Second, if participants had not been treated with oral hypoglycemic agents or insulin injection, they underwent HbA1c (Hemoglobin A_{1c}) measurement for screening of impaired glucose tolerance. The value for HbA1c is estimated as an NGSP (US National Glycohemoglobin Standardization Program) equivalent value (%) calculated by the formula HbA1c (%) = HbA1c (JDS, Japanese Diabetes Society) (%) + 0.4%, considering the relational expression of HbA1c (JDS)(%) measured by the previous Japanese standard substance and measurement methods and HbA1c (NGSP) [12]. If their HbA1c levels were ≥6.0%, they were also regarded as affected. HbA1c ≥6.0% is the level defined as possible diabetes mellitus in the 2007 survey of the Ministry of Labor, Health and Welfare of Japan [1]. In addition to these subjects, 6 index cases from other families with a 3-generation history of diabetes were included in the study (Supplementary Fig. 1). In these families, although we confirmed the affected status of some of the family members, DNA samples were available only for the index cases but not for other family members. Together with the 4 index cases from the families included in the linkage analysis, a total of 10 unrelated cases with a 3-generation history of diabetes were available for DNA sequencing. The clinical features of family members and additional index cases are shown in Table 1.

2.2. Normoglycemic controls

An annual medical check-up program was performed in Nyukawa district of Takayama City, Japan. Nine-hundred ninety local residents (430 men, 560 women) were recruited in the program and consented to donate their DNA. From 2002 to 2007, participants underwent physical examination and blood tests including fasting plasma glucose and HbA1c every year. We selected normoglycemic controls from the

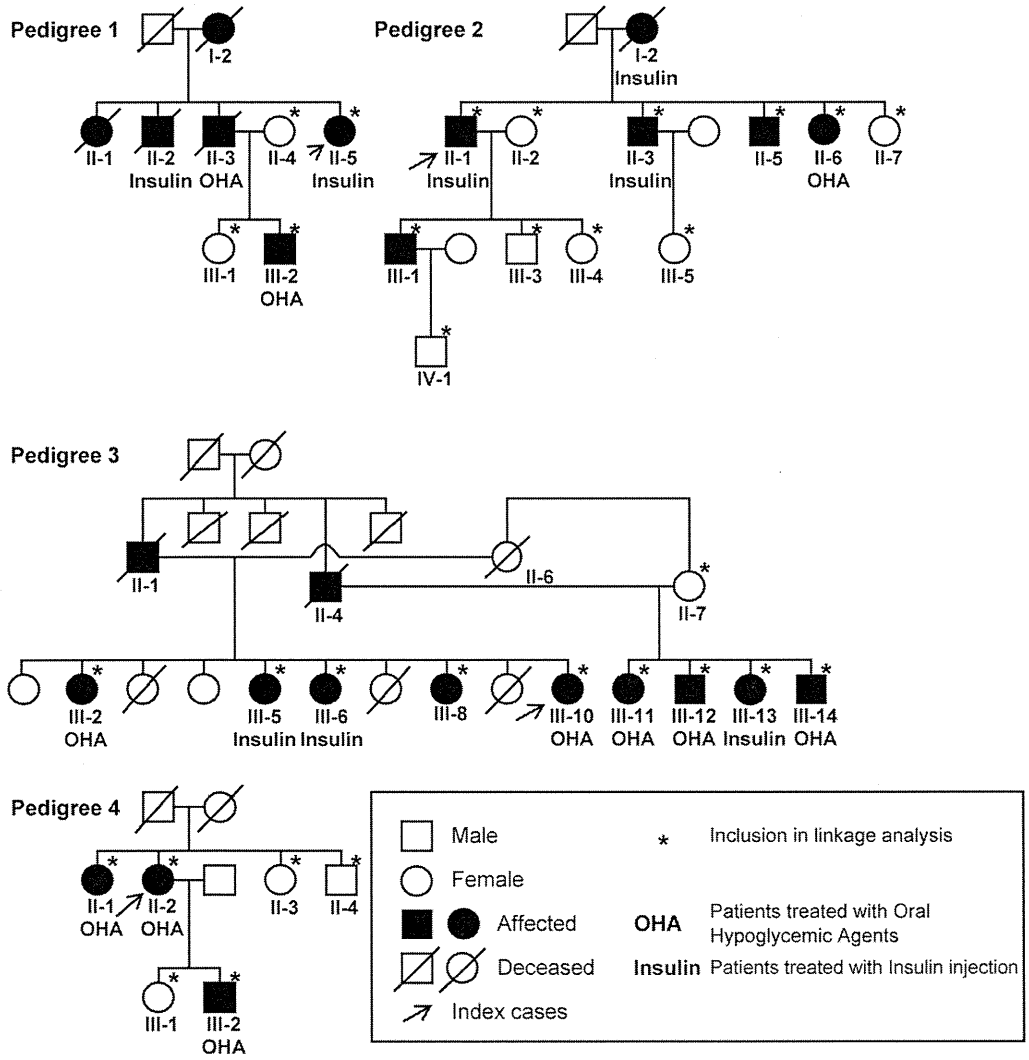

Fig. 1. Four pedigrees with familial aggregated diabetes mellitus.

Table 1
Characteristics of family members and additional index cases.

	ID	Current age	Sex	BMI	HbA1c (%)	Age when diagnosed (diagnosis)	Current therapy
Pedigree 1	II-4	70	F	16.2	5.0		
	II-5	71	F	22.5	10.6	60 (DM)	Insulin 66 U/d
	III-1	40	F	21.9	5.4		
	III-2	37	M	26.0	6.9	20 (DM)	Insulin
Pedigree 2	II-1	79	M	19.2	7.5	50 (DM)	Insulin 25 U/d
	II-2	77	F	18.6	5.6		
	II-3	76	M	17.9	7.2	45 (DM)	Insulin
	II-5	74	M	18.2	6.0	64 (IGT)	Diet
	II-6	71	F	18.4	6.6	N/A (DM)	Oral drug
	II-7	68	F	19.9	5.9		
	III-1	53	M	24.2	6.0	53 (IGT)	Diet
	III-3	51	M	20.4	5.6		
	III-4	47	F	19.3	5.2		
	III-5	46	F	19.6	4.9		
	IV-1	23	M	19.9	5.6		
Pedigree 3	II-7	92	F	22.3	5.9		
	III-2	77	F	23.9	9.3	30 (DM)	Oral drug
	III-5	72	F	22.0	8.1	60 (DM)	Insulin 16 U/d
	III-6	69	F	19.8	8.0	65 (DM)	Insulin 16 U/d
	III-8	66	F	19.1	6.5	64 (IGT)	Diet
	III-10	59	F	19.3	10.2	57 (DM)	Oral drug
	III-11	67	F	20.4	6.9	62 (DM)	Oral drug
	III-12	66	M	21.1	N/A	57 (DM)	Oral drug
	III-13	64	F	20.0	6.6	25 (DM)	Insulin
	III-14	62	M	20.2	10.3	50 (DM)	Oral drug
Pedigree 4	II-1	76	F	28.2	6.7	60 (DM)	Oral drug
	II-2	73	F	25.1	6.4	50 (DM)	Oral drug
	II-3	67	F	19.0	5.5		
	II-4	64	M	N/A	5.4		
	III-1	52	F	20.4	5.3		
	III-2	50	M	20.8	6.2	35 (DM)	Oral drug
Additional index cases	1	57	M	25.7	7.1	30 (DM)	Oral drug
	2	47	F	22.9	10.0	36 (DM)	Insulin 20 U/d
	3	68	F	19.7	7.1	45 (DM)	Insulin 19 U/d
	4	60	F	24.7	10.4	40 (DM)	Insulin 51 U/d
	5	60	F	28.0	9.7	50 (DM)	Insulin 8 U/d
	6	54	F	34.5	9.1	40 (DM)	Insulin

BMI: body mass index, DM: diabetes mellitus, IGT: impaired glucose tolerance.

participants in the cohort. Subjects defined as normoglycemic controls had the following characteristics: HbA1c <6.0% and fasting plasma glucose <5.5 mmol/l during 5-year follow-up span, and age ≥55. The number of subjects that satisfied the definition was 206 (81 men, 125 women).

2.3. Genotyping family members

Genomic DNA was extracted from blood samples with a QIAamp DNA Blood Mini Kit (Qiagen Inc). PCR amplification from genomic DNA was performed with fluorescence-labeled (6-FAM, HEX, NED) and tailed primers. PCR primers to analyze microsatellite markers comprised an approximately 10 cM human index map (ABI Prism Linkage Mapping Set Version 2.5: 382 markers for 22 autosomes), and other microsatellite fine markers were designed according to information from the UniSTS map. PCR reactions were carried out in 7.5 μl with 50 ng genomic DNA, using AmpliTaq Gold DNA Polymerase (Applied Biosystems) in a 2-step amplification program. DNA fragments were analyzed on an Applied Biosystems 3130 Genetic Analyzer. Genotyping errors and inconsistent relationships were checked with the use of GENEHUNTER (version 2.1) software [13]. If the results of genotyping were missed or ambiguous, we treated them as an unknown genotype in the linkage analysis. The rate of genotyping failure was 0.057% (7/11842).

2.4. Linkage and haplotype analyses

Both affected and unaffected family members were included in the linkage analysis. Participants with HbA1c level <6.0% were considered unaffected if the age was ≥55 and unknown if the age was <55, considering the assumed age-dependent penetrance of diabetes. The purpose of including members assigned as unknown was to increase the accuracy of haplotype estimation in affected members, although inclusion did not increase the statistical power. Multipoint parametric analyses for autosomes were run using GENEHUNTER assuming an autosomal dominant model [13]. Because locus heterogeneity could be associated with diabetes, LOD (log of the odds) score and HLOD (heterogeneity LOD) score were calculated. The disease allele frequency was set at 0.00001 and a phenocopy frequency of 0.00001 was assumed. Population allele frequencies for each microsatellite marker were assigned equal portions for individual alleles. We used a 2-stage design: first, all chromosomal regions were screened by genotyping at an approximately 10 cM density (screening), and the regions where LOD scores were highest were considered potentially interesting. Second, these regions were further finely mapped at approximately 1- to 2-cM densities (fine mapping). Regions where LOD scores were above 3.3, a level corresponding to genome-wide significance [9], were considered linkage regions. Haplotypes were constructed with the GENEHUNTER program.

2.5. Prioritization of candidate genes

The 23.6-Mb linkage region on chromosome 2p25-22 contained 106 genes annotated in Ensemble genome browser (http://www.ensembl.org). The genes were computationally prioritized using Endeavour (http://www.esat.kuleuven.be/endeavour/) [14]. We selected 6 MODY genes (*HNF4A*, *GCK*, *HNF1A*, *PDX1*, *HNF1B*, and *NEUROD1*) as training genes because a dominant mode of inheritance

was assumed in the highly clustered families in linkage analysis. We adopted all databases available in Endeavour, which prioritized glucokinase regulator (*GCKR*) at the first rank.

2.6. Sequencing

We directly sequenced the coding exons of 6 MODY genes (*HNF4A*, *GCK*, *HNF1A*, *PDX1*, *HNF1B*, and *NEUROD1*) in the 10 index cases. We sequenced *GCKR* including all exons found in the National Center for Biotechnology Information (NCBI) Evidence Viewer (http://www.ncbi.nlm.nih.gov) and the 2-kb promoter region in the index cases from families and in control subjects. We also selected other 7 genes that are highly prioritized within the 11th rank (10.3%) in the linkage region using Endeavour excluding 3 genes with known metabolic functions unrelated to glucose metabolism (Supplementary Table 1). We sequenced the entire coding exons of the 7 genes in the index cases from families included in the linkage analysis. Forward and reverse PCR primers for each exon were selected in an intronic sequence 50 bp away from the intron/exon boundaries and primers to amplify the *GCKR* promoter region were also selected. Sequencing primer data for *GCKR* is shown in Supplementary Table 2. PCR products were run on 2% agarose gel, and the appropriate bands were excised and then purified with the use of the QIAquick Gel Extraction Kit (Qiagen). Sequencing results were analyzed on an ABI Prism 3130 Avant DNA sequencer (Applied Biosystems). Any nucleotide changes identified in sequencing were searched for SNPs (single nucleotide polymorphisms) in the dbSNP database (http://www.ncbi.nlm.nih.gov/SNP/).

2.7. Genotyping SNPs

If minor allele frequencies (MAF) of nucleotide changes identified in sequencing were unregistered in the HapMap JPT database on dbSNP as of April 2010 and the minor allele appeared in <2 of all subjects, MAF was determined in the expanded population. We defined mutation as MAF <1% [15]. To determine whether each nucleotide change was a mutation or not, we genotyped 105 normoglycemic controls randomly selected from the cohort (Supplementary Table 3), because genotyping of 210 normal chromosomes is necessary to achieve 80% power to detect a polymorphism present in 1% of the population [16]. The PCR-RFLP (restriction fragment length polymorphism) method for *HNF1A* R583G, *GCKR* g.-689G>A, *GCKR* g.-299G>A, *GCKR* E252K and *FOSL2* R198H and Taqman method for *GCKR* g.6859C>G were used.

2.8. Statistical analysis

Frequencies of mutations (MAF<1%) and common nucleotide changes (MAF≥1%) identified in *GCKR* sequencing in the index cases and in normoglycemic controls were compared by the Fisher exact test with SAS software (version 8.2).

2.9. Ethics

The methods used in this study were approved by the Ethics Committee of the Kyoto University Institutional Review Board, and approved written informed consent was obtained from each participant.

3. Results

3.1. Characteristics of family members

Four families with a 3-generation history of diabetes were enrolled in this study (Fig. 1, Table 1). Every family included no less than 1 member that had been diagnosed with diabetes before the age of 50. Sixteen members (6 men, 10 women) had previously been diagnosed with diabetes. Thirteen out of the 16 members with diabetes were lean (BMI<25). Six members were treated with insulin and another 10 members were treated with oral hypoglycemic agents. Twelve family members who had not been diagnosed with diabetes underwent HbA1c measurement and 3 of them had HbA1c level ≥6.0%. These 3 members had already been diagnosed with impaired glucose tolerance before this study and were included as affected members in the study.

3.2. Exclusion of MODY gene mutations in the index cases

For the 10 index cases, we performed direct sequencing in entire coding exons of the MODY genes. The detected missense SNPs were *HNF1A* I27L (rs1169288), *HNF1A* S487N (rs2464196), *HNF1A* R583G, and *HNF4A* T117I (rs1800961) (Supplementary Table 4). *HNF1A* R583G is a mutation that is reported to cause MODY [17], thus we excluded the carrier of the mutation (additional index case #6, Table 1) from further investigation. *HNF1A* I27L and *HNF1A* S487N are common in the general population (MAF = 0.386 and 0.341, respectively in HapMap-JPT). *HNF4A* T117I was associated with late-onset type 2 diabetes but it was not the cause of MODY in a previous report [18].

3.3. Linkage analysis

A total of 30 members (19 affected members) from 4 families were included in the linkage analysis, assuming an autosomal dominant model. The genome-wide linkage results in the screening are shown in Fig. 2. Regions of potential interest by multipoint LOD and HLOD scores were observed on chromosomes 2p24 and 7q34. After fine mapping, 2p25-22 was revealed to be a significant linkage region (Fig. 3, LOD and HLOD = 3.47) while the region on 7q34 was discarded. The size of the region with positive HLOD score was 23.6 Mb (D2S2199–D2S2230). In the region, a haplotype segregated in affected and unaffected members in the pedigrees 1, 2, and 3, but not in the pedigree 4.

3.4. Candidate genes

We searched candidate genes in the implicated linkage region by applying a gene prioritization approach implemented in Endeavour software. We selected 6 MODY genes as training genes. The 2 top-ranked genes were glucokinase regulatory protein (*GCKR*) and nuclear receptor coactivator 1 (*NCOA1*). *GCKR* ranked high in prioritization using gene–gene interaction databases (first rank in 5 out of 7 interaction databases), mainly because the interaction of glucokinase and glucokinase regulatory protein has been demonstrated in previous studies [19,20]. *NCOA1* also ranked high in prioritization using gene–gene interaction databases (second rank in 2 out of 7 interaction databases), because nuclear receptor coactivator 1 has been reported to interact with HNF4α (Hepatocyte Nuclear Factor 4α) as a coactivator [21]. Together with *GCKR* and *NCOA1*, genes that are highly prioritized within the 11th rank (10.3% of annotated genes) were considered candidate genes except 3 genes with well-characterized metabolic functions unrelated to glucose metabolism (Supplementary Table 1).

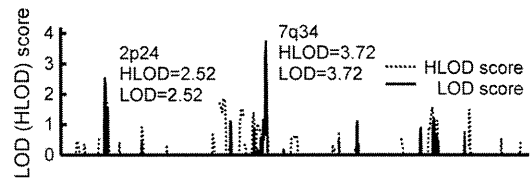

Fig. 2. Multipoint HLOD and LOD scores in genome-wide linkage analysis for 4 pedigrees.

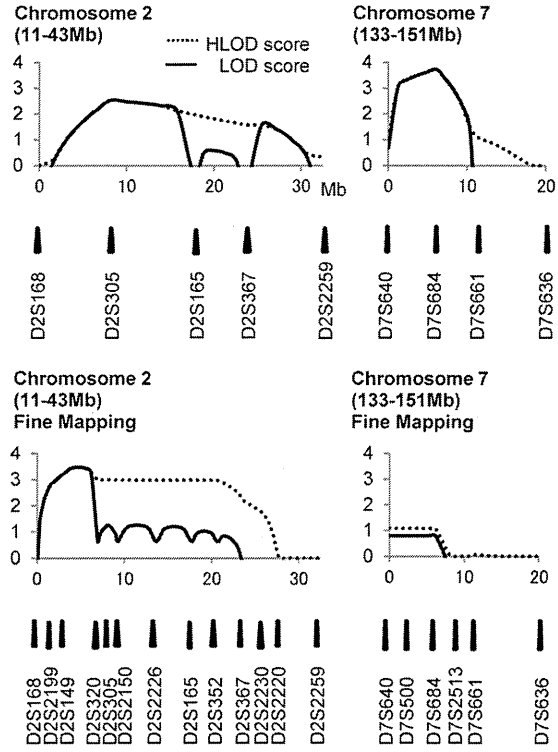

Fig. 3. Multipoint HLOD and LOD scores in fine mapping of D2S168–D2S2259 and D7S640–D7S636.

3.5. Direct sequencing in GCKR and other candidate genes

We performed direct sequencing in exons and the 2-kb promoter region of *GCKR*. Sequencing was performed in 9 index cases from families and in 18 normoglycemic controls in parallel. The 18 control subjects were randomly selected from 206 normoglycemic controls (Supplementary Table 3). Detected sequence changes in the 9 index cases and 18 controls are shown in Table 2. Five nucleotide changes (g.-959 Insertion AATGTTG, E66E, E77G, g.9709G>A, and L446P) were considered to be common variants, because the minor allele was found in not less than 2 subjects out of a total of 27 case and control subjects. To determine whether or not each of the other nucleotide changes (g.-689G>A, g.-299G>A, E252K and g.6859C>G) was a mutation (MAF<1%), genotyping was performed in a total of 105 normoglycemic controls. g.-689G>A, g.-299G>A and g.6859C>G were not detected in the 105 controls, and were regarded as mutations, while E252K was detected in 4 controls out of 105 (MAF = 1.9%) and was regarded as a common change. The number of alleles having mutations was thus significantly larger in the index cases from families than in the controls (3/18 alleles vs. 0/36 alleles, P = 0.033, Fisher exact test).

We performed direct sequencing in the entire coding exons of other 7 candidate genes in index cases from 4 families. One misssense mutation *FOSL2* R198H (MAF = 0.004 in normoglycemic controls) was detected. No other mutations were detected in other 6 genes (Supplementary Table 5).

3.6. Segregation of the mutations with the phenotype in pedigrees

In index cases from the 4 families included in the linkage analysis, 3 sequence changes of *GCKR* were detected (g.-959 Insertion AATGTTG, g.6859C>G and L446P). We tested the segregation of *GCKR* g.6859C>G, a mutation detected in pedigree 3, with the phenotype in the pedigree. Another 2 changes (*GCKR* g.-959 Insertion AATGTG and *GCKR* L446P) were commonly detected in controls (3/36 alleles and 11/36 alleles respectively). In pedigree 3, *GCKR* g.6859C>G was detected in all 9 affected members, but was not detected in the unaffected member (II-7). We performed linkage analysis and haplotype construction in 2p25-22 using the *GCKR* g.6859 genotype together with the microsatellite markers. The parametric multipoint LOD score for pedigree 3 was 2.67 at the *GCKR* g.6859 locus. Haplotype analysis revealed that all affected individuals in pedigree 3 shared a disease haplotype within D2S2199–D2S2230, which includes *GCKR* g.6859G (Fig. 4). In pedigree 3, another sequence change, *GCKR* L446P, was detected, but *GCKR* L446P did not co-segregate with the disease. Haplotype analysis revealed that the minor allele of *GCKR* L446P (g.11169C) resided on a different haplotype than *GCKR* g.6859G in affected subjects III-11, 12, 13, 14 (Fig. 4).

We tested the segregation of *FOSL2* R198H, a mutation detected in pedigree 4, with the phenotype. *FOSL2* R198H was detected in 2 affected subjects (II-2, II-22) but not detected in one subject (II-1).

4. Discussion and conclusions

Recent progress in genome-wide association studies has identified tens of type 2 diabetes susceptibility genes. Even so, only a small

Table 2
Mutations and common nucleotide changes in exons and the promoter of *GCKR* in 9 index cases in families and in 18 controls.

Position	Change	Description	Effect	Detected number of alleles				p^a	Minor allele frequency [MAF]
				Index cases from families (n = 9)		Controls (n = 18)			
				Major	Minor	Major	Minor		
Mutations (MAF<1%)									
Promoter	g.-689G>A			17	1	36	0	0.33	0.000[b]
Promoter	g.-299G>A			17	1	36	0	0.33	0.000[b]
Exon 9	g.6859C>G	Noncoding exon		17	1	36	0	0.33	0.000[b]
Total				15	3	36	0	0.033	
Common changes									
Promoter	g.-959 insAATGTTG			16	2	33	3	1.00	N/D
Exon 2	g.468G>A	Synonymous	E66E	17	1	35	1	1.00	N/D
Exon 3	g.671A>G	Missense	E77G	17	1	33	3	1.00	0.024[c]
Exon 10	g.8817G>A	Missense	E252K	18	0	35	1	1.00	0.019[b]
Exon 11	g.9709G>A	Noncoding exon		17	1	33	3	1.00	0.123[c]
Exon 14	g.11169T>C	Missense	L446P	8	10	25	11	0.087	0.467[c]

GenBank accession no. NT_022184.15.
[a] Fisher exact test.
[b] Frequency in 105 normoglycemic controls.
[c] Frequency in HapMap-JPT.

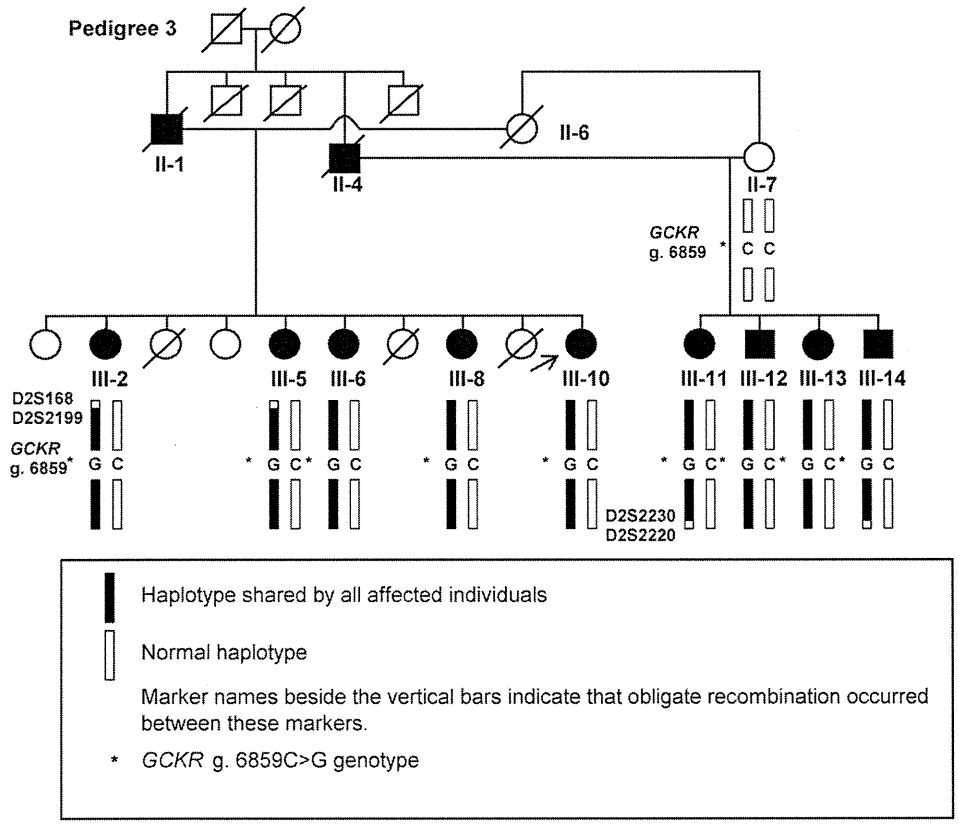

Fig. 4. Haplotype analysis in the D2S168–D2S2259 region and the *GCKR* g.6859C>G genotype for pedigree 3.

portion of the genetic background of diabetes has been explained in the Japanese population. The loci identified in association studies have only very small effect sizes. We hypothesized that rare disease variants with larger effect sizes remain to be discovered that may explain a greater part of the genetic background. Family-based linkage study is an important alternative for the identification of rare disease variants. Indeed, studies with large families with highly clustered diabetes have revealed important mutations involved in MODY and other dominantly inherited diabetes, including a *KCNJ11* mutation [22]. We therefore recruited families with a 3-generation history of diabetes. The validity of our strategy was strengthened by the fact that one case out of the 10 index cases recruited in our study carried a previously reported rare disease variant *HNF1A* R583G.

Our family analysis revealed a significant linkage region on chromosome 2p25-22 that has not been reported in previous Japanese sib-pair analyses [3–5]. Because our approach was based on a higher degree of familial clustering than sib-pair analyses, the linkage region suggested in the present study might well go undetected in sib-pair analyses that include an admixture of sib-pairs with both low and high degrees of familial clustering. In the present study, we conducted a computational approach targeting the linkage region on chromosome 2p25-22. One hundred and six known genes were present in this linkage region. Prioritization of the candidate gene was possible by integrating the information available from multiple publicly available databases [14]. *GCKR* and other 7 gens ranked high in the prioritization, and were selected as candidate genes.

GCKR regulates glucokinase (GCK), the first glycolytic enzyme, in liver. *GCKR*-null mice exhibit elevated postprandial glucose [19]. Adenoviral-mediated overexpression of *GCKR* in mouse liver increases GCK activity and lowers fasting blood glucose. It was suggested that GCKR, a competitive inhibitor of GCK activity, also has a paradoxical role in extending GCK half-life by stabilizing the enzyme [20]. If so, diminished expression of GCKR in human might cause decreased GCK activity in liver and lead to impaired liver glucose uptake, which suggests the *GCKR* mutation as a possible cause of the disease in linked families.

We sequenced entire exons and the 2-kb promoter region of *GCKR* in 9 index 3-generation cases and in 18 control subjects. The rare variants were significantly more frequent in index cases from families than in control subjects. In addition, exonic rare variant g.6859C>G in pedigree 3, which was not detected in 105 control subjects, was clearly segregated in all 9 affected members in pedigree 3. Previous reports have shown the association of common *GCKR* variants with fasting plasma glucose, glucose level after glucose challenge, and diabetes risk in various ethnic groups [23–30]. In Japanese population, a common variant *GCKR* rs780094 is associated with fasting glucose and diabetes risk [27,30]. Our family study suggests the effect of rare *GCKR* variants on diabetes susceptibility that has not been revealed by previous association studies. A recent study has shown the excess of rare *GCKR* variants in individuals with hypertriglyceridemia [31], which supports our idea that rare *GCKR* mutations also affect the diabetes susceptibility.

On the other hand, the only one mutation in other 7 highly prioritized genes was *FOSL2* R198H and it did not co-segregate with the phenotype in the pedigree. Therefore, we tentatively eliminate the possibility that these genes are involved in familial clustering of diabetes patients in the current pedigrees.

Our study has several limitations. First is the large size (23.6 Mb) of the linkage region. Only 4 families could be included in the linkage analysis because we limited the cohort to 3-generation families with ≥2 affected members who donated DNA. Further efforts to recruit large families are needed to narrow down the linkage region. Second, because the *GCKR* g.6859C>G mutation was in a non-coding exon, confirming the relevance of the mutation as the cause of the disease is difficult. Investigation of the effect of the mutation in human liver, where GCKR is predominantly expressed [32], is required, but liver specimens of family

members are currently unavailable. Although we tried to determine the mRNA level in peripheral blood of family members, GCKR mRNA was only barely detectable with the RT-PCR method (data not shown), so comparison of the GCKR mRNA level between affected and unaffected members was not possible. We speculate that the g.6859C>G mutation might affect GCKR function in liver through mRNA transcription or splicing processes [33]. *GCKR* g.-689G>A and g.-299G>A mutations located in the promoter also might affect the expression of GCKR, but TRANSFAC database [34] expected no binding sites of transcription factors at the two promoter mutations.

In conclusion, with systematic investigation we propose that *GCKR* is a susceptibility gene in Japanese families with clustered diabetes. A family-based approach may be a promising strategy to elucidate the complex genetic background of common diseases including type 2 diabetes.

Supplementary materials related to this article can be found online at doi:10.1016/j.ymgme.2010.12.009.

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ORIGINAL ARTICLE

GLP-1 receptor agonist attenuates endoplasmic reticulum stress-mediated β-cell damage in Akita mice

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ABSTRACT

Aims/Introduction: Endoplasmic reticulum (ER) stress is one of the contributing factors in the development of type 2 diabetes. To investigate the cytoprotective effect of glucagon-like peptide 1 receptor (GLP-1R) signaling *in vivo*, we examined the action of exendin-4 (Ex-4), a potent GLP-1R agonist, on β-cell apoptosis in Akita mice, an animal model of ER stress-mediated diabetes.

Materials and Methods: Ex-4, phosphate-buffered saline (PBS) or phlorizin were injected intraperitoneally twice a day from 3 to 5 weeks-of-age. We evaluated the changes in blood glucose levels, bodyweights, and pancreatic insulin-positive area and number of islets. The effect of Ex-4 on the numbers of C/EBP-homologous protein (CHOP)-, TdT-mediated dUTP-biotin nick-end labeling (TUNEL)- or proliferating cell nuclear antigen-positive β-cells were also evaluated.

Results: Ex-4 significantly reduced blood glucose levels and increased both the insulin-positive area and the number of islets compared with PBS-treated mice. In contrast, there was no significant difference in the insulin-positive area between PBS-treated mice and phlorizin-treated mice, in which blood glucose levels were controlled similarly to those in Ex-4-treated mice. Furthermore, treatment of Akita mice with Ex-4 resulted in a significant decrease in the number of CHOP-positive β-cells and TUNEL-positive β-cells, and in CHOP mRNA levels in β-cells, but there was no significant difference between the PBS-treated group and the phlorizin-treated group. Proliferating cell nuclear antigen staining showed no significant difference among the three groups in proliferation of β-cells.

Conclusions: These data suggest that Ex-4 treatment can attenuate ER stress-mediated β-cell damage, mainly through a reduction of apoptotic cell death that is independent of lowered blood glucose levels. (J Diabetes Invest, doi: 10.1111/j.2040-1124.2010.00075.x, 2011)

KEY WORDS: Apoptosis, Endoplasmic reticulum stress, Glucagon-like peptide-1

INTRODUCTION

Type 2 diabetes is a chronic metabolic disorder characterized by the loss of β-cell function and mass. The mechanisms underlying the loss of β-cell function and mass are not fully understood, but recent studies have shown that endoplasmic reticulum (ER) stress is one of the causes of β-cell damage in diabetes[1]. Owing to increased demand for insulin secretion, β-cells show a highly developed ER[1]. The ER has a number of important functions, such as post-translational modification, folding and assembly of newly synthesized secretory proteins[2–4]. Thus, the ER plays an essential role in cell survival. ER function can be impaired by various conditions, including inhibition of protein glycosylation, reduction in formation of disulfide bonds, calcium depletion from the ER lumen, impairment of protein transport from the ER to the Golgi and expression of malfolded proteins[1]. Various physiological or pathological conditions that compromise ER functions are collectively termed ER stress[1–3]. To alleviate ER stress and promote cell survival, an adaptive response, known as unfolded protein response (UPR) is activated. UPR comprises translational attenuation, induction of chaperones and ER stress-associated degradation (ERAD). However, prolonged activation of UPR can ultimately lead to cell death by apoptosis.

Increased demand for insulin secretion under certain conditions, such as chronic hyperglycemia, might result in β-cell overload. Chronic hyperglycemia in diabetes can therefore induce persistent ER stress, cause β-cell dysfunction and finally lead to a reduction in β-cell mass through apoptosis[1].

Glucagon-like peptide 1 (GLP-1) is a physiological incretin, an intestinal hormone released in response to nutrient

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ingestion that stimulates glucose-dependent insulin secretion. A growing body of evidence suggests that GLP-1 not only increases insulin secretion and upregulates insulin biosynthesis, but also stimulates β-cell proliferation and neogenesis[5–9], and inhibits β-cell apoptosis[9–16], resulting in increased β-cell mass. However, demonstration of an *in vivo* effect in the animal models of type 2 diabetes is problematic, because enhancement of GLP-1R signaling lowers blood glucose levels as result of its insulinotropic action, and it is difficult to evaluate the direct cytoprotective effects of GLP-1 in conditions of similar glucose toxicity.

In the present study, we investigated the cytoprotective effect of GLP-1R signaling *in vivo* on ER stress-mediated apoptotic cell death by using Akita mice, an animal model of ER stress-mediated diabetes mellitus. Akita mice have a point mutation in the insulin 2 gene, resulting in misfolding of insulin that leads to severe ER stress[17,18]. To exclude the possibility that the effect of Ex-4 on β-cells is mediated through improved blood glucose levels, we used three groups of mice: Akita mice treated with phosphate-buffered saline (PBS), Ex-4, or the sodium-coupled glucose transporter inhibitor phlorizin, which decreases blood glucose levels without increasing insulin secretion.

MATERIALS AND METHODS

Experimental Animals

Male C57BL/6 mice and male Akita mice were obtained from Shimizu (Kyoto, Japan). The animals were housed under a light/dark cycle of 12 h with free access to food and water. All experiments were approved by the Kyoto University Animal Care Committee.

In vivo Treatment

The mice were given twice daily intraperitoneal injections of PBS, Ex-4 (24 nmol/kg) or phlorizin (0.3 g/kg) for 2 weeks (from 3 to 5 weeks-of-age). Blood glucose levels were measured every third day by enzyme electrode method using a portable glucose analyzer (Glutest sensor; Sanwakagaku, Nagoya, Japan). Blood samples were collected from tail cuttings from these mice fed *ad libitum*. At the end of the experimental period, blood samples were collected from the inferior vena cava under anesthesia to determine the plasma glycoalbumin levels (Oriental Yeast, Tokyo, Japan). Pancreas samples from each of the animal groups were obtained for histological evaluation, and islets were isolated for measurement of insulin content and RNA extraction.

Evaluation of Pancreatic Insulin-Positive Area and Number of Islets

The pancreas samples were fixed in Bouin's solution. Serial 5-μm paraffin-embedded tissue sections were mounted on slides. After rehydration, sections were incubated with polyclonal rabbit anti-insulin antibodies (Santa Cruz Biotechnology, Santa Cruz, CA, USA), with a biotinylated goat anti-rabbit antibody (DAKO, Carpinteria, CA, USA), and then with a streptavidin peroxidase conjugate and substrate kit (DAKO) using standard protocols. The total pancreas area and insulin-positive area were quantified on five distal, random, non-overlapping sections from five mice of each group using a BZ-8100 microscope equipped with a BZ-Analyzer (KeyEnce, Osaka, Japan). Insulin-positive areas and the number of islets of each group were adjusted by total pancreas area[15].

Measurement of Insulin Contents of Isolated Islets

Pancreatic islets were isolated by collagenase digestion. To determine insulin contents, islets were homogenized in 400 μL acid ethanol (37% HCl in 75% ethanol, 15:1000 [v/v]) and extracted at 4°C overnight. The acidic extracts were dried by vacuum, reconstituted and subjected to insulin measurement. The amount of immunoreactive insulin was determined by radioimmunoassay (RIA).

Measurement of mRNA Expression of C/EBP-Homologous Protein and BiP in Isolated Islets

Measurement of mRNA expression of C/EBP-homologous protein (CHOP) and BiP was carried out by quantitative reverse transcription polymerase chain reaction (RT–PCR) as described previously[19]. Briefly, total RNA was extracted from isolated islets with an RNeasy mini kit (Qiagen, Valencia, CA, USA) and treated with DNase (Qiagen). cDNA was prepared by SuperScript Reverse Transcriptase system (Invitrogens, Carlsbad, CA, USA) according to the manufacturer's instructions. CHOP mRNA levels and BiP mRNA levels in the islets were measured by quantitative RT–PCR using an ABI PRISM 7000 Sequence Detection System (Applied Biosystems, Foster City, CA, USA). The sequences of forward and reverse primers to evaluate

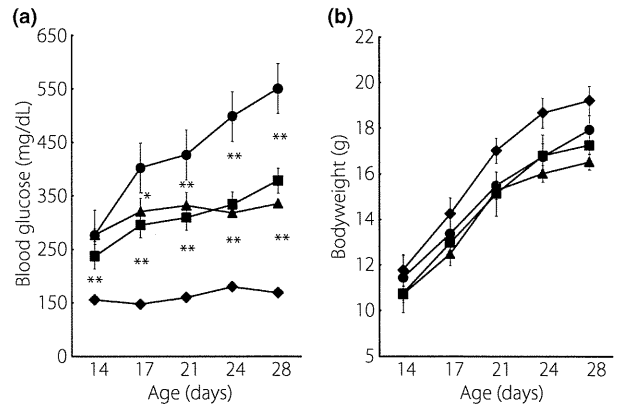

Figure 1 | Ex-4 significantly reduced blood glucose levels in Akita mice. (a) Blood glucose concentration and (b) bodyweight were measured in wild-type C56BL/6 mice (closed diamond, $n = 10$), Akita mice treated with PBS alone (closed circle, $n = 10$), Ex-4 (closed square, $n = 12$) and phlorizin (closed triangle, $n = 10$). Each symbol represents mean ± SE. $^{*}P < 0.05$, $^{**}P < 0.01$ *vs* PBS-treated Akita mice.