high contents of methylated histone H3 and heterochromatin proteins such as HP1β, may protect the maternal genome from active demethylation. On the other hand, Dnmt1s is absent from decondensing sperm and is gradually recruited to the paternal genome during the first cell cycle. This time course is similar to those of some epigenetic changes such as K9 dimethylation and K27 trimethylation of histone H3 (Morgan et al., 2005; Santos et al., 2005). Di/trimethylated H3-K9 and trimethylated H3-K27 are specifically targeted by the chromodomains of HP1 and polycomb proteins, respectively (Margueron et al., 2005). In fact, HP1β is also recruited to the paternal genome during a similar period (Santos et al., 2005). Because HP1β and its interacting partner SUV39H1 can associate with Dnmt1 (Fuks et al., 2003), these factors may mediate the recruitment of Dnmt1s to the paternal genome and cooperate with it in reestablishing an epigenetic state equivalent to the maternal one.

Immunostaining demonstrates cell cycle-coupled dynamics of Dnmt1s localization during at least the first two cell cycles. The effect of leptomycin B on Dnmt1s localization indicates that nuclear Dnmt1s appears to translocate to the cytoplasm in the G2 phase via CRM1/exportin-mediated nuclear export. This phenomenon may be highly characteristic of preimplantation embryos at this stage, because endogenous and forcedly-expressed Dnmt1s is localized in the nucleus throughout cell cycle in somatic cells such as NIH3T3 cells and HeLa cells (Easwaran et al., 2004, and our unpublished data). Dnmt1 contains a leucine-rich region in its C-terminus, which is close to the consensus sequence of the nuclear export signal (NES), which is recognized by CRM1/exportin (Kutay and Guttinger, 2005). This region may act as a functional NES in the G2 phase of preimplantation embryos.

Interestingly, EGFP-Dnmt1o was also localized to the nucleus and thereafter translocated to the cytoplasm. We speculate that the initial localization to the nucleus and translocation to the cytoplasm thereafter do not require the Dnmt1s-specific N-terminal region. It also raises a possibility that *de novo*-synthesized Dnmt1o may first localize to the nucleus and may be thereafter sequestered to the cytoplasm by an active mechanism. It has been previously reported that Dnmt1o interacts and colocalizes with annexin V (Ohsawa et al., 1996), a calcium-sensitive phospholipid binding protein (Schlaepfer et al., 1987). This interaction is postulated to lead to active sequestration of Dnmt1o in the cytoplasm of unfertilized oocytes and preimplantation embryos (Doherty et al., 2002). This may explain the difference in subcellular localization between Dnmt1s and Dnmt1o.

At present, there is no evidence supporting the relation between this phenomenon and genome-wide demethylation. However, it might be possible that the disappearance of Dnmt1s from the nucleus in G2 decreases the opportunity for this enzyme to be recruited to hemi-methylated CpG regions or nuclear complexes containing proteins interactive with it after the S phase. Indeed, previous reports have demonstrated that Dnmt1s associates with chromatin (preferentially constitutive heterochromatin) during the G2 and M phases through a mechanism different from a replication dependent one in the S phase (Easwaran et al., 2004). Thus, the depletion of nuclear Dnmt1s in G2 may be related to the limited maintenance methylation during preimplantation development.

Decreases in methylated CpG dinucleotides in the LTR of IAPs and the paternal allele of *H19* in response to microinjection of N48 or Dnmt1 siRNA suggest nuclear-localized Dnmt1s to be involved in maintenance methylation during preimplantation development. The presence of Dnmt1s in the nucleus and its function in maintenance methylation appear to compensate for the limited role of Dnmt1o, which apparently translocates to the nucleus only at the eight-cell stage (Howell et al., 2001), during preimplantation development. In preimplantation embryos, methylation states are maintained only in limited genomic sequences, in contrast to the situation in somatic cells. Taken together with the observation that the localization of Dnmt1s fluctuates via nucleocytoplasmic shuttling in preimplantation embryos, these findings indicate that this characteristic behavior of Dnmt1s may restrict its recruitment to certain genomic regions, allowing large portions of the genomic DNA to be demethylated. The mechanism by which Dnmt1s is recruited to particular regions in the ubiquitously methylated genome of preimplantation embryos should be further investigated.

In the present study, about 50% to 60% of CpG dinucleotides in the LTR of IAPs and the paternal allele of *H19* remained methylated after microinjection of N48 or Dnmt1 siRNA. This partial demethylation may be due to the presence of Dnmt1o and/or incomplete inactivation of Dnmt1s with the methods used in this study. In our preliminary experiment, however, embryos injected with Dnmt1 siRNA tended to show growth retardation after implantation, as compared to control siRNA-injected embryos (data not shown). This result may support the idea that Dnmt1s activity in preimplantation embryos is required for normal postimplantation development, although it may also be possible that the effect of injected siRNA was retained after implantation to affect the growth thereafter.

Recently, Sasaki's group established oocyte-specific Dnmt1 knockout mice and demonstrated that Dnmt1, but not Dnmt3a and 3b, is mostly responsible for maintenance DNA methylation during preimplantation development (Ryutaro Hirasawa and Hiroyuki Sasaki, personal communication). Taken together with only partial reduction in DNA methylation in Dnmt1o-specific knockout embryos reported previously (Howell et al., 2001), their results are consistent with us in that Dnmt1s may compensate the absence of Dnmt1o in the nucleus except for the 8-cell stage during preimplantation development. Dnmt1s-specific gene knockout is expected to further clarify this issue.

In conclusion, the present study has revealed the presence of Dnmt1s in the nucleus and its nucleocytoplasmic shuttling in preimplantation embryos. Inactivation of Dnmt1s by microinjection of Dnmt1s-specific antibody and siRNA resulted in decreases of methylated CpG dinucleotides in the genomic regions whose methylation patterns must be maintained after fertilization. These findings may contribute to the understanding of the mechanism underlying epigenetic regulation during preimplantation development.

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# SH3 domain of the phosphatidylinositol 3-kinase regulatory subunit is responsible for the formation of a sequestration complex with insulin receptor substrate-1

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**Abstract**

Class IA phosphatidylinositol 3-kinase (PI 3-kinase), which is composed of a 110 kDa catalytic subunit and a regulatory subunit, plays a key role in most insulin dependent cellular responses. To date, five mammalian regulatory subunit isoforms have been identified, including two 85 kDa proteins (p85α and p85β), two 55 kDa proteins (p55γ and p55α), and one 50 kDa protein (p50α). In the present study, we overexpressed these recombinant proteins, tagged with green fluorescent proteins (GFP), in CHO-IR cells and investigated intracellular localizations in both the presence and the absence of insulin stimulation. Interestingly, in response to insulin, only p85α and p85β redistributed to isolated foci in the cells, while both were present throughout the cytoplasm in quiescent cells. In contrast, p55s accumulated in the perinuclear region irrespective of insulin stimulation, while p50α behaved similarly to control GFP. Immunofluorescent antibodies against endogenous IRS-1 revealed IRS-1 to be co-localized in the p85 foci in response to insulin. As both insulin receptors and p110α catalytic subunits were absent from these foci on immunofluorescence study, only p85 and IRS-1 were suggested to form a sequestration complex in response to insulin. To determine the domain responsible for IRS-1 complex formation, we prepared and overexpressed the SH3 domain deletion mutant of p85α in CHO-IR cells. This mutant failed to form foci, suggesting the SH3 domain of regulatory subunits to be responsible for formation of the p85-IRS-1 sequestration complex. In conclusion, our study revealed the SH3 domain of PI 3-kinase to play a critical role in intracellular localizations, including formation of foci with IRS-1 in response to insulin.


*Keywords:* PI-3kinase; CHO-IR cells; IRS-1; Insulin; Akt

Class IA phosphatidylinositol 3-kinase (PI 3-kinase), which is composed of a catalytic 110 kDa protein (p110) associated with a regulatory subunit, has been implicated in the regulation of various cellular response activities, including proliferation, differentiation, membrane ruffling, prevention of apotosis, and insulin stimulated glucose uptake [1–5]. The SH2 domain of the regulatory subunit has been shown to bind directly to the tyrosine-phosphorylated YXXM motif of several activated receptor tyrosine kinases [6]. To date, five mammalian regulatory subunit isoforms have been identified, including two 85 kDa proteins (p85α and p85β), two 55 kDa proteins (p55γ and p55α), and one 50 kDa protein (p50α). All five isoforms share two SH2 domains but have different NH2-terminal sequences. The most well known 85 kDa isoforms contain SH3 and bcr homology (BH) domains in their N-termini [7]. The recently cloned 55 kDa isoforms contain a unique 34 amino acid sequence in their N-termini [8,9]. The

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50 kDa isoform contains only a six amino acid sequence in its N-terminal portion, which is apparently too short to interact with other molecules [10].

In this study, we overexpressed these recombinant proteins tagged with green fluorescent proteins (GFP) in CHO-IR cells and investigated intracellular localizations in the presence and absence of insulin stimulation. Only p85α and p85β redistributed to discrete foci in CHO-IR cells, while other isoforms did not. A recent study also demonstrated that GFP-p85α translocates to similar foci in CHO-K1 cells in response to insulin-like growth factor-1 (IGF-1) stimulation [11]. We have demonstrated these isolated foci to be composed of p85 and IRS-1 by immunohistochemistry and western blotting using an immunoprecipitation method, and found the SH3 domain located in the N-terminal portion of p85 to be responsible for the formation of foci with IRS-1. As monomeric p85 was previously demonstrated to down-regulate insulin signaling by competing with the p85-p110 dimer for IRS-1 binding [12], the formation of p85-IRS-1 foci is likely to be involved in the mechanism of negative regulation of insulin signaling.

## Materials and methods

*cDNA constructs of each PI 3-kinase regulatory subunit isoform.* Rat cDNAs encoding the full-length amino acid sequences of p85α, p85β, p55α, p55γ, and p50α [13], as well as the GFP cDNA (CLONTECH, Laboratories, Inc.) at each N-terminus, were ligated into the EcoRI sites of pSRα vectors. cDNA of the SH3 domain deletion mutant (SH3D) of p85α was prepared as previously described by PCR methods [14] and similarly inserted into pSRα vectors. Fragments prepared by PCR were fully sequenced and observed to have no unexpected mutations.

*Cell culture and transfections.* CHO-IR cells were maintained in DMEM with 4500 mg/L glucose, containing 10% fetal calf serum (Life Technologies, Inc.) at 37 °C in 5% $CO_2$. Lipofectamine reagent, Opti-MEM I, was purchased from Gibco-BRL Life Technologies (Eggenstein, Germany). One day before transfection, CHO-IR cells were trypsinized and seeded onto a 60-mm plastic culture dish at $6 \times 10^5$ cells/dish. The following day, the transfection procedures were performed using 30 μl of lipofectamine diluted in 300 μl of Opti-MEM I and 6 μg of plasmid DNA diluted in 300 μl of supplemental Opti-MEM-I per 60-mm dish. Cells were incubated in the presence of the lipofectamine-DNA mix for 5 h at 37 °C, in 5% $CO_2$, and then incubated overnight in DMEM-10% FCS. Forty-eight hours after transfection, each transfected 60-mm dish was used for experiments.

*Antibodies and Western blotting.* Western blotting was performed as previously described [15]. Commercial antibodies against murine GFP (Chemicon International, CA), phospho-Akt (Ser 473) (Cell Signaling Technology, CA), phophotyrosine, 4G10 (Upstate Biotechnology, NY), and IRS-1 (Cell Signaling Technology, CA) were purchased. After blotting with the indicated secondary antibody, detection was performed using an ECL chemiluminescent kit (Amersham Pharmacia Biotech, UK). Quantitations were performed using a Molecular Imager (Bio-Rad Lab, CA). Immunoprecipitation was performed as previously described [16], using anti-IRS-1 and GFP antibodies. Immunoprecipitates were then boiled in Laemmli sample buffer, subjected to SDS–PAGE, and finally to Western blotting using the anti-phosphotyrosine (4G10) or GFP antibodies.

*Immunofluorescence analysis.* Immunofluorescence studies were performed as previously described [15]. Cells were plated at near-confluent density on glass coverslips and fixed in 4% paraformaldehyde–PBS for 20 min at room temperature. Coverslips were washed three times in PBS, then quenched for 15 min in 0.2% Triton X-100. After a further three washes in PBS, coverslips were blocked for 30 min in 2% horse serum-PBS and then washed twice in PBS. Commercial primary antibodies against IRS-1 (Cell Signaling Technology, CA), insulin receptor (Santa Cruz Biotechnology, Germany), Caveolin (BD Biosciences, CA), and p110α [17] were used. These antibodies were diluted in 0.1% horse serum-PBS, and incubations were carried out at 4 °C overnight. Tetramethyl rhodamine isothiocyanate (TRITC)-conjugated anti-mouse immunoglobulin secondary antibody (Zymed Lab., CA) diluted in 0.1% horse serum–PBS was applied after three 5 min washes in PBS. After 1 h of incubation, at RT, coverslips were washed three times in PBS for 5 min each and then mounted in 1% propyl gallate–50% glycerol–PBS and finally observed under a microscope.

*Method of deliverying peptides into CHO-IR cells.* We delivered peptides into CHO cells using Chariot Transfection Reagent (Active Motif, CA). Briefly, 6 μl of Chariot were diluted in 60% DMSO up to 100 and 100 μl of PBS were added to 50 μg of synthesized proline-rich peptides (PRM1, PPTPKPRPPRPLPVAP). The 100 μl proline dilution was added to the 100 μl Chariot dilution, followed by incubation at RT for 60 min to allow the Chariot-proline complex to form. The cells to be transfected in a six-well tissue culture plate were overlaid with the 200 μl Chariot-proline complex, followed by addition of 400 μl of serum-free medium and incubation for 1hr. Then, we added 1 ml of complete growth medium to the cells and continued the incubation for 1 h. Next, we aspirated the complete growth medium, washed twice with 2 ml of PBS, added serum free medium containing 0.2% BSA and incubated the cells at 37 °C in 5% CO2 for 5 h. After incubation with or without 100 nM insulin for 10 min and washing once with PBS, the cells were fixed with 4% paraformaldehyde for 10 min. After washing with PBS, the cells were observed by fluorescence microscopy. Positive control peptides, 2 μg of β-galactosidase, were transfected into the cells using the same techniques, except for β-galactosidase staining, achieved using a β-galactosidase staining kit (Active Motif, CA).

## Results

The schematic structures of five wild-type and one SH3 deletion mutant regulatory subunit isoform of PI 3-kinase are shown in Supplementary Fig. 1. First, we overexpressed wild-type recombinant proteins tagged with GFP in CHO-IR cells and investigated intracellular localizations in both the presence and the absence of insulin stimulation (Fig. 1). Control GFP were found to exhibit intracellular localizations with a greater preference for the nucleus. Interestingly, in contrast to control GFP, p85α, and p85β redistributed to discrete foci in the cells in response to insulin, while they were seen throughout the cytoplasm in quiescent cells. Other isoforms showed no changes in localization with insulin stimulation. The p55α and p55γ exhibited concentrated accumulations around the perinuclear region. In particular, p55γ was restricted to the perinuclear region, while p55α was also distributed throughout the cytoplasm. On the other hand, the distribution of p50α was very similar to that of control GFP.

To investigate the properties of these isolated foci, we searched for proteins co-localized with overexpressed p85-GFP proteins. First, we performed immunofluorescence analyses using antibodies against the insulin receptor, caveolin and the catalytic subunit of PI 3-kinase, p110α, as primary antibodies. However, the signals obtained from these studies were not associated with the foci observed in the cytoplasm when p85α-GFP proteins were overex-

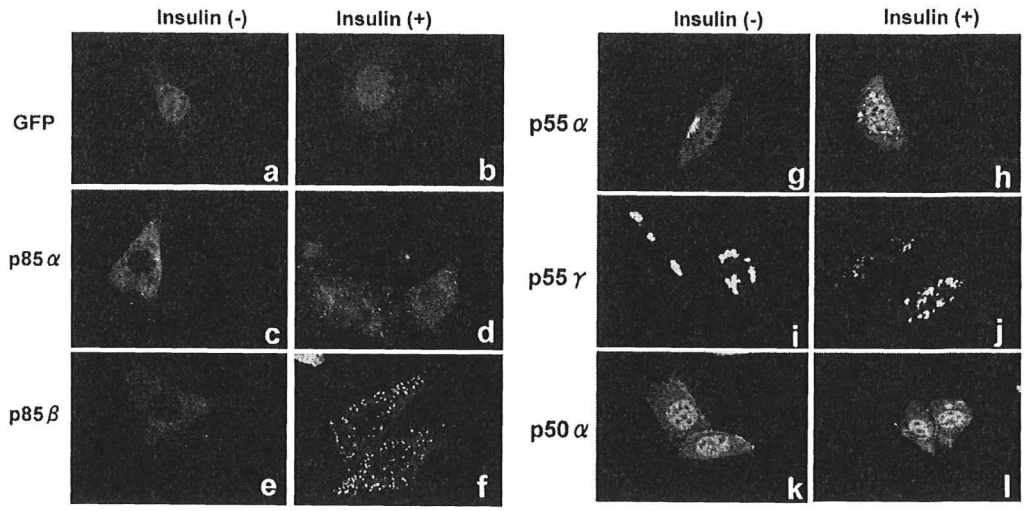


Fig. 1. The localizations of each PI 3-kinase regulatory subunit-GFP protein in CHO-IR cells in the absence and presence of insulin. CHO-IR cells were seeded onto a 60-mm plastic culture dish at $6 \times 10^5$ cells/dish. The following day, transfection procedures were performed using 30 μl of lipofectamine diluted in 300 μl of Opti-MEM I and 6 μg of pSRα vector DNA containing cDNA of GFP (a,b), p85α-GFP (c,d), p85β-GFP (e,f), p55α-GFP (g,h), p55γ-GFP (i,j), and p50α-GFP (k,l). Cells were incubated in the presence of the lipofectamine-DNA mix for 5 h, and then incubated overnight in DMEM containing 10% FCS. Forty-eight hours after transfection, each of the transfected 60-mm dishes was used for experiments. Before the experiments, CHO-IR cells were serum starved and stimulated with insulin for 10 min (b, d, f, h, j, and l). The results shown are representative of three experiments.

pressed (data not shown). Interestingly, only the signals observed in an immunofluorescence study using antibodies against IRS-1 corresponded to with these foci (Fig. 2h), suggesting that IRS-1 co-localized with these p85 foci in response to insulin. Though we cannot rule out the possibility that the p85-IRS-1 complex contains other unex-

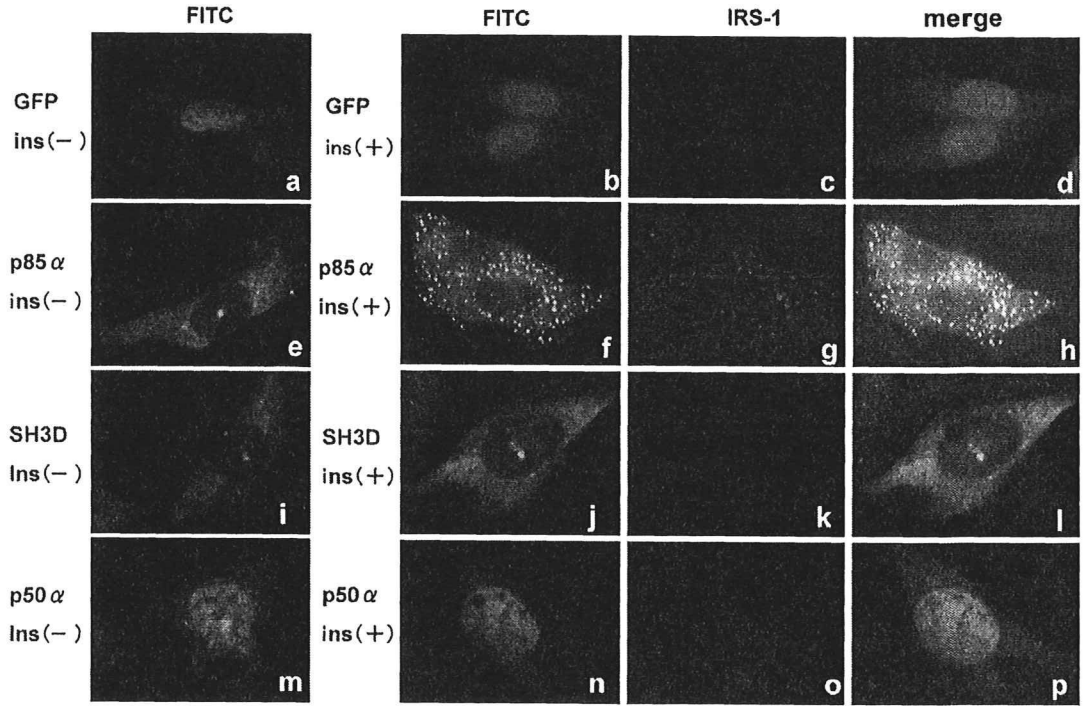


Fig. 2. Immunofluorescence analyses of PI 3-kinase regulatory subunit-GFP proteins. CHO-IR cells were plated at near-confluent density and were transfected with GFP (a–d), p85α-GFP (e–h), SH3D-GFP (i–l) or p50α-GFP(m–p). Cells were serum starved and stimulated with insulin for 10 min. Cells were fixed in 4% paraformaldehyde–PBS for 20 min, then quenched for 15 min in 0.2% Triton X-100. Commercial primary antibodies against IRS-1 were diluted in 0.1% horse serum–PBS, and incubations were carried out at 4 °C overnight. TRITC-conjugated anti-mouse immunoglobulin secondary antibody diluted in 0.1% horse serum-PBS was applied after three 5 min washes in PBS. After a 1 h incubation, coverslips were mounted in 1% propyl gallate–50% glycerol–PBS and were observed under a microscope. Results shown are representative of three experiments.

pected proteins, both the insulin receptor and p110α catalytic subunits are absent from these foci according to immunofluorescence results, suggesting that only p85 and the IRS-1 dimer form a sequestration complex in response to insulin. As p55s and p50α did not form foci, we expected that the domain responsible for IRS-1 complex formation would be either the SH3 domain or the bcr homology (BH) domain. Thus, we prepared and overexpressed the SH3 domain deletion mutant (SH3D) of p85α-GFP in CHO-IR cells. This mutant failed to form foci (Fig. 2j), i.e., the SH3 domain of regulatory subunits is likely to be responsible for formation of the p85-IRS-1 sequestration complex. Based on a previous report that SH3 domain-proline rich motif inertactions mediate dimerization of PI-3 kinase regulatory subunits [18], we examined whether these interactions are involved in formation of the sequestration complex with IRS-1. After confirming that β-galactosidase, as a positive control peptide, was properly transfected in our experiments (Supplementary Fig. 2a), proline-rich motif peptides were similarly transfected into CHO-IR cells. As shown in Supplementary Fig. 2e, proline-rich peptides did not affect p85-IRS-1 complex formation, indicating that SH3-domain-proline-rich motif interactions are unlikely to be involved in this complex formation.

Though p85α-IRS-1 complexes formed in response to insulin stimulation, as demonstrated by immunofluorescence analysis, we attempted to further demonstrate these direct associations by immmunoprecipitation. After confirming that almost equal amounts of p85α, SH3D, and p50α-GHP proteins had been expressed in CHO-IR cells (Fig. 3, upper panel), we performed immunoprecipitation experiments using either anti-IRS-1 or anti-GFP antibody and blotted the transferred sheets with anti-GFP or anti-phopho-tyrosine antibody (4G10), respectively. As expected, an insulin-dependent IRS-1 association with p85α-GFP was detected (Fig. 3, middle and lower panels). Despite the lack of IRS-1 complex formation, IRS-1 associations with both the SH3D mutant and p50α-GFP were also observed. Moreover, only IRS-1-SH3D mutant binding was present in the absence of insulin stimulation. Thus, even though the overexpressed regulatory subunits fail to form discrete foci, these subunits do actually bind to IRS-1 in the presence of insulin.

Next, we investigated downward signaling by analyzing Ser473-Akt phosphorylation in the presence of insulin with overexpression of each isoform. As shown in Fig. 4, p85α and SH3D mutant-GFP overexpressions markedly diminished insulin dependent Akt phosphorylations, while p50α-GFP overexpression did not affect Akt phosphorylation as compared with control cells. Based on a previous report demonstrating monomeric p85 to down-regulate insulin signaling by competing with the p85-p110 dimer for IRS-1 binding [12], p85α-GFP and the SH3D mutant also negatively suppressed insulin signaling by removing IRS-1 from p85-p110-IRS trimers.

## Discussion

In this study, we overexpressed five class IA PI 3-kinase regulatory subunit isoforms tagged with GFP in CHO-IR cells and investigated intracellular localizations in response to insulin stimulation. p85α and p85β redistributed to discrete foci in CHO-IR cells, while other isoforms did not. p55α and p55γ preferentially remained in the perinuclear

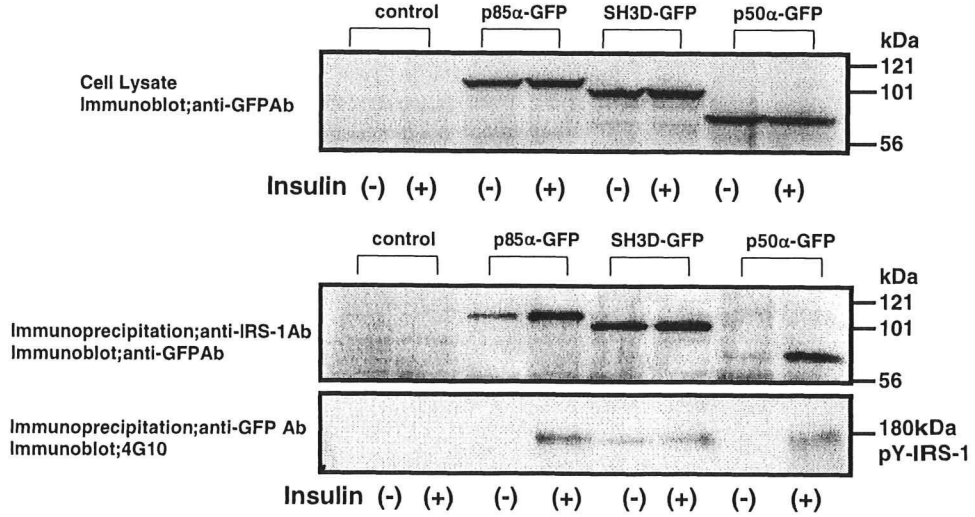


Fig. 3. Direct associations between IRS-1 proteins and each PI 3-kinase regulatory subunit isoform. CHO-IR cells were transfected with only the pSRα vector, pSRα DNA containing cDNA of p85α-GFP, SH3D-GFP, or p50α-GFP. After serum starvation, cells were stimulated with insulin for 10 min. Supernatants including tissue protein extracts were resolved on 10% SDS–polyacrylamide gel, followed by electrophoretic transfer to a nitrocellulose membrane. Membranes were incubated for 1 h at RT with anti-GFP antibody. After blotting with anti-GFP antibody, detection was performed using an ECL chemiluminescence kit (upper panel). Immunoprecipitation was performed using anti-IRS-1 (middle panel) and GFP antibodies (lower panel). Immunoprecipitates were then boiled in Laemmli sample buffer, subjected to SDS–PAGE, and finally to Western blotting using anti-GFP (middle panel) and anti-phosphotyrosine antibodies (lower panel). Three independent experiments were performed and similar results were obtained.

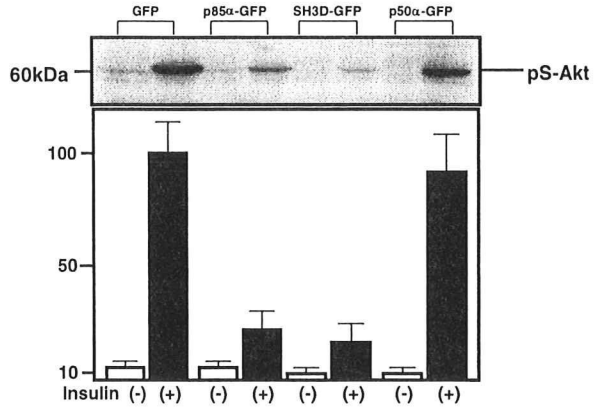


Fig. 4. Effects of overexpressing each isoform of the PI 3-kinase regulatory subunit on Ser473-Akt phosphorylation in CHO-IR cells. CHO-IR cells were transfected with only pSRα vector, pSRα DNA containing cDNA of p85α-GFP, SH3D-GFP or p50α-GFP. After serum starvation, cells were stimulated with insulin for 10 min. Supernatants including tissue protein extracts were resolved on 10% SDS–polyacrylamide gel, followed by electrophoretic transfer to a nitrocellulose membrane. Membranes were incubated for 1 h at RT with anti-phospho-Akt (Ser473) antibody. After blotting with the indicated secondary antibody, detection was performed using an ECL chemiluminescent kit. Quantitations were performed using a Molecular Imager. Three independent experiments were performed and similar results were obtained.

region, while p50α exhibited localizations very similar to that of the control GFP. The signal sequence of p55s is located in the N-terminal domain, which is composed of a unique 34 amino-acid sequence. It was previously reported that this 34 amino-acid sequence has a high affinity for α/β tubulin [19] or the retinoblastoma tumor suppressor protein (Rb), a key regulator of cell cycle progression [20]. Further study is needed to investigate whether perinuclear localizations are related to the associations with these proteins.

Though PI 3-kinase plays a key role in mediating insulin signals downstream from IRS-1, mice lacking the p85α or p85β subunits of PI 3-kinase, paradoxically, show high insulin sensitivity [21,22]. There are two possible explanations for this discrepancy. First, p50α subunits were previously demonstrated to exhibit a markedly higher capacity for activation of associated PI 3-kinase via insulin stimulation and to have a higher affinity for tyrosine-phosphorylated IRS-1 than other isoforms [10]. In mice lacking p85s, there are more p50α subunits and they substitute for the missing p85s subunits [21,22], thereby producing enhanced insulin sensitivity. In fact, the overexpression of p50α-GFP also resulted in high insulin sensitivity being maintained in this study. Second, p85s regulatory subunits have two SH2 domains separated by an inter-SH2 domain, through which they bind p110 catalytic subunits, and in addition, monomeric p85s and p85s–p110s mutually compete for IRS-1 binding [12]. Thus, the molecular balance between p85s and p110s might have a major effect on insulin signaling downstream from PI 3-kinase. We can speculate that fewer p85s subunits means greater insulin sensitivity. Inversely, if an excess of monomeric p85s is present, insulin signaling might be inhibited by p85s-IRS-1 dimers, which have no ability to transmit insulin signals, and thus serve as a dominant negative form.

Subsequently, it was clearly demonstrated that p85α-IRS-1 dimers form a sequestration complex in response to IGF-1 stimulation [11]. We observed similar p85-IRS-1 complexes in the case of insulin stimulation in p85s-GFP transfected CHO-IR cells and showed the p85α-SH3 domain to be responsible for complex formation. Based on a previous report describing the isolated p85α-SH3 domain as binding only one of its endogenous proline-rich motifs, PRM1 (Fig. 1) [18], we examined whether SH3-PRM1 interactions are involved in forming the sequestration complex with IRS-1. However, PRM1 peptides were incapable of disrupting the p85α-IRS-1 complex, suggesting that other interactions with the SH3 domain, such as the SH3-BH domain [23], might be involved in this complex formation.

In conclusion, when five PI 3-kinase regulatory subunit isoforms tagged in their C-terminal tails with GFP were overexpressed in CHO-IR cells, only p85α and p85β redistributed to discrete foci in response to insulin. We immunohistochemically demonstrated that these isolated foci are composed of p85 and IRS-1 and found the SH3 domain located in the N-terminal portion of p85 to be responsible for the formation of foci with IRS-1. These p85-IRS-1 complex formations represent negative regulation of insulin signaling due to a molecular imbalance between p85s and p110s.

## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.bbrc.2007.10.187.

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# Regulation of gut-derived resistin-like molecule β expression by nutrients

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ABSTRACT

Resistin was initially identified as a protein, secreted by adipocytes, which inhibits insulin action and adipose differentiation. The three proteins homologous to resistin were identified and given the names resistin-like molecules (RELM) α, β and γ. Resistin and RELMα are abundantly expressed in adipose, but RELMβ and RELMγ are secreted mainly from the gut. Since nutrient composition greatly affects insulin sensitivity, we investigated the regulatory effects of various nutritional factors in food on the expressions of resistin family proteins.

First, mice were given diets with different nutritional compositions (high-carbohydrate, high-protein and high-fat) for 2 weeks. RELMβ mRNA expression in the intestines was markedly suppressed by the high-protein and high-carbohydrate diets, while slightly but not significantly upregulated by the high-fat diet. In the epididymal fat, resistin expression was unchanged, while RELMα expression was markedly decreased by the high-carbohydrate diet. Taking into consideration that humans have neither RELMα nor RELMγ, our subsequent studies focused on RELMβ expression. We used the human colon cancer cell line LS174T. Treatments with insulin and TNFα as well as stearic acid, a saturated free fatty acid, upregulated RELMβ expression, while D-glucose downregulated RELMβ. These results suggest RELMβ expression to be regulated directly by nutrients such as glucose and saturated free fatty acids including stearic acid, as well as by hormones including insulin and TNFα. These regulations may play an important role in the nutrient-associated induction of insulin resistance.



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## 1. Introduction

Resistin and its related proteins, *i.e.* resistin-like molecules (RELMs) α, β and γ, are a family of recently identified proteins [1,2]. They share an N-terminal signal sequence and a C-terminal region with a unique structure that contains 10 cysteine residues [3]. Resistin was identified as an adipocyte secreted factor, expression of which is increased in genetically obese (*ob/ob* and *db/db*) mice [4]. Furthermore, administration of resistin reportedly impairs glucose tolerance and reduces insulin action in normal mice, both of which are reversed by immunoneutralization with anti-resistin antibody [4]. Resistin knock-out mice were also described as having lower fasting blood glucose [5]. However, there are conflicting observations regarding its function as a factor responsible for insulin resistance [6–9].

RELMα is a secreted protein of 111 amino acids that has been identified in rats and mice and is expressed in the lungs, white adipose tissue and the intestines. There is a difference between the two species in that RELMα expression in white adipose tissue is much lower in rats than in mice [2,3]. This protein has been shown to inhibit the differentiation of adipocytes *in vitro* [10]. RELMα is induced by Th2 type cytokines in rodent pulmonary epithelial cells, and thus is likely to be involved in the inflammatory response [11]. RELMγ was also initially identified in the nasal respiratory epithelium of rats [2], and was revealed to be expressed in bone marrow, peripheral blood granulocytes, the spleen, lungs and pancreas as well as the large and small intestines of mice [2,12,13].

RELMβ is highly expressed in goblet cells of the murine colon and secreted in response to bacterial colonization [14], and thus was suggested to play an important role in defense against nematode parasitization in mice [15]. On the other hand, we previously reported that RELMβ and RELMγ are present in blood, and that their serum concentrations and expressions in the colon were elevated in insulin resistant models such as obese *db/db* mice and high-fat-fed mice [16]. In addition, transgenic mice which overexpressed RELMβ in the liver, exhibited hyperglycemia, hyperlipidemia and fatty liver [17]. Thus, we consider intestine-derived RELMβ to be involved in insulin resistance.

The first objective of this study was to investigate the regulatory effects of nutritional factors in different diets on the expressions of resistin and RELMs. Interestingly, the expression of RELMβ, but not resistin, was found to be strongly influenced by different dietary compositions. Although there are four genes encoding this protein family in the mouse, only resistin and RELMβ have been identified in the human genome sequence [2]. Thus, we focused on the regulation of RELMβ expression, and performed additional experiments using cultured cells to examine whether nutritional factors, as well as hormones such as insulin and TNFα, are direct regulators of RELMβ expression. Herein, we show the regulation of gut-derived RELMβ to be regulated by both nutrients and hormones, and that its upregulation may be involved in the pathogenesis of diet-derived insulin resistance.

## 2. Materials and methods

### 2.1. Reagents and antibodies

All reagents were of analytical grade and anti-RELMβ antibody was purified as previously described [17].

### 2.2. Animal studies

Six-week-old mice (C57BL/6J) were purchased from CLEA Inc and housed under conventional conditions. All animal studies were performed after 2–3 days acclimation period and mice were anesthetized with pentobarbital. To determine RELMβ expression levels in fed and fasted states, the colon was excised from both mice fed *ad libitum* and those fasted for 18 h ($n = 3$ per group). In the fasted state, both the colon and the ileum were collected to assess the correlation between RELMβ mRNA levels in these tissues ($n = 22$). In the dietary studies, animals were divided into four groups receiving different diets, *i.e.* high-carbohydrate (CA), high-protein (P), high-fat (HF) and control (C) diets, and were fed *ad libitum* for 2 weeks ($n = 4$–5 per group) or fed once ($n = 6$ per group), to assess both acute and chronic effects of these diets. The compositions of the diets are shown in Table 1. With 2 week feeding, at the end of the 2-week period, the animals were fasted for 18 h. Then, blood, colon and epididymal fat, as a representative white adipose tissue, samples were collected. Tissue samples were homogenized in an adequate amount of ice-cold Isogen (Nippon Gene) directly for mRNA extraction or ice-cold Lysis Buffer (10 mM HEPES pH 7.4, 150 mM NaCl, 2 mM EDTA, 1% Triton-X 100, 2 mM PMSF, 2 μg/ml aprotinin, 5 μg/ml leupeptin) after careful removal of stool, for Western blotting. Serum was separated, after a sufficient time at room temperature to allow coagulation, by centrifugation at 3000 rpm for 20 min followed by 1 min at 15000 rpm. Lipid and other parameters were measured in the sera obtained.

Animal care and procedures for the experiments were performed according to the Japanese guidelines for the care and use of experimental animals.

**Table 1 – Dietary compositions**

| | Control diet (3.58 Kcal/g) | | High carbohydrate (3.55 kcal/g) | | High protein diet (3.47 kcal/g) | | High fat diet (6.66 kcal/g) | |
|---|---|---|---|---|---|---|---|---|
| | %weight | %kcal | %weight | %kcal | %weight | %kcal | %weight | %kcal |
| Protein | 23.3 | 26 | 13 | 14 | 70 | 79.8 | 24.2 | 14.6 |
| Fat | 5.3 | 13.3 | 1 | 4.4 | 1 | 5.7 | 60 | 81 |
| Carbohydrate | 53.8 | 60.1 | 80 | 81.6 | 10 | 12.5 | 7.3 | 4.4 |

### 2.3. *Intraperitoneal glucose tolerance tests*

Glucose tolerance tests were performed after the 2-week feeding period. After an overnight fast, 2 g/kg D-glucose was injected intraperitoneally after the initial glucose measurement. Glucose levels were again determined at 15, 30, 60, 90 and 120 min after the injection. Glucose was measured by tail snipping. Three or four mice from each group were subjected to this test.

### 2.4. *Cell culture*

LS174T cells were obtained from the Cell Resource Center for Biomedical Research (Sendai, Japan), and cultured in RPMI 1640 (Sigma) medium supplemented with 10% FCS (Invitrogen), Penicillin 100 U/ml and Streptomycin 100 μg/ml (GIBCO Invitrogen) at 37 °C in 5% $CO_2$. Cells were cultured on 24 well plates (IWAKI) for the extraction of mRNA for stimulation tests. At 80% confluence, each well was washed twice with PBS and subsequently incubated under various conditions described below for 24 h, and the cells were then subjected to the mRNA extraction.

For insulin and TNFα stimulation, insulin and TNFα were added to RPMI 1640 to give final concentrations of 100 nM and 100 ng/ml, respectively. For glucose stimulation, RPMI 1640 supplemented with D-glucose to achieve final concentrations of 5, 11 or 25 mM was used and RPMI 1640 containing L-glucose at the same concentrations was used for the controls. Furthermore, linoleic acid (LA), oleic acid (OA) and stearic acid (SA) resolved in ethanol and conjugated with 20% bovine serum albumin (BSA) were added to RPMI 1640 to give two final concentrations, 0.5 and 2.0 mM, for each FFA. For control samples, medium adjusted only with ethanol and BSA was used.

### 2.5. *RNA isolation and quantification by real time quantitative polymerase chain reaction*

Total RNA was extracted from murine tissue samples, or cultured LS174T cells, using Isogen (Nippon Gene) according to the manufacturer's instructions. The cDNA was synthesized from total RNA using a First Strand cDNA Synthesis Kit for RT-PCR (Roche Diagnostics) according to the manufacturer's instructions. The oligonucleotide primers were designed using program Primer 3 (http://frodo.wi.mit.edu/cgi-bin/primer3/) and produced by Japan Bio Service, (Saitama, Japan). mRNA expressions for RELMs and resistin were quantified on a Light Cycler Instrument (Roche) using Light Cycler DNA Master SYBR Green I. The results were standardized against internal controls, m36B4 or h36B4 for the mouse tissue and LS174T cell-derived mRNA, respectively. The primer sequences used for human RELMβ (hRELMβ), mouse resistin (mResistin), mouse RELMβ (mRELMβ), mouse RELMγ (mRELMγ), m36B4 and h36B4 are shown in Table 2. The primers for hRELMβ and h36B4 were used as described previously [14,18].

### 2.6. *Histological analysis*

Colonic tissues were routinely embedded in paraffin; approximately 5 μm-thick slices were obtained from these samples. Slices were stained with hematoxylin and eosin (HE) to compare the number of goblet cells. Immunostaining was performed according to the microwave antigen-retrieval technique, using purified anti-mRELMβ antibody (1:500) and a VECSTATIN ABC kit (Vector labs), following the manufacturer's instructions.

### 2.7. *Western blotting*

Twenty micrograms of protein extracted from homogenized colonic tissue or 4 μl of serum was boiled in Laemmli sample buffer containing 100 mmol/l dithiothreitol. Samples were subjected to SDS-PAGE, transferred to Hybond-P membranes (GE Healthcare, Bioscience Inc.), and immunoblotted using purified anti-mRELMβ antibody (1:1000). Proteins were visualized with enhanced chemiluminescence (ECL) and exposed to ECL film (GE Healthcare, Bioscience Inc.). The band intensity was analyzed as described previously [16].

### 2.8. *Statistical analysis*

Stat View-J 5.0 software for windows (SAS Institute Inc.) was used for statistical analysis. Results are expressed as mean ± S.E. In the multiple comparisons, ANOVA followed by the post hoc Fisher's PLSD test was used to compare means between pairs of groups. The unpaired t-test was also used to compare means between pairs of groups.

## 3. Results

### 3.1. *Characterizations of feeding groups, energy intake and changes in serum lipid, glucose and insulin levels*

The body weights, epididymal fat weights, glucose levels, insulin levels and serum lipid levels at the start and after 2

**Table 2 – Primers used for real-time PCR**

| | Sense | Antisense |
|---|---|---|
| m-Resistin | TCATTTCCCCTCCTTTTCCT | AAGCGACCTGCAGCTTACA |
| m-RELMα | TCCAGCTAACTATCCCTCCACTGT | CAGTAGCAGTCATCCCAGCA |
| m-RELMβ | CAAAAAGCTAGAACTGAGCTCCAG | TAGTAATATGAAGACAATGAGTCAGG |
| m-RELMγ | CTTGCCAATCGAGATGACTG | TTTCCAAGTTGGGATTGTGC |
| m-36B4 | GCTCCAAGCAGATGCAGCA | CCGGATGTGAGGCAGCAG |
| h RELMβ | CACCCAGGAGCTCAGAGATCTAA | ACGGCCCCATCCTGTACA |
| h-36B4 | CCACGCTGCTGAACATGCT | TCGAACACCTGCTGGATGAC |

**Table 3a – Characteristics of the dietary groups of the study**

| | Control | High carbohydrate | High protein | High fat |
|---|---|---|---|---|
| Body weight (g) | 19.2 ± 0.32 | 19.2 ± 0.15 | 19.4 ± 0.33 | 19.2 ± 0.22 |
| Blood glucose (mg/dl) | 66.4 ± 3.24 | 67.8 ± 6.34 | 64.7 ± 4.21 | 57.9 ± 3.03 |
| Insulin (ng/ml) | 2.91 ± 0.09 | 3.20 ± 0.31 | 2.80 ± 0.50 | 3.72 ± 0.17 |
| Triglyceride (mg/dl) | 73.8 ± 5.32 | 69.6 ± 4.47 | 76.3 ± 6.56 | 65.9 ± 3.40 |
| Cholesterol (mg/dl) | 82.6 ± 3.07 | 61.8 ± 6.51 | 84.6 ± 4.79 | 80.5 ± 7.27 |
| NEFA (μEq/l) | 1.33 ± 0.06 | 1.28 ± 0.18 | 1.14 ± 0.07 | 1.00 ± 0.05 |

Values are indicated as mean ± S.E. ($n$ = 4–6).
No statistically significant differences between the feeding groups were observed.

**Table 3b – Characteristics of the dietary groups at the end of the 2-week feeding period**

| | Control | High carbohydrate | High protein | High fat |
|---|---|---|---|---|
| Body weight (g) | 21.1 ± 0.6 | 20.4 ± 0.6 | 19.7 ± 1.0 | 23.0 ± 0.3 |
| Blood glucose (mg/dl) | 84.6 ± 6.0 | 90.0 ± 8.4 | 120.6 ± 21.7 | 125.4 ± 17.0 |
| Insulin (ng/ml) | 5.82 ± 1.16 | 4.47 ± 0.66 | 4.64 ± 2.70 | 14.50 ± 3.43* |
| Triglyceride (mg/dl) | 60.7 ± 4.8 | 49.5 ± 4.6 | 45.2 ± 9.8 | 61.2 ± 4.1 |
| Cholesterol (mg/dl) | 87.4 ± 6.0 | 108.1 ± 5.0* | 46.2 ± 6.4* | 98.3 ± 5.3 |
| NEFA (μEq/l) | 0.92 ± 0.09 | 0.86 ± 0.01 | 0.94 ± 0.10 | 0.92 ± 0.04 |
| Epididymal fat (mg) | 115.8 ± 16.1 | 49.6 ± 2.6* | 129.1 ± 29.9 | 404.6 ± 17.0* |

$n$ = 4–6.
* $p < 0.05$.

weeks of feeding are shown in Tables 3a and 3b, respectively. Body weights, glucose levels and lipid profiles at the beginning of the feeding period did not differ significantly among the groups (Table 3a). Body weights of the three different dietary groups did not differ significantly from that of the control group at the end of the 2-week feeding period, though the high-fat group tended to be heavier (Table 3b). Furthermore, the epididymal fat mass of the high-fat group was significantly larger than that of the control group at the end of the 2-week feeding period (C 115.8 ± 16.1 mg, HF 404.6 ± 17.0 mg; $p < 0.01$) (Table 3b). The high-carbohydrate group had a significantly reduced adipose tissue mass as compared to the control group (C 115.8 ± 16.1 mg, CA 49.6 ± 2.6 mg; $p < 0.05$) (Table 3b).

In contrast to the adipose depot mass, serum total cholesterol was slightly elevated in the high-carbohydrate group by the second week (C 87.4 ± 6.0 mg/dl, CA 108.1 ± 5.0 mg/dl; $p = 0.02$). The high-protein group, however, had significantly lower levels at the end of the second week (C 87.4 ± 6.0 mg/dl, P 46.2 ± 6.4 mg/dl; $p < 0.01$) (Table 3b). Serum non-esterified fatty acids (NEFA) and triglyceride levels did not differ significantly among the groups.

### 3.2. *Impaired glucose tolerance in the high-fat diet group*

To assess whether these diets impair glucose tolerance, intraperitoneal glucose tolerance tests were performed at the end of the 2-week feeding period, as described in Section 2 (Fig. 1). The high-fat group showed a significantly greater glucose rise than the control group, and showed this serum glucose elevation was sustained beyond the 120 min of the test. No such obvious glucose intolerance was detected in either the high-carbohydrate or the high-protein group.

### 3.3. *Expression levels of RELMβ and RELMγ in the colon, and of resistin and RELMα in white adipose tissue*

RELMβ expression profiles in fasted and fed states, and the correlations between levels in the colon and ileum are presented in Fig. 2. In the fasted state, the RELMβ protein level was downregulated 43.3 ± 17.2% as compared with that in the fed state (*ad libitum*), which suggests that the diet itself affects RELMβ expression (Fig. 2A and B). There was a positive correlation between RELMβ mRNA levels in the ileum and the colon ($r^2 = 0.604$, $p = 0.0002$), although the RELMβ mRNA level

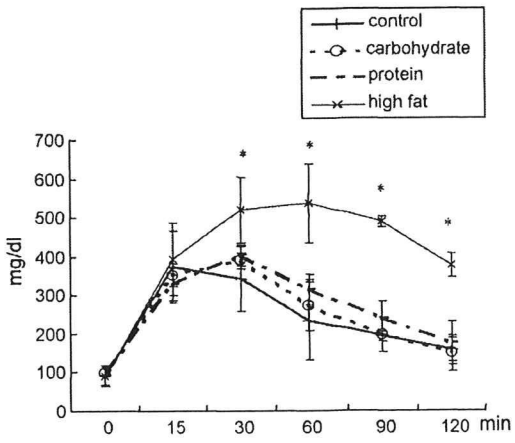


**Fig. 1 – Impaired glucose tolerance in the high-fat diet group. The results of intra-peritoneal glucose tolerance tests done at the end of the second week are shown. Asterisks (*) denote glucose values significantly different from those of the control group. Bars indicate standard errors ($n$ = 3–4).**

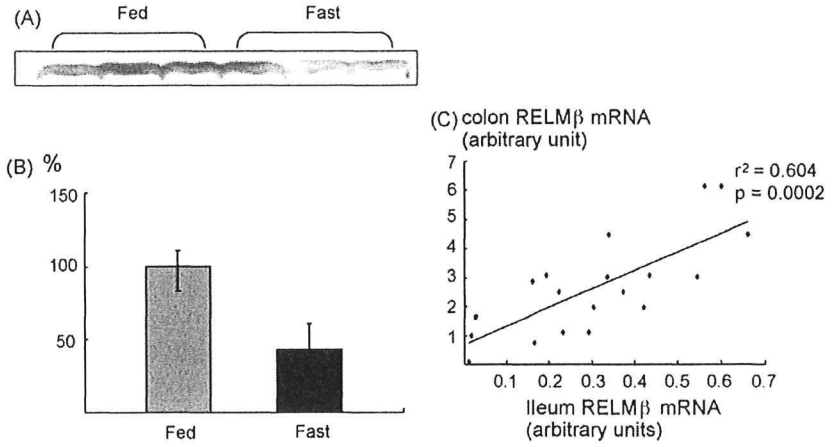


**Fig. 2 – Altered expressions of RELMβ in fed and fasted states and comparison of RELMβ expressions in the ileum and colon. The protein level is shown as band (A), quantification as band (B), using NIH image. Asterisks (*) denote values in the state, which are significantly different from those in the fed state. Bars indicate standard errors ($n = 3$). The RELMβ mRNA level is shown in a scatter plot. The X-axis represents RELMβ from the ileum, the Y-axis that from the colon. Scales of the two are arbitrary but the values correspond to each other.**

in the colon was more variable than that in the ileum, being up to 10 times higher (Fig. 2C). A positive correlation between RELMβ levels in serum and the colon was demonstrated previously [16].

As shown in Fig. 3A, interestingly, it was revealed that the high-carbohydrate and high-protein diets had markedly decreased RELMβ mRNA expression by the end of the 2-week feeding period (C $1.0 \pm 0.34$, CA $0.002 \pm 0.001$; $p = 0.02$, P $0.09 \pm 0.06$; $p < 0.01$) in the colon, while RELMβ mRNA expression in the high-fat group was slightly higher than that of the control group, but this difference was not statistically significant (Fig. 3A). In the ileum and serum, the same tendency was observed, as shown in Fig. 3B and C, although only serum RELMβ in the high protein group changed significantly (C $1.00 \pm 0.15$, CA $0.67 \pm 0.33$, P $0.46 \pm 0.02$, $p < 0.02$, F $1.31 \pm 0.16$ in serum, C $1.00 \pm 0.24$, CA $0.73 \pm 0.10$, P $0.68 \pm 0.06$, F $0.95 \pm 0.23$ in the ileum). These results suggest a strong influence of nutritional components on RELMβ expression in the colon. Furthermore, a single feeding produced no significant change in RELMβ mRNA ($1.00 \pm 0.13$, CA $1.06 \pm 0.23$, P $0.84 \pm 0.04$ or F $0.82 \pm 0.07$) in the colon. The RELMβ mRNA level was changed by the diet itself, although repetitive and chronic stimulation was needed for those dietary components to change the RELMβ mRNA level.

The resistin mRNA analysis of white adipose tissue conducted during the second week of the feeding period, showed no significant differences among the groups (Fig. 4A). The RELMα mRNA expression levels in white adipose tissue

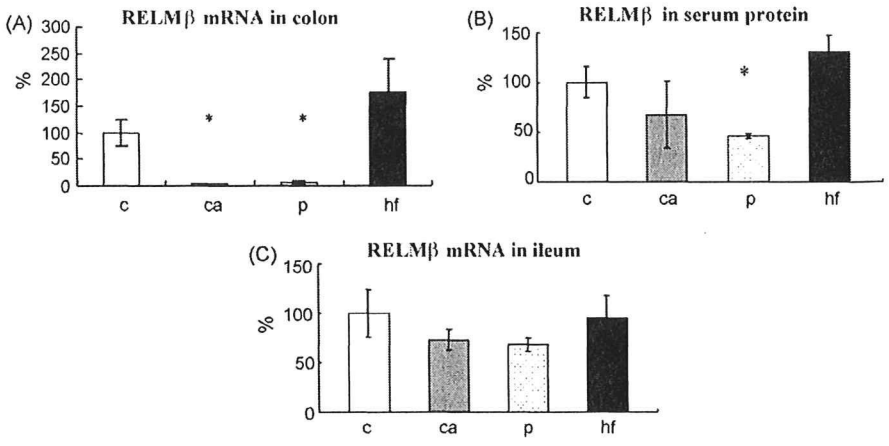


**Fig. 3 – Altered expressions of RELMβ in the colon, ileum and serum in response to various dietary compositions. The mice were given a control, high-carbohydrate, high-protein or high-fat diet for 2 weeks. RELMβ expressions in the colon (A), serum (B) and ileum (C) were investigated and the data are presented as percentages of the control group values. Asterisks (*) denote values significantly different from those of the control group. Bars indicate standard errors ($n = 4$–6).**

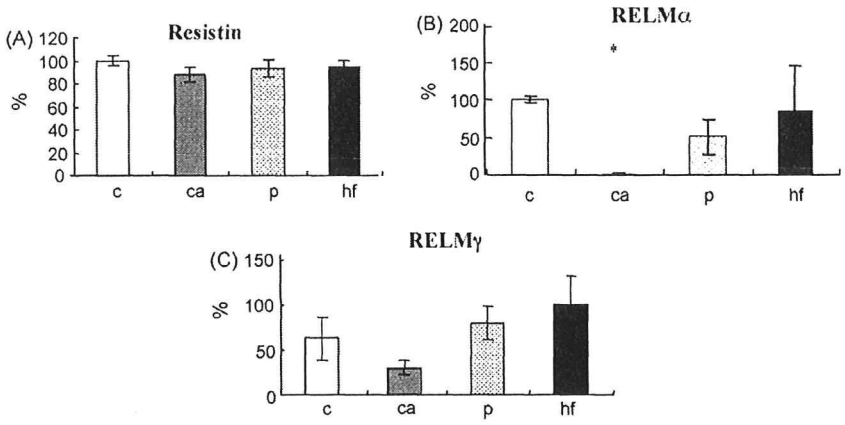


**Fig. 4 – Expressions of resistin and RELMα mRNAs in adipose tissue and RELMγ in the colon in response to various dietary compositions. The mice were given a control, high-carbohydrate, high-protein or high-fat diet for 2 weeks. The expressions of resistin (A) and RELMα (B) mRNAs in adipose tissue and RELMγ (C) in the colon were investigated and the data are presented as percentages of the control group values. Asterisks (*) denote values significantly different from those of the control group. Bars indicate standard errors ($n$ = 4–6).**

are presented in Fig. 4B. RELMγ mRNA expressions in the colon did not differ among the dietary groups (Fig. 4C). Two-week feeding of a high-carbohydrate diet significantly suppressed RELMα expression as compared to the control group, while the high-protein and high-fat diets had no marked effects.

### 3.4. *Histological analysis*

Representative RELMβ immunohistochemistry of the colon, the major RELMβ production site, for each dietary group, is presented in Fig. 5. The high-carbohydrate and high-protein

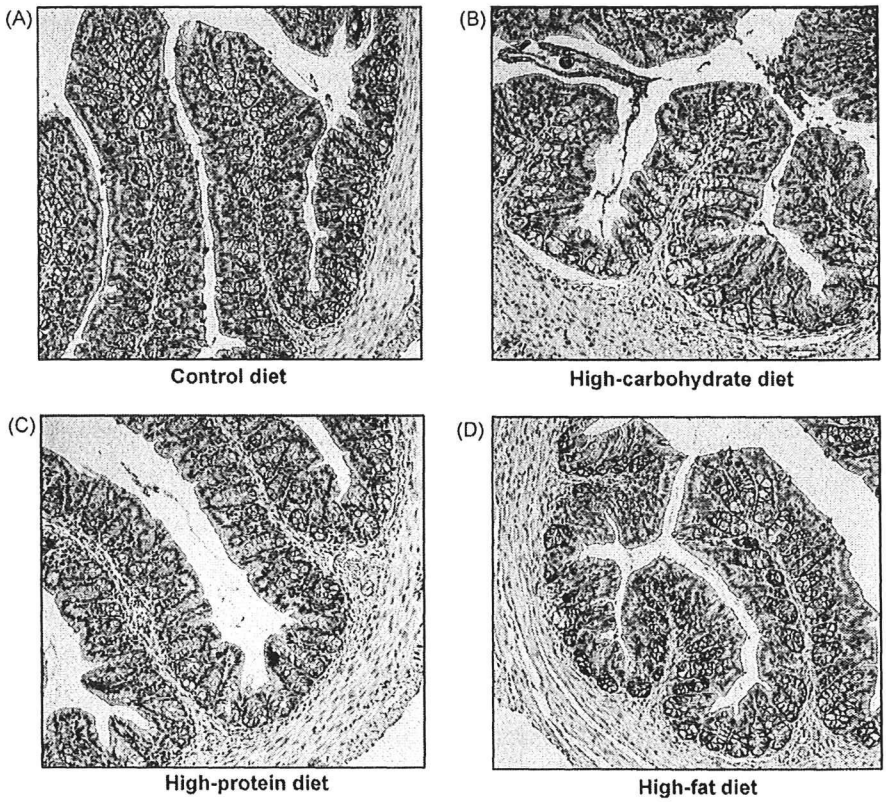


**Fig. 5 – Colonic Immunohistochemistry of RELMβ. Colonic immunohistochemistry of RELMβ (magnification 100×) for each dietary group is shown. RELMβ is identifiable by its brown appearance. (A) Control diet, (B) high-carbohydrate diet, (C) high-protein diet, (D) high-fat diet.**

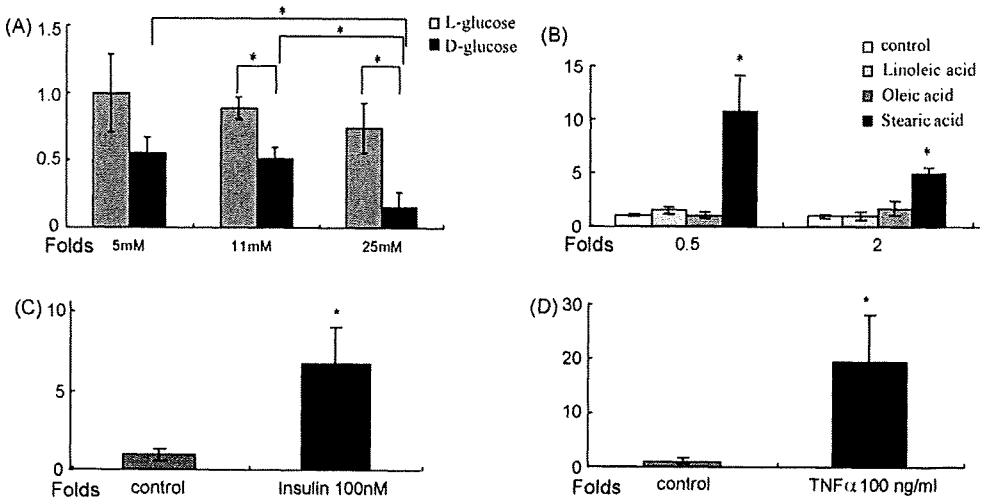


**Fig. 6 – hRELMβ mRNA expression in LS174T cells with different stimuli. The hRELMβ mRNA expressions in LS174T cells after 24 h stimulation, with the agents shown at the indicated concentrations, are presented. (A) The cells were incubated with D-glucose or L-glucose at concentrations of 5 mM, 11 mM and 25 mM. The data are presented as the fold increase compared to the L-glucose group. (B) The cells were incubated with or without linoleic acid, oleic acid or stearic acid at concentrations of 0.5 and 2 mM. The data are shown as fold increases compared to the group without stimulation. (C) The cells were incubated with or without 100 nM insulin. (D) The cells were incubated with or without 100 ng/ml TNFα. Data from four separate experiments are presented and the bars indicate standard errors. The asterisks (*) denote values significantly different from those of the control group.**

diet groups showed significantly less RELMβ expression than the control and high-fat diet groups. HE-stained preparations from all dietary groups were compared for the number of goblet cells. The absence of significant differences in numbers of intestinal goblet cells, among the groups, was also confirmed.

### 3.5. *Changes in hRELMβ mRNA expression in a human colon cancer cell line with various stimulations*

Expressions of hRELMβ mRNA in the human colon cancer cell line LS174T, were compared after stimulation with D-glucose or L-glucose, insulin, TNFα and three types of FFA, as described in Section 2. The results are presented in Fig. 6. Stimulation with D-glucose at 5, 11 and 25 mM significantly reduced the RELMβ mRNA expression in a concentration dependent manner (Fig. 6A). The three FFA exerted different effects on mRNA expression. Stearic acid stimulation resulted in marked upregulation of the RELMβ mRNA level (0.5 mM stearic acid, $10.7 \pm 3.3$ fold; $p < 0.01$, 2.0 mM stearic acid, $3.4 \pm 0.38$ fold; $p < 0.01$), while linoleic and oleic acids had no significant effects (Fig. 6B).

Stimulation with 100 nM insulin induced a 6.7-fold increase in mRNA expression ($p < 0.01$) (Fig. 6C). TNFα stimulation markedly increased RELMβ mRNA expression, by approximately 20 fold ($p < 0.01$) (Fig. 6D).

## 4. Discussion

One major factor contributing to Type 2 diabetes mellitus is insulin resistance, and obesity is known to be the most common factor inducing insulin resistance. Pathophysiological states (i.e. insulin resistance, obesity, and low-grade inflammation) are major and synergistic components of the metabolic syndrome. It was recently demonstrated that adipocytes are not only a lipid depot site, but also actively produce and secrete hormones and cytokines [19]. Resistin is one of these adipocyte-derived proteins and was suggested to play a role in the development of insulin resistance [4].

In addition, it was revealed that resistin and three structurally related RELMs constitute a resistin family [2,3,14]. Only RELMβ among these three RELMs is present in humans. Intestinal RELMβ secretion is reportedly increased in response to bacterial colonization [14] and has been suggested to be involved in the defense mechanism against nematode infestation in mice [15]. On the other hand, administration of RELMβ via the bloodstream induces acute hepatic insulin resistance [20], and transgenic mice over-expressing RELMβ in the liver were shown to exhibit hyperglycemia, hyperlipidemia and fatty liver [17]. These findings suggest that RELMβ is involved in both inflammatory responses intrinsic to the intestine and insulin resistance, particularly in the liver, and therefore may be an important link between these two pathophysiological states. Taking the aforementioned background factors into consideration, we carried out this study to investigate the regulatory effects of various nutritional factors in food on the expressions of RELMβ and other isoforms.

The effects of different nutritional components of diets are now receiving attention, especially in relation to obesity. With the intention of preventing and treating obesity and related diseases, intervention trials have been undertaken [21,22]. Diets rich in carbohydrate and low in fat have been employed, and have been found to reduce the incidence of diabetes by up

to 60%. Diets of similar composition are also recommended by medical societies for the treatment of diabetes [23,24]. Another study revealed that a high-protein diet resulted in substantial and sustained improvements in waist circumference, triglycerides and insulin, whereas with a high carbohydrate diet these changes were more modest [25]. In patients with Type 2 diabetes, a high protein diet reportedly improved glucose metabolism, due to the stimulatory effect of protein on insulin secretion [26].

In the present study, neither the high-carbohydrate nor the high-protein diet for 2 weeks induced either hyperinsulinemia or hyperglycemia in the fasting condition, nor was there any obvious glucose tolerance impairment in mice. Furthermore, epididymal fat tissue masses in both groups were reduced or were similar to those of the control group. These results are in a good accordance with the reported observations in a clinical trial [25]. In this study, we first demonstrated RELMβ expression in mice to be strongly influenced by whether the animals were fasted or fed, and differences in dietary nutritional composition, while resistin expression in adipose tissues did not differ significantly among the dietary groups. Resistin levels in white adipose tissue are reportedly higher in insulin resistant rodent models [4], though others have described contrasting observations [6–8]. Post-transcriptional and/or post-translational modifications, that consequently affect the secretion rate of the protein, have been suggested as possible explanations for this discrepancy.

Since RELMβ is the only RELM in humans, we focused on the regulation of colonic RELMβ expression, which was significantly suppressed in both the high-protein and the high-carbohydrate group. The histological investigations ruled out suppressed RELMβ expression due to a reduced number of goblet cells, and indicated that RELMβ secretion is markedly influenced by nutrients. Therefore, we speculate that protein and carbohydrate exert suppressive effects, or alternatively that an as yet unknown lipid, induces RELMβ expression. We also considered the possible involvement of insulin and TNFα, serum concentrations of which are increased in high-fat diet-induced insulin resistance. To examine these possibilities, a human colon cancer cell line, LS174T, which has been shown to express human RELMβ (RELMβ) under basal conditions [14], was subjected to various culture conditions. The initial incubation of these cells with D-glucose induced significantly lower RELMβ expression, in a D-glucose concentration dependent manner, than the same L-glucose concentrations. Subsequently, it was revealed that only the saturated FFA, i.e. stearic acid, had significant inducing effects on RELMβ mRNA expression, while the other two free fatty acids had little impact.

We also demonstrated insulin and TNFα to markedly increase RELMβ expression. Induction of RELMβ expression by TNFα is an observation in good accordance with previous study results showing induction of RELMβ expression by Th2 cytokines such as Il-4 and IL-13 [15]. Furthermore, the presence of several STAT6 and NFκB elements in the promoter region of human RELMβ was disclosed by sequence analysis [14].

Taking these results together, we can suggest possible mechanisms underlying diet-induced RELMβ regulation. First, repetitive and chronic stimulation by certain free fatty acids, such as stearic acid, or glucose, *per se*, increased and decreased RELMβ expression, respectively. Second, although no supporting data were obtained in this study, it is reasonable to speculate that the different nutritional compositions of foods would affect bacterial colonization in the colon, and that differences in bacterial colonization might affect RELMβ expression either directly or indirectly (*i.e.* systemic hormonal changes) through local Th2 cytokine production. Finally, a high-fat diet enlarges adipocytes, which in turn induces the secretion of various proteins such as TNFα while high-carbohydrate and high-protein diets reduce adipocyte size. In addition, FFA also reportedly induces the release of TNFα from macrophages [27]. TNFα secreted by adipocytes and macrophages would then induce the expression of RELMβ. We speculate that some or all of these mechanisms are involved in the nutrient-induced regulation of RELMβ. The high concentrations of RELMβ secreted by the intestines would reach the liver via the blood stream and thus contribute to the development of insulin resistance.

In conclusion, this study has clearly shown intestinal RELMβ expression to be strongly influenced by the nutritional compositions of foods. Up-regulation by inflammatory mediators, together with the previous demonstration of the RELMβ association with insulin resistance, suggests a role for this protein as a cytokine contributing to the pathogenesis of insulin resistance and thereby to that of the metabolic syndrome.

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# Replication of Genome-Wide Association Studies of Type 2 Diabetes Susceptibility in Japan

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**Background:** In Europeans and populations of European origin, several groups have recently identified novel type 2 diabetes susceptibility genes, including *FTO*, *SLC30A8*, *HHEX*, *CDKAL1*, *CDKN2B*, and *IGF2BP2*, none of which were in the list of functional candidates.

**Objective and Design:** The aim of this study was to replicate in a Japanese population previously identified associations of single nucleotide polymorphisms (SNPs) within 10 candidate loci with type 2 diabetes using a relatively large sample size: 1921 subjects with type 2 diabetes and 1622 normal controls.

**Results:** A total of 15 SNPs were genotyped. Eight SNPs in five loci were found to be associated with type 2 diabetes: rs3802177 [odds ratio (OR) = 1.16 (95% confidence interval (CI) 1.05–1.27); $P = 4.5 \times 10^{-3}$] in *SLC30A8*; rs1111875 [OR = 1.27 (95% CI 1.14–1.40); $P = 1.4 \times 10^{-5}$] and rs7923837 [OR = 1.27 (95% CI 1.13–1.43); $P = 1.0 \times 10^{-4}$] in *HHEX*; rs10811661 [OR = 1.27 (95% CI 1.15–1.40); $P = 1.9 \times 10^{-6}$] in *CDKN2B*; rs4402960 [OR = 1.23 (95% CI 1.11–1.36); $P = 8.1 \times 10^{-5}$] and rs1470579 [OR = 1.18 (95% CI 1.07–1.31); $P = 8.3 \times 10^{-4}$] in *IGF2BP2*; and rs7754840 [OR = 1.28 (95% CI 1.17–1.41); $P = 4.5 \times 10^{-7}$] and rs7756992 [OR = 1.27 (95% CI 1.15–1.40); $P = 9.8 \times 10^{-7}$] in *CDKAL1*. The first and second strongest associations were found at variants in *CDKAL1 and CDKN2B*, both of which are involved in the regenerative capacity of pancreatic β-cells.

**Conclusion:** Some of these variants represent common type 2 diabetes-susceptibility genes in both Japanese and Europeans. (***J Clin Endocrinol Metab* 93: 3136–3141, 2008**)

Type 2 diabetes is a complex disease with several genes and environmental factors involved in onset and development. To date, a number of genes have been reported to be associated with type 2 diabetes. Most of these were investigated because of their assumed relevance to the pathogenesis of type 2 diabetes based on their functions. However, because the pathogenesis of

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Abbreviations: BMI, Body mass index; *CDKAL1*, cyclin-dependent kinase inhibitor 5 regulatory subunit associated protein 1-like 1 gene; *CDKN2B*, cyclin-dependent kinase inhibitor 2B gene; CI, confidence interval; *EXT2*, exostosin 2; *FTO*, fat mass and obesity associated gene; *GCKR*, glucokinase regulatory protein gene; *HHEX*, hematopoietically expressed homeobox gene; HOMA, homeostasis model assessment; HOMA-β, homeostasis model assessment of β-cell function; HOMA-IR, homeostasis model assessment of insulin resistance; *IGF2BP2*, IGF2 mRNA binding protein 2 gene; LD, linkage disequilibrium; OR, odds ratio; *SLC30A8*, zinc transporter gene; SNP, single nucleotide polymorphism; TG, triglyceride.

type 2 diabetes is yet to be elucidated completely, the candidate-gene approach is limited in power to detect novel disease-susceptibility genes. A strongly associated type 2 diabetes gene, transcription factor 7-like 2, has been identified by a genome-wide linkage study (1). Several groups confirmed a significant association between type 2 diabetes and this gene in various populations, with some noteworthy exceptions (2–7). Genome-wide association studies using 300,000–500,000 single nucleotide polymorphisms (SNPs) and high throughput technology overcome the limitation of function-based investigation, and novel susceptibility genes for type 2 diabetes, including zinc transporter (*SLC30A8*), hematopoietically expressed homeobox (*HHEX*), cyclin-dependent kinase inhibitor 2B (*CDKN2B*), IGF2 mRNA binding protein 2 (*IGF2BP2*), and CDK5 regulatory subunit associated protein 1-like 1 (*CDKAL1*), have recently been identified. In addition, the fat mass and obesity associated gene (*FTO*) and glucokinase regulatory protein gene (*GCKR*) were associated with body mass index (BMI) and serum triglyceride (TG) level, respectively (8–13). All of these proven genes for type 2 diabetes have been reproducibly associated in multiple studies (14). Meanwhile, exostosin 2 (*EXT2*), *LOC387761* (11), and an intergenic signal (rs9300039) (9) were identified in a single study and have not been replicated. However, most of the populations analyzed were of European ancestry, except in the case of *CDKAL1*, which was replicated in subjects from Hong-Kong. To distinguish variants that are common and reproducible susceptibility genes, it is important to replicate the associations of candidate SNPs with type 2 diabetes in various ethnic groups. In this study we examined the association of recently identified risk SNPs in 10 candidate loci with type 2 diabetes in a relatively large sample set of Japanese subjects.

## Subjects and Methods

### Subjects

Three sample sets were involved. The Kobe set and the Gunma set subjects were recruited from hospitals in Hyogo and Gunma prefecture, respectively. The Consortium set subjects were recruited from seven districts in Japan by the Study Group of the Millennium Genome Project for Diabetes Mellitus. The inclusion criteria for normal, control subjects of these three sets were as follows: 1) older than 60 yr, 2) glycosylated hemoglobin $A_{1c}$ values less than 5.8%, and 3) no past history of type 2 diabetes. Type 2 diabetes was diagnosed in accordance with World Health Organization criteria. Other forms of diabetes were excluded based on the clinical data. The clinical and laboratory characteristics of the study subjects are shown in supplemental Table 1, which is published as supplemental data on The Endocrine Society's Journals Online web site at http://jcem.endojournals.org. Written, informed consent was obtained from all participants. This study was approved by the ethics committee of each participating institute (6).

### Genotyping

There were 15 SNPs genotyped using TaqMan SNP Genotyping Assays (Applied Biosystems, Foster City, CA). These SNPs were selected based on previous reports (8–13) and HapMap linkage disequilibrium (LD) data of Japanese. Departures from Hardy Weinberg Equilibrium were defined as $P < 0.001$ in cases and controls (11). Because SNP rs13266634 in *SLC30A8* was deviated from Hardy Weinberg Equilibrium, SNP rs3802177 in the same gene, which is in strong LD with rs13266634 ($r^2 = 0.96$, HapMap LD data of Japanese), was also examined. The genotyping success rate in the three sample sets was more than 96%. The genotypes determined by TaqMan methods were identical to those determined by direct sequencing for 48 samples. The risk allele of each SNP is shown in supplemental Table 2.

### Clinical assessment

The clinical profile of each subject was directly determined at entry. Association studies were performed between the candidate SNPs and BMI, homeostasis model assessment (HOMA) [HOMA of insulin resistance (HOMA-IR) and HOMA of β-cell function (HOMA-β)], or serum TG level. Subjects who had not been treated with insulin were evaluated for HOMA-IR and HOMA-β. Data are expressed as means ± SD.

### Statistical analysis

The differences in SNPs between type 2 diabetic and nondiabetic subjects were compared using $\chi^2$ test and multiple logistic regression analysis under additive, dominant, and recessive models for SNPs. The Cochran-Armitage trend test was also performed with the additive model. There was no heterogeneity among the samples in regard to the recruiting districts. We considered statistical significance at $P$ values less than 0.0033 (0.05/15) in the association study for SNPs after Bonferroni correction. The relation of the variants in these genes with BMI, HOMA-IR, HOMA-β, and TG was assessed by ANOVA for each SNP. The HOMA-IR, HOMA-β, and TG data were log transformed for normality. Statistical analysis was performed with the StatView program (version 5.0-J; SAS Institute Inc., Cary, NC). LD analysis was performed with Haploview (http://www.broad.mit.edu/personal/jcbarret/haploview).

## Results

There were 15 SNPs from 10 candidate loci examined for association with type 2 diabetes with a criterion of significance of $P$ value less than $0.05/15 = 0.0033$ after Bonferroni adjustment. Eight SNPs in five loci, *SLC30A8* (rs3802177), *HHEX* (rs1111875, rs7923837), *CDKN2B* (rs10811661), *IGF2BP2* (rs4402960, rs1470579), and *CDKAL1* (rs7754840, rs7756992), were found to be associated with the occurrence of type 2 diabetes (Tables 1 and 2). The $P$ values of association for *CDKN2B* (rs10811661) and *CDKAL1* (rs7754840 and rs7756992) were about $1.9 \times 10^{-6}$, $4.5 \times 10^{-7}$, and $9.8 \times 10^{-7}$, respectively. The next strongest association was found for *IGF2BP2* (rs4402960 and rs1470579) and *HHEX* (rs1111875 and rs7923837) at a $P$ value of $10^{-4}$–$10^{-5}$. SNP rs3802177 of *SLC30A8* showed a nominal association, which disappeared after adjustment for age, sex, and BMI. No association of the other SNPs with type 2 diabetes was detected.

Association studies were also performed between *FTO* and BMI and *GCKR* and serum TG level using the samples with serum data according to previous reports. A nominal association of *GCKR* (rs780094) with serum TG level both in case and control subjects was found in our samples, as previously reported in Caucasians (10). In control subjects the mean values of serum TG were 1.07 ± 0.53, 1.13 ± 0.49, and 1.18 ± 0.55 mmol/liter for CC, CT, and TT genotype, respectively ($P = 0.097$). In cases, these values were 1.32 ± 0.73, 1.43 ± 1.57, and 1.56 ± 1.05 mmol/liter for CC, CT, and TT genotype, respectively ($P = 0.063$). Association of the SNP of *FTO* (rs9939609) with BMI

**TABLE 1.** Association results between 15 SNPs in 10 candidate loci and type 2 diabetes in Japanese

| Gene | SNP ID | Genotype T2DM | | | Genotype CONT | | | RAF | | P value | Armitage trend | P value[a] | OR | 95% CI | | RAF-C | OR -C |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | RR | Rr | rr | RR | Rr | rr | T2DM | CONT | | | | | Upper | Lower | | |
| *SLC30A8* | rs13266634 | 690 | 806 | 334 | 522 | 725 | 327 | 0.60 | 0.56 | $3.2 \times 10^{-3}$ | $4.5 \times 10^{-3}$ | 0.17 | 1.16 | 1.05 | 1.27 | 0.65 | 1.12 |
| *SLC30A8* | rs3802177 | 649 | 885 | 306 | 473 | 808 | 291 | 0.59 | 0.56 | $3.2 \times 10^{-3}$ | $3.0 \times 10^{-3}$ | 0.065 | 1.16 | 1.05 | 1.27 | | |
| *HHEX* | rs1111875 | 212 | 784 | 852 | 132 | 603 | 828 | 0.33 | 0.28 | $9.6 \times 10^{-6}$ | $1.4 \times 10^{-5}$ | $8.4 \times 10^{-5}$ | 1.27 | 1.14 | 1.40 | 0.53 | 1.13 |
| *HHEX* | rs7923837 | 98 | 633 | 1113 | 60 | 467 | 1049 | 0.22 | 0.19 | $8.8 \times 10^{-5}$ | $1.0 \times 10^{-4}$ | $6.7 \times 10^{-3}$ | 1.27 | 1.13 | 1.43 | 0.62 | 1.22 |
| *LOC387761* | rs7480010 | 1226 | 556 | 68 | 1018 | 481 | 67 | 0.81 | 0.80 | 0.33[a] | 0.33[a] | 0.29 | 1.06 | 0.94 | 1.20 | | |
| *EXT2* | rs3740878 | 260 | 842 | 731 | 211 | 738 | 629 | 0.37 | 0.37 | 0.73[a] | 0.74[a] | 0.63 | 1.02 | 0.92 | 1.12 | | |
| *CDKN2B* | rs10811661 | 683 | 891 | 283 | 486 | 770 | 326 | 0.61 | 0.55 | $1.7 \times 10^{-6}$ | $1.9 \times 10^{-6}$ | $5.8 \times 10^{-6}$ | 1.27 | 1.15 | 1.40 | 0.83 | 1.20 |
| *CDKN2B* | rs564398 | 1342 | 482 | 47 | 1122 | 416 | 41 | 0.85 | 0.84 | 0.67[a] | 0.67[a] | 0.65 | 1.03 | 0.90 | 1.17 | 0.56 | 1.12 |
| *GCKR* | rs7800944 | 421 | 903 | 534 | 312 | 782 | 492 | 0.47 | 0.44 | 0.029[a] | 0.030[a] | 0.017 | 1.11 | 1.01 | 1.22 | | |
| Inter gene | rs9300039 | 1068 | 684 | 105 | 903 | 565 | 111 | 0.76 | 0.75 | 0.41[a] | 0.42[a] | 0.15 | 1.05 | 0.94 | 1.17 | | |
| *IGF2BP2* | rs4402960 | 230 | 835 | 787 | 143 | 675 | 759 | 0.35 | 0.30 | $7.9 \times 10^{-5}$ | $8.1 \times 10^{-5}$ | $9.4 \times 10^{-4}$ | 1.23 | 1.11 | 1.36 | 0.29 | 1.14 |
| *IGF2BP2* | rs1470579 | 260 | 874 | 738 | 165 | 735 | 694 | 0.37 | 0.33 | $9.0 \times 10^{-4}$ | $8.3 \times 10^{-4}$ | $2.8 \times 10^{-3}$ | 1.18 | 1.07 | 1.31 | 0.30 | 1.17 |
| *CDKAL1* | rs7754840 | 446 | 881 | 543 | 262 | 781 | 538 | 0.47 | 0.41 | $3.2 \times 10^{-7}$ | $4.5 \times 10^{-7}$ | $3.5 \times 10^{-7}$ | 1.28 | 1.17 | 1.41 | 0.31 | 1.12 |
| *CDKAL1* | rs7756992 | 537 | 876 | 442 | 330 | 818 | 438 | 0.53 | 0.47 | $8.0 \times 10^{-7}$ | $9.8 \times 10^{-7}$ | $3.9 \times 10^{-6}$ | 1.27 | 1.15 | 1.40 | 0.26 | 1.20 |
| *FTO* | rs9939609 | 88 | 596 | 1165 | 63 | 520 | 995 | 0.21 | 0.20 | 0.68[a] | 0.68[a] | 0.74 | 1.03 | 0.91 | 1.15 | | |

ORs, 95% CIs, and *P* values are given for 15 SNPs identified in French, decode, Diabetes Genetics Initiative, Wellcome Trust Case Control Consortium, and Finland-United States Investigation of Noninsulin-Dependent Diabetes Mellitus Genetics studies. SNPs are shown with the risk allele (R) and risk allele frequency (RAF) and the exact count of each genotype in type 2 diabetic (T2DM) patients and controls (CONT). Risk allele-specific ORs and *P* values were calculated using an additive genetic model that in logistic regression is multiplicative on the OR scale. $r^2 = 0.83$ (rs13266634 and rs3802177), 0.22 (rs1111875 and rs7923837), 0.001 (rs10811661 and rs10811661), 0.87 (rs4402960 and rs1470579), and 0.69 (rs7754840 and rs7756992) in controls of this study. ID, Identification; OR-C, OR in Caucasians; r, nonrisk allele; RAF-C, risk allele frequency in Caucasian controls.

[a] *P* values adjusted for age, sex, and BMI.