heterozygosities, and this further confirms that the Ainu population has experienced admixture with the two surrounding populations. In fact, we came to know through discussion with the Ainu people that there were some Mainlaind Japanese individuals who married Ainu people in Biratori Town when blood collection was conducted. These genetically non-Ainu people might have been included in the 'Ainu' samples we used. Another information from the Ainu representatives of the Biratori Town was that some Sakhalin Ainu people migrated to that town after the World War II. There is a possibility that the five outliers in the red circle in Figure 1a are Sakhalin Ainu people.

Another possible reason for the low average heterozygosity in the Ainu compared with other populations is ascertainment bias in which SNPs included in the Affymetrix 6.0 genechip were chosen based on their polymorphism in only a few ascertained populations.

Possible mother population for the alternative admixture events with the Ainu population

Unlike admixture with the Mainland Japanese, it is difficult to ascertain the other potential source of admixture in the Ainu without a proper source population. Previous studies did support the idea of contact with Northern populations, which may have contributed to the genetic diversity in the Ainu. Archeological data point to an introduction of a distinct culture, which was quite different from the Satsumon culture, by the Okhotsk people into Hokkaido during the 7th–10th centuries.[52] The cultural contact with these northern peoples seemed to continue until recently. Genetic studies using mitochondrial DNA[24] and human leukocyte antigen loci[32] support this idea by showing close affinities between the Ainu and the Nivkhi who live in the Sakhalin Island and the Amur River region. It would therefore be interesting to collect samples from populations from that area in future studies to have a clearer view of the relationships between the Ainu and Northeast Asian populations.

Perspectives

We still have no clear clues on homelands of the Jomon and the Yayoi people, who constituted the two major genetic components of the modern human populations in the Japanese Archipelago. It should be noted that Omoto[53] conducted a pioneering study on the phylogenetic relationship of the Ainu population considering various degrees of admixture. When a 60% admixture with the Mainland Japanese was assumed for the modern Ainu population, the ancestral Ainu population was clustered with Sahulian (Papuan and Australian).[53] This sort of simulations based on the real data is needed.

We should also integrate evidences from various research fields such as archeology and morphology. There is a long history of craniofacial studies on Jomon, Yayoi and historical populations in the Japanese Archipelago.[1,3,54] Although metric characters were mostly used, studies on nonmetric characters are promising,[55–58] for they are expected to be more under genetic controls than metric ones. Hanihara's analysis[58] suggested the existence of gene flows between the Hokkaido Jomon people and the Okhotsk people. An application of the computed tomography images for measuring nonmetric cranial variations in living humans was already started,[59] and genome-wide association studies of morphological characters are waiting to be initiated. In fact, the genetic background of shovel-shaped incisors found frequently in East Asian individuals was recently deciphered,[60] and the nonsynonymous polymorphism on the *EDAR* gene showed the greatest difference in SNP genotype frequencies between the Mainland Japanese and Ryukyuan clusters,[36] followed by another nonsynonymous polymorphism on the *ABCC11* gene that is responsible for the earwax phenotypic differences.[61] Similar statistical analyses will be conducted in the near future using the genome-wide SNP data produced by this study. Genomic DNA polymorphisms are not restricted to SNPs, but also include insertion–deletion type polymorphisms such as microsatellite polymorphisms (for example, Li *et al.*[62]).

Ancient DNA data are very important for understanding the evolutionary history of the present-day organisms. Because of technical difficulties, most of the ancient DNA data available regarding the origin of peoples in the Japanese Archipelago are mitochondrial DNAs,[63–71] with exceptions of the *ABCC11* gene[72] and the ABO blood group gene.[73] If the genome-wide nuclear DNA polymorphism data can be obtained for ancient DNA samples found from the Japanese Archipelago, we will be able to have a much wider scope on the history of peoples in this Archipelago.

Conclusion

We demonstrated that the Ainu are genetically closer to the Ryukyuan than they are to the Mainland Japanese in this study. The close association between the Ainu and the Ryukyuan, despite their current geographical locations, which is at the two opposing ends of the Japanese Archipelago, may be interpreted as having a shared common ancestry probably dating back to the Jomon period. The population tree in Figure 4b also places the Mainland Japanese in an intermediate position between the Ainu/Ryukyuan and the Continental population clusters. This observation, coupled with the very short external branch in the Mainland Japanese, strongly suggests that they are the result of admixture between the two genetically distinct ancestors, namely the Jomon people and the Yayoi ancestors. Our analysis revealed a great genetic variation within the individuals of the Ainu group, brought about by admixture with the mainland Japanese and possibly another population from Northeast Asia. Figure 5 depicts a plausible time course of the human populations in the three regions of the Japanese Archipelago based on the findings of this study, though many features are still speculative. In conclusion, our results support the more

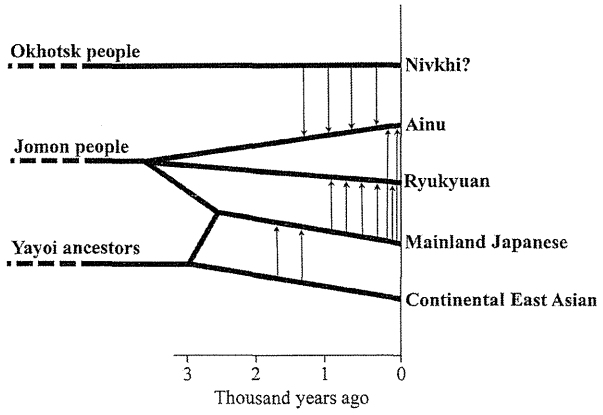

Figure 5 A scenario of the evolutionary history of the human populations in the three regions of the Japanese Archipelago based on the results of this study and archeological evidences.[52] The Northern, the Central and the Southern populations, corresponding to the Ainu, the Mainland Japanese and the Ryukyuan in the present day, were assumed to diverge simultaneously, sometime during the Jomon period, although we do not have a precise time estimate. The admixture of the indigenous Jomon people and Yayoi migrants was assumed to occur sometime after the Yayoi period started 3000 years ago.[76] Vertical arrows designate gene flows in historical times, but their timings and frequencies are rather speculative.

than 100-year-old hypothesis of von Baelz[4] that the Ainu and the Ryukyuan have shared genetic ancestry, and the admixture hypothesis (for example, Torii[74] and Kanaseki[75]) that the mainland Japanese are the result of admixture between the ancestral Yayoi people and the indigenous Jomon people.

The SNP genotype data determined in this study are available upon requests to corresponding authors, under the conditions of collaboration with us and with an appropriate approval of human genomic DNA research ethics committee of institutions to which researchers involved in the data analyses belong.

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ORIGINAL ARTICLE

The Radioprotective 105/MD-1 Complex Contributes to Diet-Induced Obesity and Adipose Tissue Inflammation

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Recent accumulating evidence suggests that innate immunity is associated with obesity-induced chronic inflammation and metabolic disorders. Here, we show that a Toll-like receptor (TLR) protein, radioprotective 105 (RP105)/myeloid differentiation protein (MD)-1 complex, contributes to high-fat diet (HFD)-induced obesity, adipose tissue inflammation, and insulin resistance. An HFD dramatically increased RP105 mRNA and protein expression in stromal vascular fraction of epididymal white adipose tissue (eWAT) in wild-type (WT) mice. RP105 mRNA expression also was significantly increased in the visceral adipose tissue of obese human subjects relative to nonobese subjects. The RP105/MD-1 complex was expressed by most adipose tissue macrophages (ATMs). An HFD increased RP105/MD-1 expression on the M1 subset of ATMs that accumulate in eWAT. Macrophages also acquired this characteristic in coculture with 3T3-L1 adipocytes. RP105 knockout (KO) and MD-1 KO mice had less HFD-induced adipose tissue inflammation, hepatic steatosis, and insulin resistance compared with wild-type (WT) and TLR4 KO mice. Finally, the saturated fatty acids, palmitic and stearic acids, are endogenous ligands for TLR4, but they did not activate RP105/MD-1. Thus, the RP105/MD-1 complex is a major mediator of adipose tissue inflammation independent of TLR4 signaling and may represent a novel therapeutic target for obesity-associated metabolic disorders. ***Diabetes* 61:1199–1209, 2012**

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Obesity is associated with chronic low-grade inflammation characterized by increased proinflammatory cytokines and infiltration of macrophages within adipose tissue (1), leading to insulin resistance (2). Although several inflammatory mediators and cell types promote these processes, precise roles of the immune system are not fully understood. Most of the infiltrated adipose tissue macrophages (ATMs) in obese adipose tissue are CD11c-positive inflammatory M1 macrophages responsible for the development of adipose tissue inflammation, which is countered by CD206-positive anti-inflammatory M2 macrophages (3,4).

Pattern recognition receptors (PRRs) such as Toll-like receptors (TLRs) quickly recognize pathogenic agents called pathogen-associated molecular patterns (5). The TLR4/myeloid differentiation protein (MD)-2 complex is indispensable for lipopolysaccharide (LPS) recognition (6,7). TLR4 requires two important adaptor molecules, myeloid differentiation factor 88 (MyD88) and TIR-domain-containing adaptor-inducing interferon-β (TRIF), to transmit its downstream signaling (5). A TLR4 homolog, radioprotective 105 (RP105), forms a complex with MD-1 (8,9). RP105 or MD-1 knockout (KO) mice show reduced proliferative responses to LPS in B cells and are impaired in hapten-specific antibody production against LPS (10–12), suggesting that the RP105/MD-1 complex cooperates with the TLR4/MD-2 complex in LPS responses. RP105/MD-1 also is expressed on macrophages (12). However, roles for RP105/MD-1 in chronic inflammation–associated metabolic disorders have not been suspected.

PRRs also can sense endogenous ligands called danger-associated molecular patterns. These include intracellular molecules such as fatty acids (FAs), heat shock proteins, and host nucleic acids, as well as extracellular components, such as hyaluronan and proteoglycans (13). These molecules can ligate PRRs, leading to activation of proinflammatory pathways and cytokine secretion. This often is referred to as "sterile" inflammation (14).

Adipose tissue–derived saturated free FAs may stimulate TLR4 and promote adipose tissue inflammation and insulin resistance (15–17). The Nlrp3 (nucleotide-binding domain, leucine-rich repeats containing family, pyrin domain-containing-3) inflammasome senses obesity-associated FAs and contributes to obesity-induced inflammation and insulin resistance (18,19). Double-stranded RNA-dependent protein kinase can sense FAs from nutrients as well as endoplasmic reticulum stress and plays critical roles in regulating insulin action and metabolism (20). Of interest, the G-protein–coupled receptor 120 recognizes unsaturated

omega-3 FAs (docosahexaenoic acid and eicosapentaenoic acid) and mediates insulin sensitizing by suppressing macrophage-induced inflammation (21). However, it remains unclear whether RP105/MD-1 has a role in sensing obesity-related natural ligand or whether the complex participates in immune responses leading to diet-induced chronic inflammation and insulin resistance.

We now report that RP105 or MD-1 KO mice were protected from high-fat diet (HFD)-induced obesity, hepatic steatosis, insulin resistance, and adipose tissue inflammation. RP105/MD-1 was expressed on macrophages in the stromal vascular fraction (SVF) of epididymal white adipose tissue (eWAT). RP105 mRNA expression was significantly increased in the visceral adipose tissue (VAT) of obese subjects. An HFD and coculture with adipocytes dramatically increased the expression of RP105 by macrophages. Endogenous TLR4 ligands, palmitic and stearic acids, did not stimulate RP105/MD-1. Therefore, the RP105/MD-1 receptor complex contributes in unique ways to diet-induced obesity and related inflammatory responses.

RESEARCH DESIGN AND METHODS

Mice. C57BL/6 mice were purchased from Japan SLC (Hamamatsu, Japan) and were used at 10 weeks of age. Mice were fed an HFD containing 60% fat (Research Diet, New Brunswick, NJ) or a standard diet containing 10% fat starting at 10 weeks of age for 12 weeks. Male mice were maintained in microisolator cages under specific pathogen-free conditions with a 12-h light/12-h dark cycle in the animal facility of University of Toyama and given free access to food and water. All experiments were performed according to the guidelines for the care and treatment of experimental animals at the University of Toyama.

Reagents. LPS from *Escherichia coli* O55:B5, palmitic, stearic, and lauric acids were purchased from Sigma-Aldrich (St. Louis, MO).

Human study. A total of 18 Japanese male patients with urological diseases who received surgery in Tokushima University Hospital were recruited in this study (Supplementary Table 1). Adipose tissue around the kidney or prostate was obtained as VAT samples. Subcutaneous adipose tissue (SAT) samples were obtained from the abdominal walls during urological surgery. This study protocol was approved by the ethics committee on human research of the University of Tokushima Graduate School and University of Toyama.

Metabolic measurements. Serum total cholesterol and alanine transaminase (ALT) were measured by Reflotron-plus (Roche Diagnostics, Mannheim, Germany). The glucose tolerance test (GTT) was performed by intraperitoneally injecting 1 g glucose/kg. For the insulin tolerance test (ITT), the mice were injected with 0.75 units of human insulin/kg i.p. (Eli Lilly, Indianapolis, IN). Blood glucose was measured by NIPRO FreeStyle FLASH (NIPRO, Osaka, Japan), and serum insulin was measured by an enzyme-linked immunosorbent assay kit (Shibayagi, Shibukawa, Japan).

Measurement of Vo_2, Vco_2, and respiratory quotient. Mice were placed in standard metabolic cages (model MK5000RQ; Muromachikikai, Tokyo, Japan) with an airflow of 0.5 L/min. Oxygen consumption (Vo_2) and carbon dioxide production (Vco_2) were measured during 3 consecutive days (three dark cycles and two light cycles). Respiratory quotient (R_Q) was calculated as a ratio of Vco_2 to Vo_2.

Isolation of adipocytes and SVF from eWAT. Mice were fasted for 12 h before dissection. Isolation of adipocytes and SVF was performed as described previously (4).

Flow cytometry analysis. The cells (1×10^5) were incubated with anti-mouse FcγR (2.4G2) to block binding of the labeled antibodies to FcγR. After 15 min, the cells were stained with predetermined optimal concentrations of the respective antibodies. 7-Amino-actinomycin D (BD Bioscience, San Diego, CA) was used to exclude dead cells. Flow cytometry analyses were conducted on a FACSCanto (Becton Dickinson, Mountain View, CA), and the data were analyzed with Flowjo software (Treestar, San Carlos, CA). The information for antibodies is listed in Supplementary Table 2.

Cell culture. RAW264.7 cells (RIKEN BioResource Center, Tsukuba, Japan) and 3T3-L1 cells (American Type Culture Collection, Manassas, VA) were maintained with DMEM containing 10% fetal calf serum and antibiotics and incubated at 37°C in a humidified 5% CO_2. 3T3-L1 cells were differentiated based on a standard protocol (22). Bone marrow–derived macrophages (BMMs) were differentiated into M1 and M2 macrophages as described previously (23).

Coculture of adipocytes and macrophages. Coculture of 3T3-L1 cells and macrophages was performed as described previously (17). RAW264.7 cells were cocultured with the 3T3-L1 cells in the absence or presence of pioglitazone (Funakoshi, Tokyo, Japan) for 24 h.

Real-time quantitative PCR. Total RNA was isolated with an RNeasy mini kit (Qiagen, Hilden, Germany) or TRIzol Reagent (Invitrogen, Carlsbad, CA). RNA was reverse transcribed with a TaqMan Reverse Transcription Reagents (Applied Biosystems, Carlsbad, CA). Real-time quantitative PCR (RT-qPCR) was performed with a TaqMan Gene Expression Master Mix (Applied Biosystems) and analyzed with an Mx3000P (Agilent Technologies, Santa Clara, CA). Relative transcript abundance was normalized for that of Hprt mRNA. The information for primers is listed in Supplementary Table 3.

Immunoprecipitation and Western blot analysis. The immunoprecipitation for RP105 was performed by using anti-RP105 (RP/14) (24). To detect RP105 by Western blotting, the anti-RP105 (0.5 μg/mL) (ProSci, Poway, CA) and horseradish peroxidase–conjugated anti-rabbit IgG (Cell Signaling, Beverly, MA) were used. Anti-actin was purchased from Sigma-Aldrich. The reactive bands were visualized by ECL Plus (GE Healthcare, Little Chalfont, Bucks, U.K.).

Immunohistochemistry analysis. Portions of the liver and eWAT were excised and immediately fixed with 4% formaldehyde at room temperature. Paraffin-embedded tissue sections were cut into 4-mm slices and placed on slides. CD11c staining was performed as described previously (4). The sections were incubated with anti–Mac-2 (macrophage surface glycoproteins binding to galectin-3), anti–MD-1 (MD113), or anti-RP105 (ProSci) for 1 h and then with ready-to-use polymered secondary antibodies for rat or rabbit monoclonal antibodies with peroxydase (Envision-PO; Dako, Glostrup, Denmark) for 1 h. Bound antibodies were detected with 3,3′-diaminobenzidine. Sections were counterstained with hematoxylin.

Statistical analysis. Statistical significance was evaluated by one-way ANOVA followed by a post hoc Tukey test. $P < 0.05$ was considered statistically significant.

RESULTS

RP105 expression dramatically increases in the adipose tissue from HFD-fed mice and obese subjects. Our initial studies evaluated the expression of genes encoding RP105/MD-1, TLRs, MD-2, and components involved in TLR signaling in the eWAT from WT mice fed with a normal diet (ND) or an HFD (Fig. 1*A*). HFD treatment markedly increased the expression of RP105 mRNA by 13-fold. The expression of MD-1, TLR1, TLR7, TLR8, and TLR9 mRNA also was increased by HFD, whereas the expression of TLR4 and MD-2 mRNA was not affected. The MyD88 and TRIF are critical adaptor molecules for TLR4 signaling (5) but are not involved in RP105 signaling (data not shown). MyD88 and TRIF mRNA, as well as TLR4 mRNA, were not increased by an HFD in eWAT (Fig. 1*A*). RP105 and MD-1 mRNAs also were significantly increased in other WAT depots, such as subcutaneous and retroperitoneal WAT, by an HFD (Supplementary Fig. 1). Levels of TLR4 mRNA in retroperitoneal adipose tissue were slightly increased by an HFD. HFD also increased RP105 mRNA in the liver, brown adipose tissue, and skeletal muscle by 1.6-, 3-, and 1.7-fold, respectively (Supplementary Fig. 2). In addition, the expression of RP105 and MD-1 mRNA in the spleen and bone marrow was not significantly affected by an HFD. Expression of TLR4, MD-2, MyD88, and TRIF in these tissues was not significantly affected by an HFD.

To test the clinical relevance of data generated from mouse models, we examined RP105 and MD-1 mRNA expression in human adipose tissue. Linear regression analyses showed a positive correlation between RP105 mRNA levels and BMI in the VAT but not the SAT (Fig. 1*B*). RP105 mRNA expression was increased in the VAT but not the SAT of obese subjects relative to nonobese subjects (Fig. 1*C*). In contrast, MD-1 mRNA expression was significantly increased in the SAT but not the VAT of obese subjects (Supplementary Fig. 3).

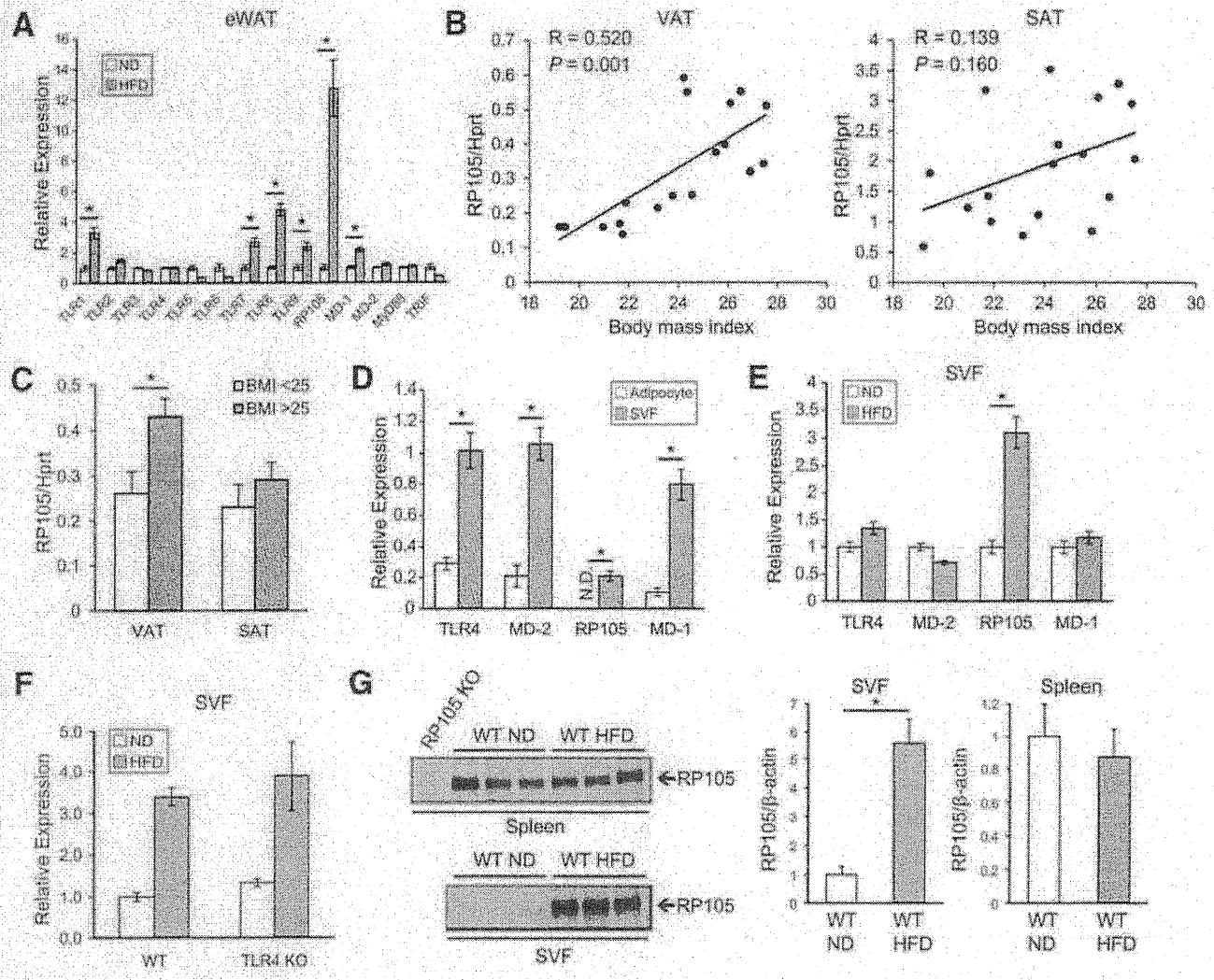

FIG. 1. RP105 and MD-1 expression in mouse and human adipose tissues. *A*: RT-qPCR of TLRs, RP105/MD-1, MD-2, MyD88, and TRIF mRNA in the eWAT from WT fed with an ND or HFD for 12 weeks (n = 8 per group). Data are presented relative to the expression in ND-fed mice, set as 1. Data are shown as means ± SE. *P < 0.05 vs. ND. *B*: Linear regression analysis of the correlation between adipose RP105 mRNA expression and BMI. *C*: RP105 mRNA expression of the human adipose tissue of nonobese (BMI <25 kg/m^2; n = 11) and obese (BMI >25 kg/m^2; n = 7) subjects. Data are shown as means ± SE. *P < 0.05. *D*: RT-qPCR of TLR4, MD-2, RP105, and MD-1 mRNA in adipocytes and SVF from WT mice on an ND (n = 8 per group). Data are shown as means ± SE. *P < 0.05 vs. adipocyte. N.D., not detected. *E*: RT-qPCR of TLR4, MD-2, RP105, and MD-1 mRNA in SVF from WT mice on an ND or HFD for 12 weeks (n = 8 per group). Data are presented relative to the expression in the ND, set as 1. Data are shown as means ± SE. *P < 0.05 vs. ND. *F*: RT-qPCR of RP105 mRNA in SVF from WT or TLR4 KO mice fed with an ND or HFD for 12 weeks (n = 7 per group). Data are presented relative to the expression in WT mice fed with an ND, set as 1. Data are shown as means ± SE. *G*: Immunoprecipitation analysis of RP105 in lysates of spleen (2 × 10^7 cells/lane) or SVF (2 × 10^6 cells/lane) from WT mice on an ND or HFD for 12 weeks. Data are presented as means ± SE normalized to β-actin expression (bar graphs). *P < 0.05 vs. WT ND.

To determine the nature of RP105-bearing cells in eWAT, we isolated adipocytes and the SVF from the eWAT of WT mice (Fig. 1*D*). In adipocytes, MD-1, TLR4, and MD-2 mRNA were expressed, whereas RP105 mRNA was not detected. The SVF expressed all the tested genes, but the level of RP105 mRNA was lower than those of others. In SVF, only RP105 was increased by an HFD (Fig. 1*E*). In addition, this change was independent of TLR4 signaling, as it was present in KO mice lacking TLR4 (Fig. 1*F*). Likewise, RP105 protein levels were increased in obese mice compared with lean mice (Fig. 1*G*). This change was not detected in the spleen. These results indicate that the expression of RP105 is associated with diet-induced obesity.

The RP105/MD-1 complex is expressed in ATMs. We then traced the expression of RP105 and MD-1 in SVF cells. Approximately 40% of the SVF cells from ND-fed mice were composed of CD45$^+$ cells, and the percentage increased to ~55% by HFD (Fig. 2*A*). In contrast, an HFD decreased the percentage of CD45$^-$ cells. RP105 and MD-1 were seen on CD45$^+$ but not CD45$^-$ cells in ND-fed mice (Fig. 2*B*). Those leukocytes were heterogeneous with respect to RP105 and MD-1 densities, and the percentages of RP105- and MD-1–bearing cells increased by HFD. The TLR4/MD-2 complex was not displayed by either CD45$^+$ or CD45$^-$ cells. The staining intensity of RP105 correlated with that of MD-1 (Fig. 2*C*). There was good correlation between transcript expression and flow cytometry results (Supplementary Fig. 4). Of interest, CD45$^-$ cells had TLR4 and MD-2 mRNA, and an HFD increased MD-2 mRNA in CD45$^-$ cells by approximately threefold.

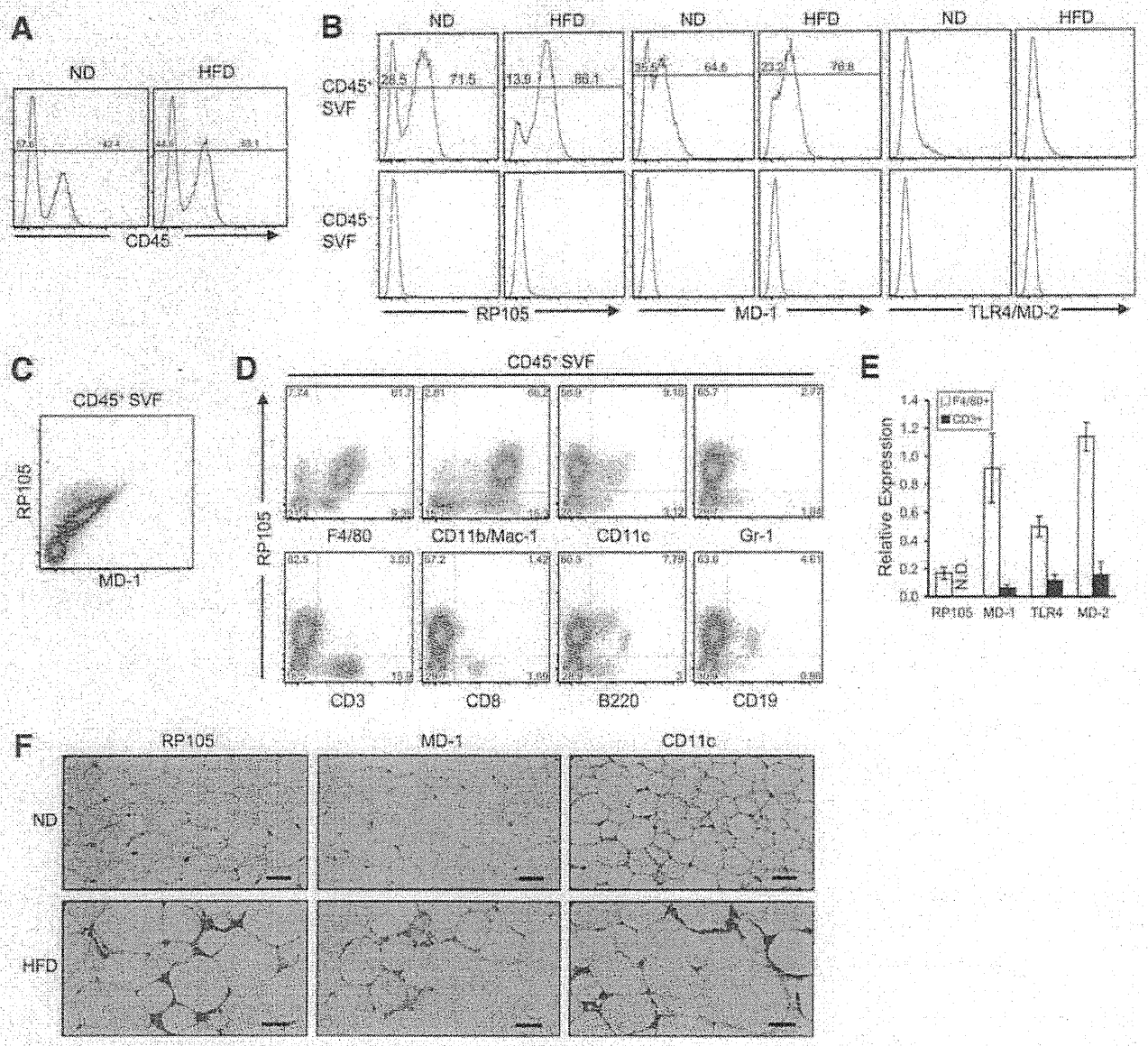

FIG. 2. ATMs are major RP105/MD-1-expressing cells in SVF. *A*: Flow cytometry analysis of CD45 expression on SVF cells from WT mice on an ND or HFD for 12 weeks. *B*: Flow cytometry analysis of RP105, MD-1, and TLR4/MD-2 expression on CD45$^+$ or CD45$^-$ SVF cells from WT mice on an ND or HFD for 12 weeks. *C*: Flow cytometry analysis of RP105 and MD-1 expression on CD45$^+$ SVF cells from WT mice on an ND. *D*: Flow cytometry analysis of CD45$^+$ SVF cells from WT mice on an ND. *E*: RT-qPCR of RP105, MD-1, TLR4, and MD-2 mRNA in F4/80$^+$ or CD3$^+$ SVF cells from WT mice on an ND. Data are shown as means ± SE. N.D., not detected. *F*: Representative histological images of eWAT from WT mice on an ND or HFD for 12 weeks stained with RP105, MD-1, and CD11c. Scale bars, 50 μm (ND) and 100 μm (HFD). All data are representative of at least two independent experiments. (A high-quality digital representation of this figure is available in the online issue.)

Additional flow cytometry analyses revealed that a majority of the RP105-expressing CD45$^+$ cells were F4/80$^+$ and CD11b/Mac-1$^+$ (Fig. 2*D*). Some RP105-expressing cells were CD11c, B220, and CD19 positive. CD8$^+$ T cells have been reported to promote the recruitment and activation of macrophages in adipose tissue (25). However, CD3$^+$ and CD8$^+$ cells did not have detectable RP105 (Fig. 2*D*). CD3$^+$ cells had no RP105 and low MD-1 mRNA (Fig. 2*E*). In addition, RP105 and MD-1 were made by CD11b/Mac-1$^+$ and CD19$^+$ cells but not CD3$^+$ cells in spleen cells of WT animals (Supplementary Fig. 5*A* and *B*). RP105 and MD-1 were predominantly expressed in ATM clusters in eWAT from HFD-fed mice (Fig. 2*F*). These RP105-/MD-1–positive cells also stained positive for CD11c. It is clear from these findings that majority of RP105-/MD-1–expressing SVF cells is ATMs.

Expression of RP105 and MD-1 on M1 macrophages reflects differentiation and is regulated by HFD and adipocytes. Additional information about RP105/MD-1 expression was obtained by examination of M1 and M2 macrophage subsets (Fig. 3*A*). Differentiated M1 macrophages were strongly positive for RP105 and MD-1 as well as tumor necrosis factor (TNF)-α and inducible nitric oxide synthase, representative M1 markers. MD-2 mRNA also was significantly increased by M1 differentiation. In contrast to the expression of arginase 1 and Mgl2 mRNA, the levels of RP105 and MD-1 mRNA in M2 were similar to those in undifferentiated BMMs. TLR4 and MD-2 mRNA were not significantly influenced by M2 differentiation. The RP105/MD-1 complex was detected on M1 and M2 ATMs from ND-fed mice (Fig. 3*B*). Of interest, RP105/MD-1 on

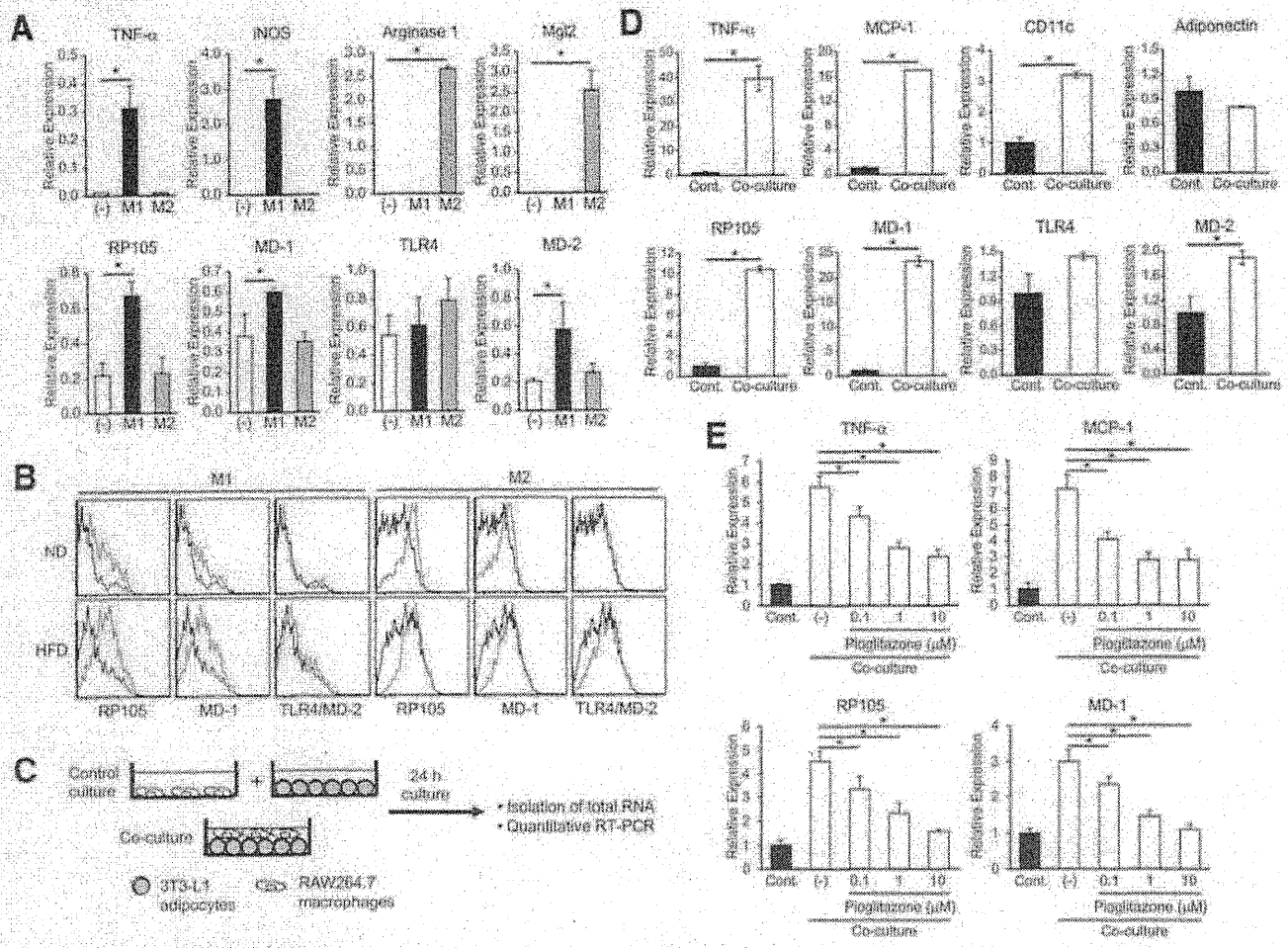

FIG. 3. Expression of RP105 and MD-1 in M1 macrophages is regulated by HFD and adipocytes. ***A*****: RT-qPCR of M1 markers (TNF-α and inducible nitric oxide synthase [iNOS]), M2 markers (arginase 1 and Mgl2), RP105, MD-1, TLR4, and MD-2 mRNA in differentiated M1 and M2 macrophages (*** $n = 3$ **per group). (−), undifferentiated BMMs. *$P < 0.05$ vs. (−).** ***B*****: Flow cytometry analysis of RP105, MD-1, and TLR4/MD-2 expression on M1 and M2 ATMs from WT mice fed with an ND or HFD for 12 weeks (blue lines, isotype control antibodies). All data are representative of at least three independent experiments.** ***C*****: Illustration of the coculture system.** ***D*****: RT-qPCR of TNF-α, MCP-1, CD11c, adiponectin, RP105, MD-1, TLR4, and MD-2 mRNA in the control and cocultured cells (*** $n = 3$ **per group). As the control, the equal numbers of each cell were cultured separately and mixed after harvest. Data are presented relative to the expression in the control culture, set as 1. *$P < 0.05$ vs. control culture.** ***E*****: RT-qPCR of TNF-α, MCP-1, RP105, and MD-1 mRNA in the control and cocultured cells with or without pioglitazone (*** $n = 3$ **per group). Data are presented relative to the expression in the control culture, set as 1. (−), coculture without pioglitazone. *$P < 0.05$ vs. coculture without pioglitazone. Data are shown as means ± SE (*** *A*, *D*, **and** *E*). **All data are representative of at least three independent experiments.**

M1 but not M2 ATMs was upregulated by an HFD. The TLR4/MD-2 complex was not displayed on ATMs from both ND- and HFD-fed mice.

To understand molecular mechanisms underlying HFD-induced upregulation of RP105/MD-1 on M1 ATMs, we prepared a coculture system composed of 3T3-L1 adipocytes and macrophages (Fig. 3*C*). Using this approach, a previous study determined that saturated FAs and TNF-α in a paracrine loop could exacerbate adipose tissue inflammation (15). We observed increased expression of TNF-α, monocyte chemoattractant protein (MCP)-1, and CD11c and decreased expression of adiponectin in the cocultured cells (Fig. 3*D*). In parallel with the upregulation of TNF-α and CD11c, RP105 and MD-1 were markedly increased in the cocultured cells compared with cells in control cultures. Because 3T3-L1 cells did not express RP105 and MD-1 mRNA, macrophages were responsible for this change (data not shown). In addition, this increase was independent of TLR4 (Supplementary Fig. 6). We also observed increased expression of TLR4 and MD-2, but these changes were smaller than those of RP105 and MD-1 (Fig. 3*D*). A peroxisome proliferator–activated receptor-γ agonist pioglitazone treatment of HFD-fed WT mice decreased M1 markers and increased M2 markers in eWAT (4). Pioglitazone stimulation decreased RP105 and MD-1 mRNA, as well as TNF-α and MCP-1 mRNA induced by the coculture in a dose-dependent manner (Fig. 3*E*). Collectively, RP105 and MD-1 are associated with differentiation and responsible for activation of M1 macrophages.

RP105 KO and MD-1 KO mice have increased energy expenditure and are protected from HFD-induced obesity and hepatic steatosis. The above observations led us to analyze RP105 KO and MD-1 KO mice in the development of obesity and insulin resistance, comparing them with WT and TLR4 targeted animals. RP105 KO and MD-1 KO mice gained significantly less weight than WT and TLR4 KO mice on an HFD, whereas no significant differences were found in body weights on an ND (Fig. 4*A*). Representative photos and magnetic resonance imaging revealed decreased fat masses in RP105 KO and MD-1 KO

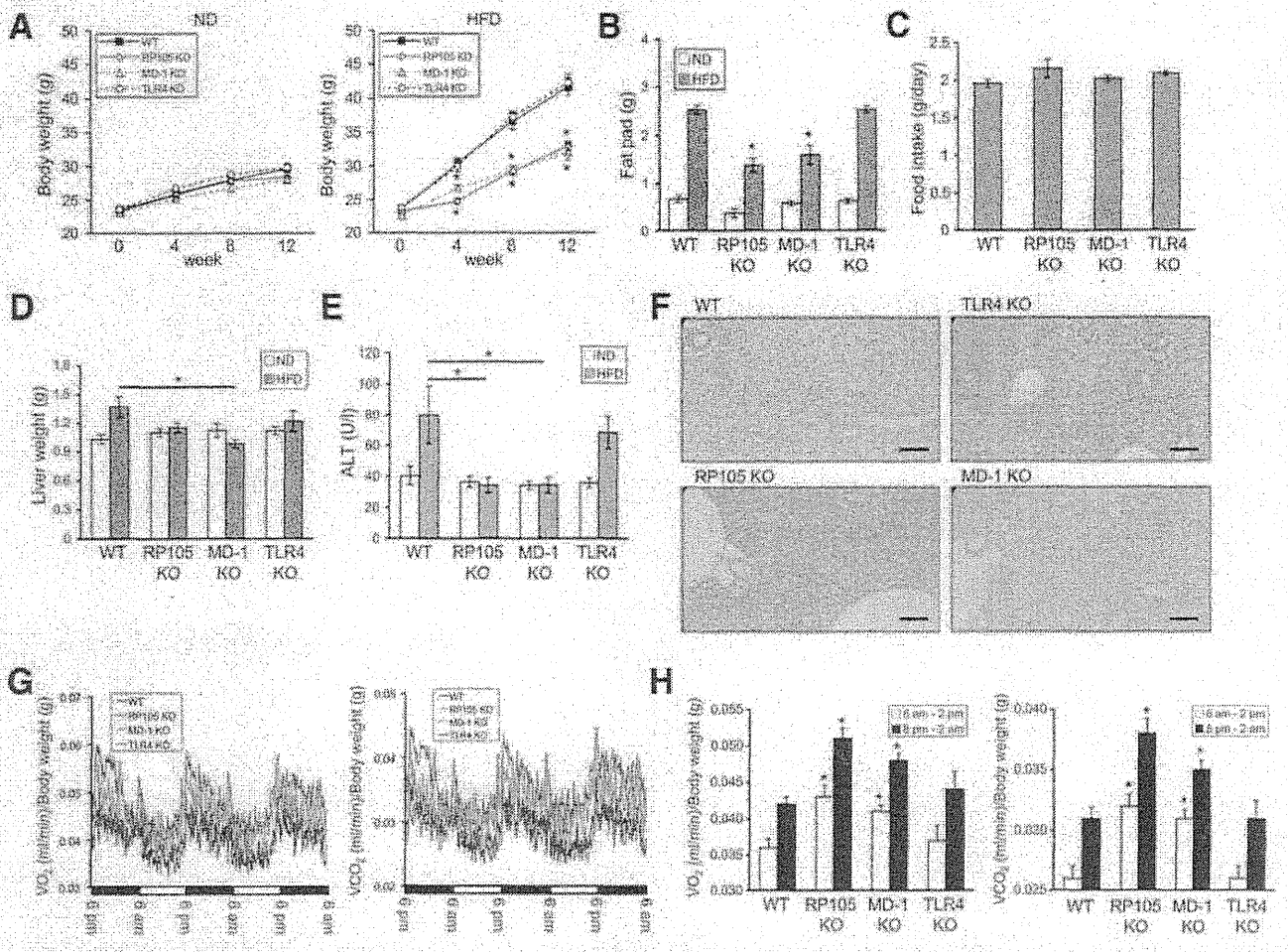

FIG. 4. RP105 KO and MD-1 KO mice with increased energy expenditure are protected from HFD-induced obesity and hepatic steatosis. *A*: Body weight changes of WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an ND or HFD (n = 12 per group). *B*: Fat-pad weights of WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an ND or HFD for 12 weeks (n = 12 per group). *C*: Food intake was measured for WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an HFD for 12 weeks (n = 12 per group). *D*: Liver weights of WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an ND or HFD for 12 weeks (n = 12 per group). *E*: Serum ALT levels were measured for 12-h fasting mice fed with an ND or HFD for 12 weeks (n = 12 per group). *F*: Representative images of hematoxylin and eosin–stained sections of livers from WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an HFD for 12 weeks. Scale bars, 200 μm. *G*: Oxygen consumption (V_{O_2}) and carbon dioxide consumption (V_{CO_2}) were measured for WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an HFD for 12 weeks (n = 6 per group). Data are shown as means. *H*: The data from 8 A.M. to 2 P.M. or 8 P.M. to 2 A.M. in *G* were calculated and shown as bar graphs. Data are shown as means ± SE (*A–E* and *H*). *P < 0.05 vs. WT (*A*, *B*, *D*, *E*, and *H*). (A high-quality digital representation of this figure is available in the online issue.)

mice on the HFD (Supplementary Fig. 7*A* and *B*). Fat-pad weights were similar in WT and TLR4 KO animals on the HFD but much smaller in RP105 KO and MD-1 KO mice (Fig. 4*B*). Daily food intakes were similar in all groups of mice (Fig. 4*C*).

Chronic exposure of mice to HFD causes hepatic steatosis. In WT mice, this is reflected in increased liver weights and levels of serum ALT (Fig. 4*D* and *E*). The latter response was abrogated in *Rp105* and *Md-1* gene–targeted animals. HFD induced macrovesicular steatosis in WT and TLR4 KO but not RP105 or MD-1 KO mice (Fig. 4*F*).

We further found no significant differences in locomotor activity in these mice (Supplementary Fig. 8*A*). RQ fluctuated between 0.70 and 0.75 in all groups of mice maintained on the HFD (Supplementary Fig. 8*B*). O_2 and CO_2 consumption were significantly increased through light and dark phases in RP105 KO and MD-1 KO mice, whereas these measurements were similar in WT and TLR4 KO mice (Fig. 4*G* and *H*). These data clearly demonstrated that RP105 KO and MD-1 KO mice are protected from HFD-induced obesity and hepatic steatosis, and energy expenditure is increased when RP105 and MD-1 are nonfunctional.

RP105 KO and MD-1 KO mice are protected from HFD-induced hypercholesterolemia and insulin resistance. All gene-targeted animals had reduced fasting serum cholesterol levels on the HFD (Fig. 5*A*). Chronic exposure to HFD increased fasting glucose and insulin levels in WT and TLR4 KO but not RP105 and MD-1 KO mice (Fig. 5*B* and *C*). The HFD caused insulin resistance and impaired glucose tolerance in WT mice, whereas the KO mice seemed to be more insulin sensitive and to have better glucose tolerance (Fig. 5*D* and *E*). Insulin sensitivities of MD-1 KO and TLR4 KO but not RP105 KO mice significantly improved compared with WT mice (Fig. 5*F*, *left*). Significant differences between WT and the KO mice were not observed in the GTT (Fig. 5*F*, *right*).

HFD-induced macrophage infiltration and adipose tissue inflammation are attenuated in RP105 KO and MD-1 KO mice. The improved insulin action in RP105- or MD-1–deficient mice led us to investigate cell subsets in

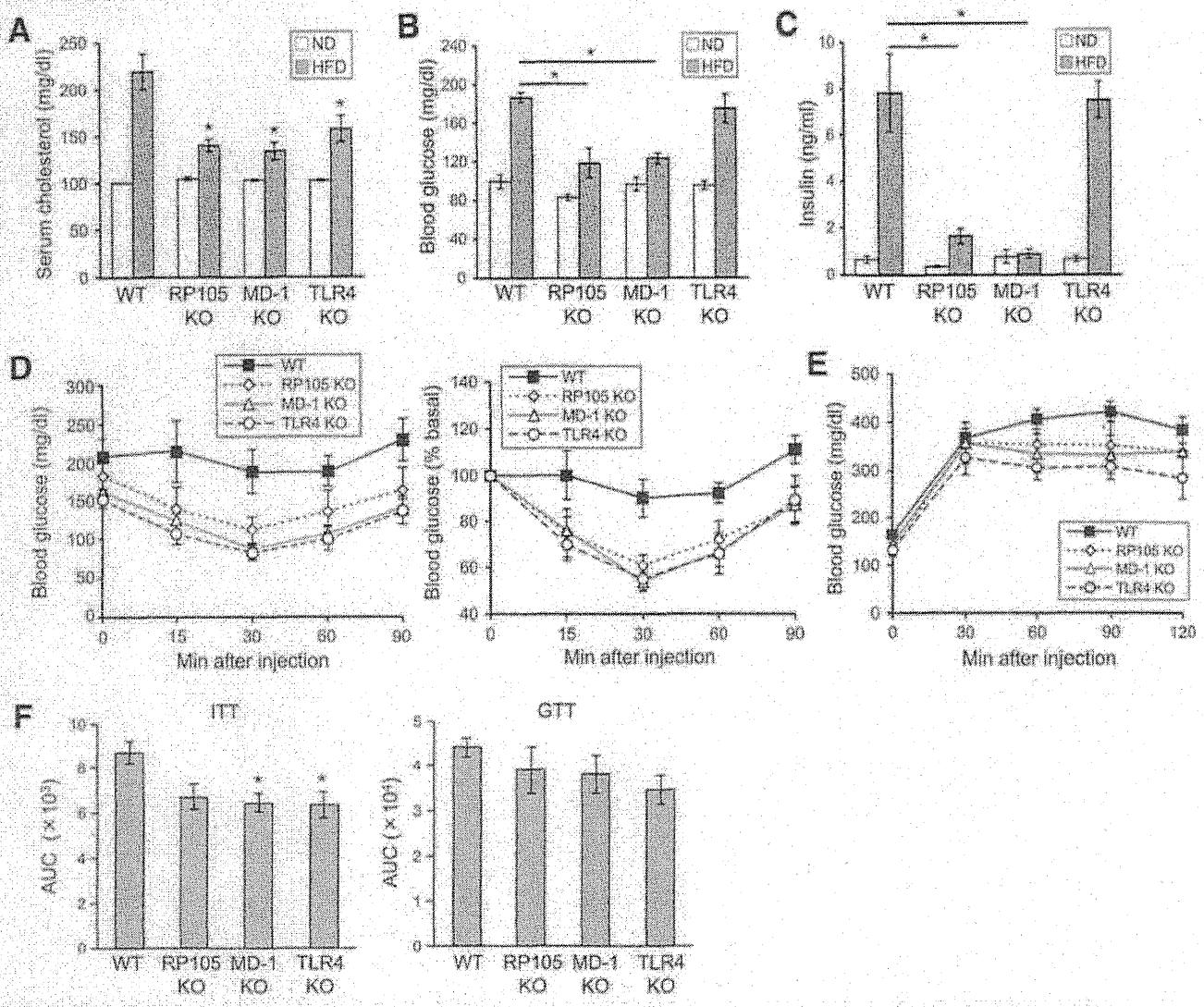

FIG. 5. RP105 KO and MD-1 KO mice are protected from HFD-induced hypercholesterolemia and insulin resistance. *A*: Serum cholesterol levels were measured for 12-h fasting mice fed with an ND or HFD for 12 weeks (n = 12 per group). *B* and *C*: Serum glucose (*B*) and insulin (*C*) levels were measured after a 12-h fasting in mice fed with an ND or HFD for 12 weeks (n = 12 per group). *D*: An ITT was performed after 3 h of fasting in mice fed with an HFD for 12 weeks (n = 6 per group). *Left*: Data are presented as absolute values. *Right*: Data are presented relative to the values of 0 min (preinjection), set as 100%. *E*: A GTT was performed after 12 h of fasting in mice fed with an HFD for 12 weeks (n = 6 per group). Data are shown as means ± SE. *F*: Area under the curve (AUC) graphs of ITT (*left*) and GTT (*right*) tests are presented. Data are shown as means ± SE. *$P < 0.05$ vs. WT.

adipose tissue and assess their expression of inflammatory genes. Compared with WT mice on an HFD, RP105 KO and MD-1 KO mice had severe reductions in the number of SVF cells and F4/80$^+$ cells in eWAT (Fig. 6*A* and *B*). In contrast, adipose tissue from TLR4 KO mice on an HFD exhibited mild reductions in these numbers compared with WT mice. The number of M1 ATMs (F4/80$^+$/CD11c$^+$/CD206$^-$) was markedly reduced in RP105- or MD-1–deficient eWAT compared with WT mice (Fig. 6*C*). M2 ATMs (F4/80$^+$/CD11c$^-$/CD206$^+$) also accumulated in eWAT during obesity (Fig. 6*C*). Their numbers were significantly reduced in RP105 KO, MD-1 KO, and TLR4 KO mice compared with WT mice. An HFD induced a large increase in ATMs, which form a crown-like structure around adipocytes in WT mice (Fig. 6*D*). We observed severe reductions of ATMs in the eWAT of RP105 KO and MD-1 KO mice. TLR4-deficient eWAT showed mild reductions in ATMs compared with WT mice. Expression of inflammatory genes, such as TNF-α, MCP-1, and IKKε, was increased by an HFD compared with an ND in WT and TLR4 KO mice (Fig. 6*E*). TNF-α and MCP-1 mRNAs also were increased by an HFD in subcutaneous and retroperitoneal adipose tissues of WT mice (Supplementary Fig. 1). In contrast, such increases were not observed in the eWAT of RP105 KO and MD-1 KO mice (Fig. 6*E*). Consistent with the reduction in the number of F4/80$^+$ cells and M1 macrophages, expression of F4/80 and CD11c mRNA was decreased in RP105- or MD-1–deficient eWAT fed with an HFD. Adiponectin expression was decreased by an HFD in WT and TLR4 KO mice but not RP105 or MD-1 deficiency. In addition, the lack of RP105/MD-1 did not affect the differentiation of BMMs into M1 subset induced by LPS plus interferon-γ (Fig. 6*F*).

We examined the activity of some of the key signaling molecules involved in adipose tissue inflammation and insulin resistance. To assess the role of Jun NH2-terminal kinase (JNK) (26,27), lysates from eWAT or SVF were

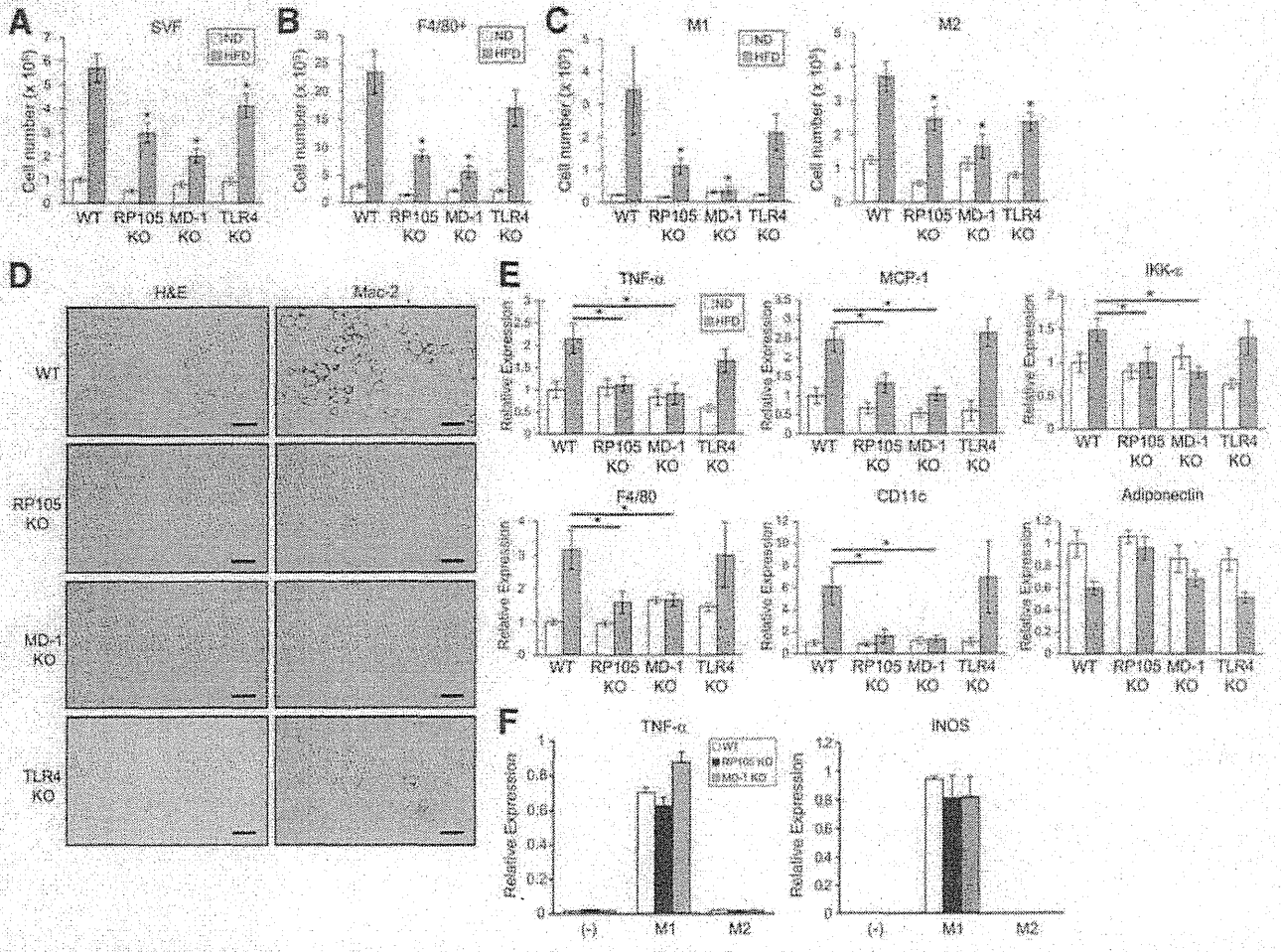

FIG. 6. Obesity-induced macrophage infiltration and adipose tissue inflammation are attenuated in RP105 KO and MD-1 KO mice. *A* and *B*: Cell number of SVF cells (*A*) and F4/80$^+$ cells (*B*) in eWAT from WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an ND or HFD for 12 weeks (n = 12 per group). *C*: Cell number of M1 (*left*) and M2 (*right*) macrophages in eWAT from WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an ND or HFD for 12 weeks (n = 12 per group). *D*: Representative histological images of eWAT from WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an HFD for 12 weeks stained with hematoxylin and eosin (H&E) and Mac-2. Scale bars, 100 μm. *E*: RT-qPCR of TNF-α, MCP-1, IKKε, F4/80, CD11c, and adiponectin mRNA in eWAT from WT, RP105 KO, MD-1 KO, and TLR4 KO mice fed with an ND or HFD for 12 weeks (n = 12 per group). *F*: BMMs from WT, RP105 KO, and MD-1 KO mice were differentiated into M1 or M2 macrophages. After 24 h, expression of M1 markers in the stimulated cells was measured by RT-qPCR. Data are shown as means ± SE (*A–C*, *E*, and *F*). *P < 0.05 vs. WT. (A high-quality digital representation of this figure is available in the online issue.)

immunoblotted with a phospho-JNK antibody. We did not observe significant increased phospho-JNK in the eWAT from WT and the KO mice by HFD (Supplementary Fig. 9*A*, *left*). An HFD produced increased phospho-JNK in SVF from WT mice (Supplementary Fig. 9*A*, *right*). Of interest, TLR4 KO but not RP105 KO and MD-1 KO mice exhibited reduced levels of phospho-JNK in SVF by HFD, suggesting that TLR4/MD-2 but not RP105/MD-1 is important for HFD-induced JNK activation. An HFD induced IκBα degradation in SVF from WT but not RP105 KO, MD-1 KO, and TLR4 KO mice, suggesting that nuclear factor (NF)-κB is activated by both TLR4/MD-2 and RP105/MD-1 (Supplementary Fig. 9*B*). IKKε is a direct transcriptional target of NF-κB (28). IKKε phosphorylation was investigated by Western blotting, as a surrogate to assay activation of the kinase. IKKε expression in eWAT was similarly increased after an HFD in WT, RP105 KO, MD-1 KO, and TLR4 KO mice (Supplementary Fig. 9*C*). Of interest, HFD increased levels of phospho-IKKε in eWAT from WT, RP105 KO, and MD-1 KO, but not TLR4 KO, mice, suggesting that IKKε phosphorylation after an HFD is downstream TLR4 but not RP105 signaling.

Because TLRs can regulate inflammatory activation, we wondered whether RP105 KO mice might also be hyporesponsive to acute inflammatory stimuli. LPS injection led to a profound elevation in proinflammatory genes in the SVF (Fig. 7). However, the levels of these genes were not affected by RP105 deficiency. Collectively, the RP105/MD-1 complex contributes to the development of diet-induced chronic, low-grade adipose tissue inflammation.

The RP105/MD-1 complex is not involved in palmitic and stearic acid–induced macrophage activation. Palmitic acid is one of the most abundant saturated FAs in plasma and is substantially elevated by an HFD (29). Furthermore, palmitic acid has been reported to be an endogenous TLR4 ligand (15–17). BSA–palmitic acid, but not BSA alone, increased TNF-α mRNA in WT BMMs (Fig. 8*A*, *upper panel*). TLR4-deficient BMMs showed a lower increase of TNF-α mRNA than WT upon BSA–palmitic acid stimulation. In contrast, WT, RP105-deficient, and MD-1–deficient BMMs

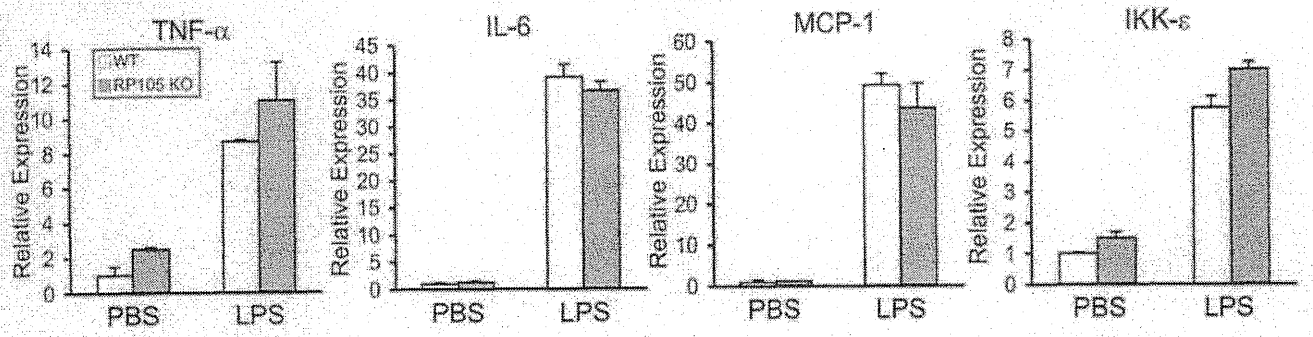

FIG. 7. RP105 does not mediate LPS-induced inflammatory responses in SVF of eWAT. WT and RP105 KO mice ($n = 3$ per group) were injected with LPS (50 μg/mice) intraperitoneally. After 3 h, SVF was isolated from eWAT and expression of TNF-α, IL-6, MCP-1, and IKKε mRNA was measured by RT-qPCR. Data are presented relative to the expression in PBS-injected WT mice, set as 1. Data are shown as means ± SE. Data are representative of at least two independent experiments.

generated similar levels of TNF-α mRNA in response to BSA–palmitic acid. BMMs also were stimulated with other saturated FAs. Upon 100 μmol/L of BSA–stearic acid stimulation, WT, RP105-deficient, and MD-1–deficient BMMs similarly increased levels of TNF-α mRNA, and this was dependent on TLR4 (Fig. 8*A*, *middle panel*). However, upon 200 μmol/L of BSA–stearic acid stimulation, we did not observe the TLR4 dependency. Although lauric acid induces NF-κB activation in RAW264.7 cells via TLR4 (30), we did not observe significantly increased TNF-α mRNA by BSA–lauric acid in BMMs from WT and all the KO mice (Fig. 8*A*, *lower panel*). Thus, although palmitic and stearic acids activate innate immunity via TLR4/MD-2, a different ligand must be recognized by RP105/MD-1 and be responsible for most of obesity-related inflammation (Fig. 8*B*).

DISCUSSION

Here, we provided evidence that RP105/MD-1 plays a major role in regulating adipose tissue inflammation and metabolic disorders. Many detrimental consequences of an HFD were ameliorated by targeting genes encoding for RP105 or MD-1. TLR4 KO mice showed reduced HFD-induced adipose tissue inflammation (Fig. 6), but our results clearly revealed more requirements of RP105/MD-1 than TLR4/MD-2 in the induction of adipose tissue inflammation and obesity. The higher levels of cell surface and transcript expression of RP105/MD-1 in eWAT might simply reflect the requirements of RP105/MD-1 (Figs. 1–3). As is demonstrated, however, RP105/MD-1 plays unique, TLR4-independent roles in adipose tissue inflammation, and a ligand and signaling pathway of RP105/MD-1 must be different from those of TLR4/MD-2 (Fig. 8*A* and Supplementary Fig. 9). A dietary or endogenous ligand other than palmitic and stearic acids might trigger upregulation of RP105 on macrophages that, in turn, accumulate in adipose tissue. The underlying mechanisms require more investigation, but some aspects are clear.

Both MD-1 and MD-2 are members of the same lipid-recognition family (31), and MD-2 is essential for LPS recognition (7). Crystal structure analyses revealed that MD-1 could recognize lipid-like molecules (32,33). An endogenous ligand for RP105/MD-1 must be something other than palmitic and stearic acids (Fig. 8*A*), inducing adipose tissue inflammation by RP105/MD-1 signaling pathway. Otherwise, it might not necessarily be a saturated FA, since some proteins and other components induce sterile inflammation via TLR4/MD-2. Other lipids or components derived from inflamed tissues might stimulate RP105/MD-1 in adipose tissue inflammation. Identification of ligands that promote adipose tissue inflammation via RP105/MD-1 would be an important achievement.

Although other TLRs have a Toll/interleukin-1 receptor (TIR) domain in the intracellular segment, RP105 has only 11 amino acids in that portion (24). This suggests that RP105 requires another molecule to transmit its signal. In B cells, CD19 regulates RP105 but not TLR4 signaling (34). The MyD88 and TRIF adaptors are involved in TLR4 (5) but not RP105 signaling (data not shown). However, little is known about how RP105 regulates chronic inflammation. The NF-κB pathway plays a crucial role in obesity-associated inflammation. HFD activates NF-κB in fat and liver and increases IKKε expression in M1 macrophages (28). IKKε KO mice do not gain weight on an HFD with increased energy expenditure (28). In addition, IKKε KO mice are protected from diet-induced hepatic steatosis, macrophage infiltration into adipose tissue, and increased expression of inflammatory genes in eWAT. The similarities between these changes and ones we attributed to RP105/MD-1 are intriguing. However, although both TLR4 and RP105 are required for HFD-induced NF-κB activation (Supplementary Fig. 9*B*), IKKε may be activated in the downstream of TLR4 but not the RP105 pathway by HFD (Supplementary Fig. 9*C*). In addition, TLR4 but not RP105 may activate JNK pathway in obese mice (Supplementary Fig. 9*A*). Thus, RP105 shares some signaling pathways with TLR4 but must have distinct ones from TLR4.

Levels of RP105 mRNA in SVF and macrophages were dramatically increased by HFD and coculture with adipocytes, respectively. We did not record similar changes in spleen, bone marrow, or even other immune cells in eWAT (data not shown). This raises the possibility of a self-amplifying, feed-forward mechanism of diet-induced inflammation. Processing or production of an RP105/MD-1 ligand by adipocytes might recruit and activate macrophages that produce cytokines capable of promoting obesity and systemic metabolic changes.

The dramatic changes in metabolic status and inflammation in RP105 KO and MD-1 KO mice we observed might have resulted from lower body weights in these KO mice. However, deletion of some genes prevents inflammation and insulin resistance but not weight gain from an HFD (35–37). Others (16) and we have demonstrated that TLR4 KO mice on an HFD have restored insulin resistance but continue to gain weight. Blunting that response to diet is desirable and unique to RP105/MD-1.

The RP105/MD-1 complex is not expressed in $CD45^-$ nonleukocytes in eWAT and RP105 expression is largely

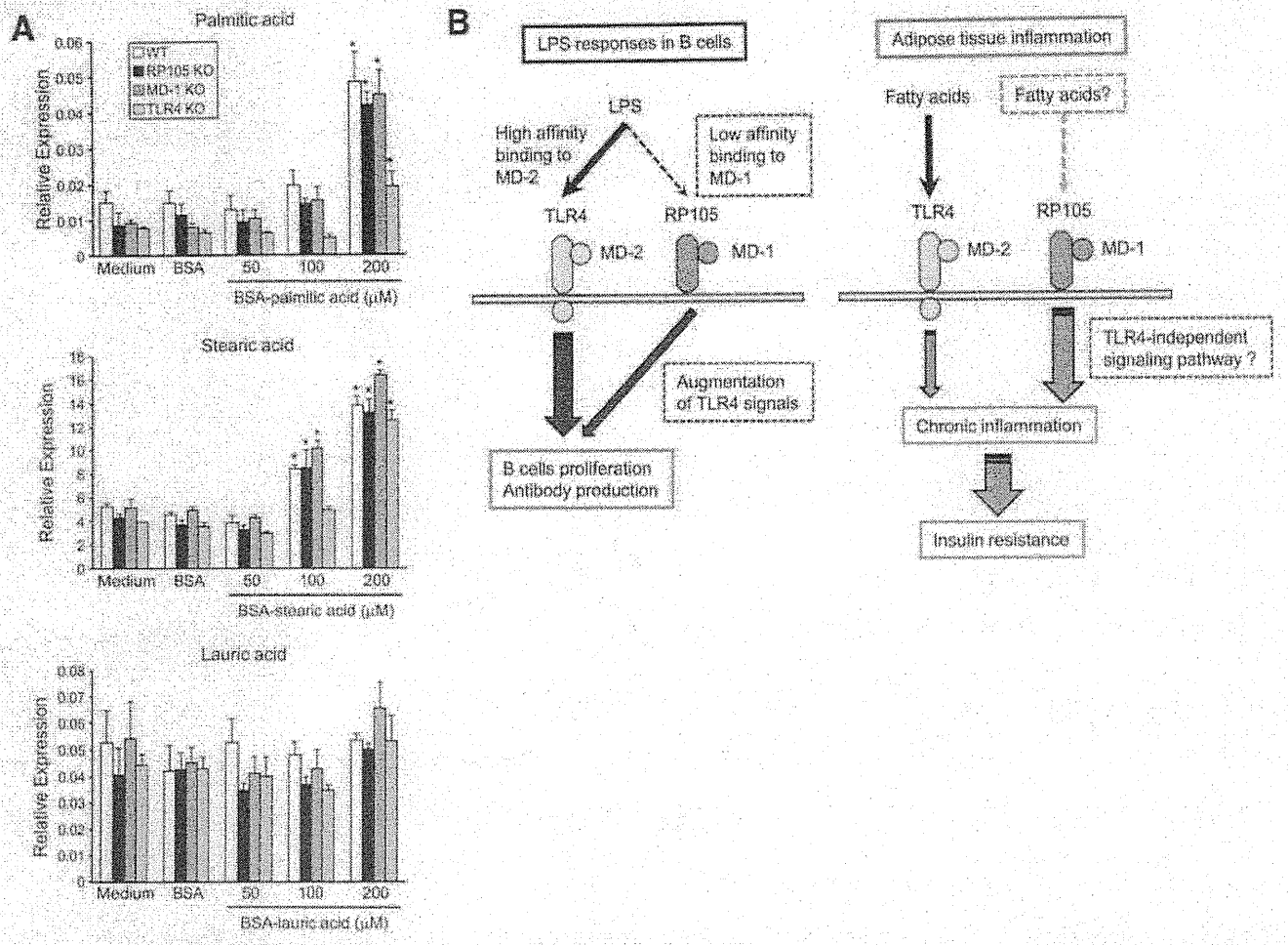

FIG. 8. Palmitate activates TLR4 but not RP105/MD-1 signaling. *A*: FAs (palmitic, stearic, and lauric acids) need to be conjugated to FA-free BSA to increase solubility. BMMs from WT, RP105 KO, MD-1 KO, and TLR4 KO mice were stimulated with the FAs conjugate to BSA or BSA control (BSA) for 24 h. Expression of TNF-α mRNA in the stimulated BMMs was measured by RT-qPCR (n = 3 per group). Data are shown as means ± SE. *P < 0.05 vs. BSA control. Similar results were obtained in three independent experiments. *B*: Hypothetical model of RP105/MD-1 activation in LPS responses in B cells and adipose tissue inflammation. The TLR4/MD-2 complex is essential for LPS recognition and responses. The RP105/MD-1 also could recognize LPS by low affinity and augment TLR4-dependent LPS responses in B cells. On the other hand, RP105/MD-1 might contribute to the development of adipose tissue inflammation and insulin resistance by palmitate-TLR4–independent manner.

restricted to the immune system (24). However, involvement of other cell types is possible. Signaling mediated by MyD88 can mediate HFD-induced leptin and insulin resistance in the central nervous system (38). Another report (39) suggests that TLR4 signaling in hematopoietic cells is important for obesity-associated insulin resistance. Although RP105 transcripts were low in the brain (data not shown), we observed that an HFD increased RP105 mRNA in the liver, brown adipose tissue, and skeletal muscle. Additional investigation will reveal if RP105/MD-1 has roles in those tissues.

To conclude, the RP105/MD-1 complex mediates much of the weight gain, insulin resistance, and sterile inflammation that result from exposure to an HFD. Future studies will clarify a precise ligand and signaling pathway of RP105/MD-1, which link this complex and adipose tissue inflammation.

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Y.W. conducted the experiments and wrote the manuscript. T.N. conducted the experiments. S.I. contributed to the knockout mice analysis. S.F., I.U., and K.To. contributed to the metabolic measurement data. K.Ts. contributed to the immunohistochemistry data. Y.I., T.W., and T.Sa. contributed to the energy expenditure data. Y.H., H.I., H.K., M.Sh., and M.Sa. contributed to the human study. T.Su. and Y.O. contributed to the coculture data. K.Ta. was involved in project planning, financing, and supervision. Y.N. conceived the study, conducted the experiments, and wrote the manuscript. S.A. and K.M. provided the knockout mice. Y.N. is the guarantor of this work and, as such, had full access to all of the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

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総　論

エピゲノムと糖尿病

亀井康富[*1*2]　小川佳宏[**1*3]

要　旨

細胞核内のクロマチン構造や染色体の構築の制御には，塩基配列の変化を伴わずに遺伝子発現を調節するエピゲノム修飾（DNA のメチル化やヒストンのメチル化・アセチル化など）が重要である．エピゲノム修飾はさまざまな疾患の発症に密接に関与し，特にがん発症におけるがん抑制遺伝子の DNA メチル化の役割について多く研究がなされている．糖尿病に関しても，エピゲノム修飾の関与を示唆する知見が得られている．

はじめに

動物の体細胞のゲノムは，一部の例外を除いて同一の塩基配列を有し，個々の細胞の特性は発現する遺伝子の組み合わせによって決定される．細胞核内のクロマチン構造や染色体の構築の制御には，塩基配列の変化を伴わずに遺伝子発現を調節するエピゲノム修飾が重要である．具体的には DNA のメチル化やヒストンのメチル化・アセチル化などであり，例えば遺伝子プロモーター領域の DNA メチル化により遺伝子発現が抑制される．これらの修飾を受けたゲノムをエピゲノムと称する．エピゲノム修飾はさまざまな疾患の発症に密接に関与し，特にがん発症におけるがん抑制遺伝子の DNA メチル化の役割について多く研究がなされている．糖尿病に関しても，エピゲノム修飾の関与を示唆する報告が複数なされており，本稿で概説する．

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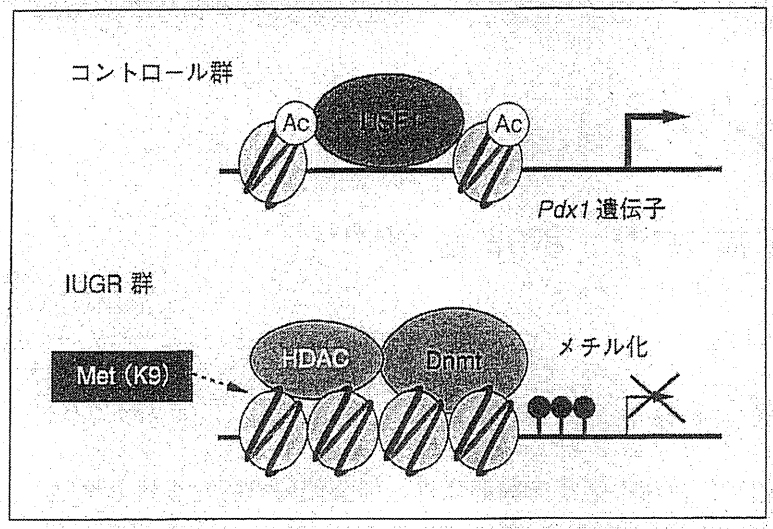
キーワード：DNA メチル化，ヒストン修飾，クロマチン構造，β 細胞

膵臓 β 細胞に対する影響

Pdx1 はホメオボックス型転写調節因子であり，膵臓の発生と β 細胞の分化に重要である．動物実験で Pdx1 の発現量を低下させると，2 型糖尿病が発症する．この *Pdx1* 遺伝子は，DNA メチル化およびヒストン修飾によるエピゲノム変化による制御を受けることが示された．妊娠中の母獣を低栄養にすると，子宮内発育遅延（intra-uterine growth retardation：IUGR）となり，産仔が成長後，糖尿病を含む生活習慣病を発症しやすいことが示されている[1]．この IUGR のモデル動物の膵臓 β 細胞では，コントロール群に比べて *Pdx1* 遺伝子プロモーターの DNA メチル化が顕著に増加し，同時に Pdx1 の発現量は低下していた．さらに，そのプロモーターに

図1　β細胞における *Pdx1* 遺伝子のエピゲノム発現制御



コントロール群の膵臓β細胞では，*Pdx1* 遺伝子プロモーター上でヒストンがアセチル化され，活性型のクロマチン構造を取っており，転写因子 USF1 が結合し，遺伝子の転写を活発にしている．IUGR 群の膵臓β細胞では，プロモーター上に Dnmt1 および Dnmt3a がリクルートされ，DNA がメチル化される．また HDAC1 や Sin3A がリクルートされ，ヒストンは脱アセチル化され，ヒストン H3K9 がジメチル化される不活性型のクロマチン構造となる．その結果，IUGR 群では *Pdx1* 遺伝子の発現が低下する．
略語：巻末の「今月の略語」参照

は DNA メチル化酵素である Dnmt1 および Dnmt3a がリクルートされていた（図1）．またクロマチン免疫沈降実験により，*Pdx1* 遺伝子プロモーターでは活性型ヒストン修飾であるヒストン H3, H4 のアセチル化およびヒストン H3K4（4番目のリシン残基）のトリメチル化が低下し，また転写抑制型ヒストン修飾であるヒストン H3K9（9番目のリシン残基）のジメチル化が増加していた．このように，IUGR により *Pdx1* 遺伝子プロモーターのクロマチン構造が転写抑制型となるために転写不活性となり，Pdx1 の発現低下，さらには2型糖尿病の発症に至ることが報告されている[1]（図1）．一方，他の研究グループが IUGR モデルラットの膵臓の DNA メチル化の網羅的な解析を行っている[2]．この報告によると，IUGR により DNA メチル化変化が観察されたのは主に遺伝子間の領域（intergenic region）であり，幾つかの遺伝子で DNA メチル化変化とその遺伝子発現が逆相関していた．DNA メチル化（特にプロモーター領域）により，遺伝子発現は抑制される（メチル化と遺伝子発現が逆相関する）ため，IUGR 群で観察された DNA メチル化変化により遺伝子発現変化が生じている可能性がある．大きな変化が観察された遺伝子は *Fgfr1*（fibroblast growth factor receptor 1），*Gch1*（GTP cyclohydrolase 1），*Vgf*（vascular growth factor nerve growth factor inducible）などであり，これらの遺伝子発現変化とβ細胞の機能低下の因果関係については今後の研究が必要である[2]．

上述のように，母親の栄養環境が子どもの成長後の糖尿病の罹患性に影響を与える可能性については，これまで多く論じられてきた．一方最近，父親の栄養環境も子どもの糖尿病

の罹患性に影響を与えうることを示唆するデータが報告された[3]．すなわち，交配前の雄ラットに高脂肪食を負荷すると，その雌性の仔において膵臓の β 細胞の *IL-13 receptor α2* 遺伝子の DNA メチル化が低下し，その遺伝子発現の増加が観察され，同時にインスリン分泌が低下し糖代謝能が悪化するというものである[3]．さらに動物実験に加えて，父親由来のエピジェネティックな影響を示唆する疫学調査が報告されている．すなわち，1890 年から 1920 年にスウェーデンで誕生した 300 人についての調査であるが，作物の収穫記録から思春期に摂取した食物量を推定し，父方の祖父の食事量が多いと孫が糖尿病に罹患しやすく，父親が飢饉を経験していると子どもが心臓病に罹患しやすいとの結果である[4]．母親の場合は胎児あるいは新生児の遺伝子に対する栄養環境の直接的な影響であると想定されるが，父親の場合は生殖系列に生じたエピゲノム変化が子孫に受け継がれる可能性が示唆される．しかしながら，具体的にどのようなメカニズムによってこのような現象が引き起こされるかについては，今後の検討が必要である．

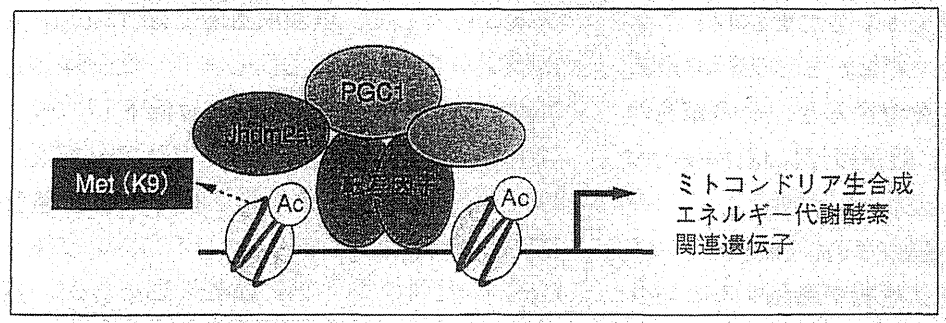
膵臓以外の臓器に対する影響

1．骨格筋 PGC1α

2 型糖尿病におけるインスリン抵抗性の原因の 1 つとして，骨格筋におけるミトコンドリアの機能低下が関連する可能性が示唆されている．PGC1 (PPARγ coactivator 1, PGC1α および PGC1β) は骨格筋におけるミトコンドリアの生合成に重要な役割を担う因子（転写共役因子）であるが，*PGC1α* 遺伝子のエピジェネティックな発現調節に関して幾つか報告されている．*PGC1α* 遺伝子の発現は，骨格筋において加齢とともに低下し，肥満者や肥満マウスにおいて抑制される[5]．骨格筋のバイオプシーにより，健常人のサンプルと比較して，糖尿病患者では *PGC1α* 遺伝子プロモーターの DNA メチル化が増加しており，PGC1α の mRNA は低下し，ミトコンドリア量およびミトコンドリアを特徴づける遺伝子群の発現も低下していた．通常 DNA メチル化はシトシン，グアニンと続く CpG の配列のシトシン塩基に生じるが，興味深いことに *PGC1α* 遺伝子プロモーターでは，CpG 以外（non-CpG）の配列のシトシンにメチル化が生じるというデータが示されている[6]．TNFα や遊離脂肪酸は骨格筋細胞にインスリン抵抗性を引き起こすことが知られるが，ヒト骨格筋初代培養細胞に TNFα や遊離脂肪酸（パルミチン酸，オレイン酸）を添加すると *PGC1α* プロモーターの non-CpG 配列の DNA メチル化が増加し，PGC1α の発現が低下した．さらに，DNA メチル化酵素である Dnmt3b のノックダウンにより，パルミチン酸によって増加する DNA メチル化が抑制された[6]．また最近，ゲノム DNA のみならずミトコンドリア DNA が DNA メチル化を受けるという報告がなされており，DNA メチル化とミトコンドリア機能との関連の解明が今後の課題とされている[7]．

一方，カロリー制限などによる脱アセチル化酵素 Sirt1 の活性化は，PGC1α タンパク質を脱アセチル化し，PGC1α の活性化に重要な役割を果たすことが報告されている[8]．また，ヒストン H3K9 脱メチル化酵素（活性型クロマチンを形成する）の *Jhdm2a* 欠損マウスは，ミトコンドリアでのエネルギー消費にかかわる遺伝子発現が低下し，肥満を発症し，血中のインスリンや中性脂肪，コレステロール含量が高く，代謝疾患の特徴を有することが報告されているが[9][10]，この現象は，PPAR/PGC1α/Jhdm2a 複合体が形成されないため熱産生に重要な UCP1 の発現が誘導されないことによるとされている（図 2）[9]．PGC1α は骨格筋以外でも，肝臓にお

図2　エネルギー代謝に重要なPGC1αを介したエピゲノム発現制御



2型糖尿病患者の骨格筋では，健常人と比較して *PGC1α* 遺伝子プロモーターの DNA メチル化が亢進されており，PGC1α およびミトコンドリア機能に重要な幾つかの遺伝子発現が低下している．ヒストン H3K9 脱メチル化酵素（活性型クロマチンを形成する）の Jhdm2a と PGC1α および転写因子複合体が形成され，エネルギー代謝に重要な遺伝子の発現調節がなされると考えられる．PGC1α は骨格筋以外でも，肝臓における糖新生，褐色脂肪組織での熱産生など，幾つかの臓器でエネルギー代謝の遺伝子活性化に役割を担っている．PGC1 のような総合的な代謝調節因子のエピジェネティック制御の異常は，糖尿病を含む代謝疾患と密接に結びつくことが示唆される．
略語：巻末の「今月の略語」参照

ける糖新生，褐色脂肪組織での熱産生など，幾つかの臓器でエネルギー代謝の遺伝子活性化に役割を担っている．PGC1 のような総合的な代謝調節因子のエピジェネティック制御の異常は，糖尿病を含む代謝疾患と密接に結びつくことが示唆される．

2．その他の遺伝子（炎症性サイトカイン，PPARγ，Glut4）

糖尿病病態におけるエピジェネティクス制御の分子機構に関して，最近複数の報告がある．例えば，2型糖尿病モデルである *db/db* マウス血管平滑筋細胞では，炎症性サイトカイン遺伝子プロモーター領域のヒストン H3K9 の低メチル化が，炎症性サイトカインの持続的な発現増加に関与する[11]．

PPARγ は核内受容体型転写因子であり，脂肪細胞の分化を促進する．PPARγ は糖尿病治療薬であるチアゾリジン誘導体により特異的に転写活性化されることが知られている．この *PPARγ* 遺伝子のプロモーターは DNA メチル化制御を受けるようである．遺伝性糖尿病モデル動物である *db/db* マウス，食餌誘導性肥満マウスの内臓脂肪において，*PPARγ* プロモーターの DNA メチル化がコントロール群に比べて増加し，発現が低下していた[12]．

また，成獣期の骨格筋では，糖輸送担体 Glut4 の低発現を示す雌性 IUGR ラットにおいて，*Glut4* 遺伝子のプロモーター領域のヒストン H3 は新生仔期に低アセチル化および高メチル化状態にあり，成獣になってもこれが維持されることが報告されている[13]．

ま と め

以上，膵臓 β 細胞およびそれ以外の組織において，糖尿病の発症に重要な遺伝子が DNA メチル化やヒストンアセチル化・メチル化などのエピゲノム修飾を受けていることが明らかになっている．エピゲノム修飾は，塩基配列の変化を伴わない可逆的な状態であり，可塑性を有するものである．DNA メチル化やヒストン脱アセチル化酵素の阻害薬は抗腫瘍薬としての開発が進められており，糖尿病分野においても将来的に臨床治療への応用が期待されるものである．

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各　論

腟炎，頸管炎，細菌性腟症と早産対策

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女性生殖器に病原性微生物が侵入してきた場合，厚いムチン層に覆われた腟ならびに子宮頸管上皮はバリアとして働いている。しかし何らかの原因で粘膜上皮に損傷が及ぶと，侵入してきた病原性微生物に対し自然免疫や獲得免疫機構が働き始める。これら防御機構が破綻してしまうと，上行性に感染や炎症が波及し，やがては子宮内感染となり流産や早産に至る。どのようにして腟炎や頸管炎が起こるについては，まだ十分には解明されていないのが現状である。

はじめに

女性の腟および子宮腟部上皮は重層扁平上皮で覆われており，さらに頸管粘液を分泌することで物理的バリアとして細菌や真菌などの微生物やウイルスなどの侵入を防御している。妊娠中にこれらの防御機構が破綻すると，病原体は上行して子宮内へと波及し，その結果，早産が引き起こされる。重要なことに，妊娠30週未満の早産の大半に絨毛膜羊膜炎や子宮内感染が認められている。

本稿では，まず腟上皮や子宮腟部における粘膜免疫系について概説し，次いで早産との関連性が明らかとなってきている代表的な感染症（細菌性腟症，マイコプラズマ，ウレアプラズマ）に対する早産予防法について触れてみたい。

1．腟・頸管における粘膜免疫

1　物理的バリアとしての腟・頸管

ヒト女性の腟や子宮腟部の粘膜は重層扁平上皮で覆われた物理的バリアであり，女性ホルモンの強い影響下に置かれている。月経周期に伴うホルモン変化により，頸管からの粘液分泌量と質が変化する。排卵時ではエストロゲンの作用により粘性が減るため，精子の通過性が高まることで妊娠しやすくなるのに対し，黄体期や妊娠中ではプロゲステロンの作用により粘性が増し，頸管に粘液栓が形成されることで微生物は子宮内へ侵入しにくい環境が作られる。

このバリアを越えて侵入してきた細菌はマクロファージや好中球などの食細胞によって貪食され，活性酸素，消化酵素，抗菌蛋白質などにより殺菌・分解される。食細胞は，炎症性サイトカインやケモカインを分泌することでさらに食細胞を誘導し，炎症が惹起される。

病原微生物が侵入した場合，自然免疫機構（innate immune system）だけでは処理しきれず，その排除にはそれぞれの微生物に特異的なリンパ球が関与する獲得免疫機構（acquired immune system）が必要となる。ヒト生殖器粘

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