

Lactic acid bacteria–derived γ-linolenic acid metabolites are PPARδ ligands that reduce lipid accumulation in human intestinal organoids

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Gut microbiota regulate physiological functions in various hosts, such as energy metabolism and immunity. Lactic acid bacteria, including Lactobacillus plantarum, have a specific polyunsaturated fatty acid saturation metabolism that generates multiple fatty acid species, such as hydroxy fatty acids, oxo fatty acids, conjugated fatty acids, and trans-fatty acids. How these bacterial metabolites impact host physiology is not fully understood. Here, we investigated the ligand activity of lactic acid bacteria-produced fatty acids in relation to nuclear hormone receptors expressed in the small intestine. Our reporter assays revealed two bacterial metabolites of y-linolenic acid (GLA), 13-hydroxy-cis-6,cis-9-octadecadienoic acid (yHYD), and 13-oxo-cis-6,cis-9-octadecadienoic acid (yKetoD) activated peroxisome proliferator-activated receptor delta (PPAR δ) more potently than GLA. We demonstrate that both yHYD and yKetoD bound directly to the ligand-binding domain of human PPAR8. A docking simulation indicated that four polar residues (T289, H323, H449, and Y473) of PPARS donate hydrogen bonds to these fatty acids. Interestingly, T289 does not donate a hydrogen bond to GLA, suggesting that bacterial modification of GLA introducing hydroxy and oxo group determines ligand selectivity. In human intestinal organoids, we determined yHYD and yKetoD increased the expression of PPARS target genes, enhanced fatty acid β-oxidation, and reduced intracellular triglyceride accumulation. These findings suggest that yHYD and yKetoD, which gut lactic acid bacteria could generate, are naturally occurring PPARS ligands in the intestinal tract and may improve lipid metabolism in the human intestine.

Gut microbiota plays diverse critical roles in host physiological processes including energy metabolism. Dysbiosis, that is, an imbalance in microbiota, is associated with metabolic disorders such as obesity (1, 2). Human gut microbiota mainly comprises of four phyla: Bacteroidetes, Firmicutes, Actinobacteria, and Proteobacteria (3, 4). Although a relationship between the gut microbiota and metabolic diseases is not fully understood, alteration of the proportion of Bacteroidetes and Firmicutes may associate with the development of obesity (5). Previous studies provided evidence that gut microbiota alters host energy harvest. For example, fecal transplantation from *ob/ob* mice to germfree mice leads to a higher increase in body fat in the WT mice (6). Gut microbiota-derived metabolites mediate host energy metabolism. For instance, changes in the amount of short-chain fatty acids (SCFAs) produced from dietary fibers have been detected in the intestinal lumen of obese patients (7, 8). SCFAs reportedly activate GPR41 and GPR43 as mediators and energy resources for host tissues (9). Activated GPR41 and GPR43 by SCFAs may function as energy sensors in gut microbiota communication connecting with the sympathetic nervous system and white adipose tissue (10, 11). In addition, long-chain fatty acids (LCFAs) may also function as nutrients and signaling molecules that target some G protein-coupled receptors (GPCRs) and are involved in systemic energy metabolism (12). However, whether LCFA derivatives converted by gut microbiota regulate host energy metabolism is unclear. In a previous study, we reported that lactic acid bacteria can enzymatically convert and produce certain fatty acids from diet-derived polyunsaturated fatty acids (PUFAs), including y-linolenic acid (GLA) (13). Lactobacillus acidophilus and Pediococcus sp. exhibit saturation metabolism on $\Delta 9$ and $\Delta 12$ double bonds in PUFAs, producing hydroxy- and oxo-fatty acids (Fig. S1) (14). These metabolites occur at significantly higher levels in specific pathogen-free mice relative to the levels in germ-free mice (13). Although these compounds are presumed to function in the human intestine at physiological concentrations, such biological activities are yet to be studied in detail.

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GLA metabolites are PPAR_δ ligands

Nuclear hormone receptors (NRs) are transcription factors activated by lipophilic ligands, including steroid hormones, fatsoluble vitamins, and dietary lipids. The NR superfamily comprises 48 members in humans (15). An N-terminal domain characterizes these receptors with activation function 1 which can activate transcription constitutively in the absence of ligand, a central DNA-binding domain, and a C-terminal ligand-binding domain (LBD) with activation function 2 (16). The transcriptional activity of NRs is regulated by the recruitment of coactivators such as steroid receptor coactivator-l (SRC-1) and corepressors such as nuclear receptor corepressor (NCoR) (17). Ligand binding induces a conformational change of the LBD of NR and releases bound corepressors. Subsequently, coactivators are associated with and activate NRs, leading to transcriptional activation. Although the classical NRs such as steroid hormone receptors are translocated from the cytoplasm to the nucleus in a liganddependent manner, other NRs including peroxisome proliferator-activated receptors (PPARs) are constitutively localized in the nucleus and associated with their response elements (18). NRs govern the expression of genes involved in diverse physiological functions including reproduction, immune response, and energy metabolism. In several studies, NRs reportedly play an important role in energy metabolism. For example, NRs that regulate energy metabolism are highly expressed in metabolic tissues, including the liver, adipose tissue, skeletal muscle, and intestines (19). In the intestines, higher levels of dietary lipophilic molecules such as fatty acids, bile acids, and fat-soluble vitamins, which can serve as physiological ligands for NRs, are observed relative to the levels found in other tissues (18, 20).

PPARs play a major regulatory role in energy metabolism among the NR superfamily. They bind to the peroxisome proliferator-response element (PPRE) on the gene promoter as a heterodimer with retinoid X receptors (21). Among three PPAR subtypes [α , γ , and δ (also referred to as β)], PPAR α , highly expressed in the liver, binds fatty acids or lipid-lowering fibrates (22) and controls the expression of target genes related to fatty acid β-oxidation and transport. PPARα-deficient mice develop hepatic steatosis during fasting or high-fat diet feeding. Contrastingly, PPARy, highly expressed in the adipose tissue as a master regulator of adipogenesis, is a target molecule of the insulin sensitizer thiazolidinedione (23). PPARδ, the most recently studied PPAR subtype, is expressed in various tissues including gastrointestinal tissues as compared to PPARα and PPARγ and regulates fatty acid and glucose metabolism in metabolic tissues (19, 24-26). PPARδ activation by its specific agonist GW1516 increases expression of genes related to fatty acid β-oxidation (e.g., CPT1A and HMGCS2). PPAR\delta also regulates cholesterol and lipoprotein metabolism in intestine (27-29). These findings show that PPAR δ plays a crucial role in intestinal energy metabolism. In addition to normal physiology, a role of PPARS on colon cancer has been reported (25, 30, 31). Although several studies showed that PPARδ is protumorigenic, protective effects of PPARδ were also reported, suggesting a complex and diverse role of PPAR δ in colon cancer.

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The present study explored the intestinal NRs activated by lactic acid bacteria–derived fatty acids. Using cell-based reporter assays, we found that two GLA (18:3n-3)-derived fatty acids, 13-hydroxy-*cis*-6,*cis*-9-octadecadienoic acid (γ HYD) and 13-oxo-*cis*-6,*cis*-9-octadecadienoic acid (γ KetoD), activate human PPAR δ potently. Additionally, γ HYD and γ KetoD stimulated fatty acid β -oxidation in human intestinal organoids. Our findings suggest that certain fatty acids produced by gut microbiota might regulate lipid metabolism in the human intestine and improve host energy metabolism.

Results

Identification of intestinal NRs activated by lactic acid bacteria-derived fatty acids

We performed cell-based luciferase reporter assays to identify intestinal NR activators and screened 50 fatty acids produced by gut lactic acid bacteria (13). For screening, chimeric receptors containing the LBD of various NRs that are highly expressed in the intestine (19) and the DNA-binding domain of the yeast transcription factor GAL4 (GAL4-NRs) were used (32). Luciferase reporter assays using HEK293 cells showed that lactic acid bacteria-derived fatty acids preferencely activates PPARs, especially PPARα and PPARδ (Fig. 1A). Other NRs were not stimulated by these fatty acids. Interestingly, some saturated metabolites of GLA, namely yHYD, yKetoD, and 10,13-dihydroxy-cis-6-octadecenoic acid (yHYE), had a more robust PPARS activation than their original compound, GLA (Fig. 1B). These activations were not seen in PPARα, indicating a PPAR subtype-selective fatty acid sensing. Similar activation of PPAR6 by saturated metabolites of linoleic acid (18:2n–6, LA) and α -linolenic acid (18:3n–3, ALA) were also observed. Because activation of PPARa and PPARy by lactic acid bacteria-derived metabolites of LA and ALA were studied previously (33-35), our present study focused on PPARδ and GLA.

To investigate the specificity of GLA, the activation of PPARs by other 18-carbon PUFAs, that is, LA and ALA (14) was analyzed (Fig. 1B). Modification of LA (HYD, KetoD, and HYE) and ALA (α HYD, α KetoD, and α HYE) had little or no effect on the ligand-induced activation of PPARa. Interestingly, 13-hydroxylation of LA and ALA, as well as GLA, potently increased PPARδ activation. 13-oxo and 13-dihydroxy LA, but not ALA, also activate PPAR6. We next investigated transactivation of full-length PPARs by fatty acids. The expression plasmid for PPARs was transfected into HEK293 cells with a luciferase reporter plasmid containing PPRE, and then luciferase activity was measured. Consistent with the GAL4-NR-related results, GLA-derived fatty acids (yHYD, yKetoD, and yHYE) but not GLA activated PPAR8 potently (Fig. 1C). In contrast, PPAR α was activated almost equally by GLA and GLA-derived fatty acids. These results indicate that GLA saturation selectively activates PPAR\delta.

yHYD and yKetoD are potential activators of PPAR δ

We also examined the activation of PPARs by other dietary PUFAs, namely docosahexaenoic acid (22:6n–3, DHA) and

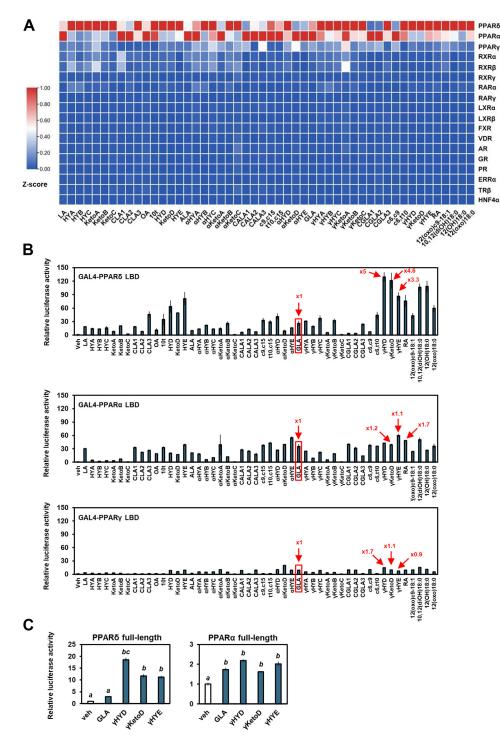


Figure 1. Gut microbial y-linolenic acid metabolites show selective activation of PPAR and PPARa. *A* and *B*, representative data of the ligand screening of GAL4-receptor luciferase assays. HEK293 cells were cotransfected with the GAL4-NRs LBD expression plasmids and a luciferase reporter gene and treated with 100 μ M fatty acids. *C*, effects of fatty acids on full-length PPARs in a luciferase reporter assay in which HEK293 cells were used. Data represent means \pm SEM (n = 3), and Tukey's test was used for analysis. Different letters indicate significant differences between groups (p < 0.05). Veh, vehicle; ALA, α -linolenic acid; GLA, γ -linolenic acid; LA, linoleic acid; LBD, ligand-binding domain; NR, nuclear hormone receptor; PPAR, peroxisome proliferator-activated receptor.

eicosapentaenoic acid (20:5n–3), which have been reported as natural occurring ligands for PPARs (36, 37). GLA-derived fatty acids, especially γ HYD and γ KetoD, activated PPAR δ more robustly than DHA and eicosapentaenoic acid as well as GLA, whereas the activation of PPAR α by these PUFAs was similar (Fig. 2, *A* and *B*); thus, GLA-derived fatty acids are potential naturally occurring activators of PPAR δ . In a luciferase reporter assay in which GAL4-PPARs were used, PPAR activations by fatty acids and PPAR agonists were dosedependent (Fig. 2, *C*–*F*). As matched with Figure 1, PPAR δ activation by γ HYD and γ KetoD was potent [effective concentration for half-maximal response (EC₅₀) = 10.6 and

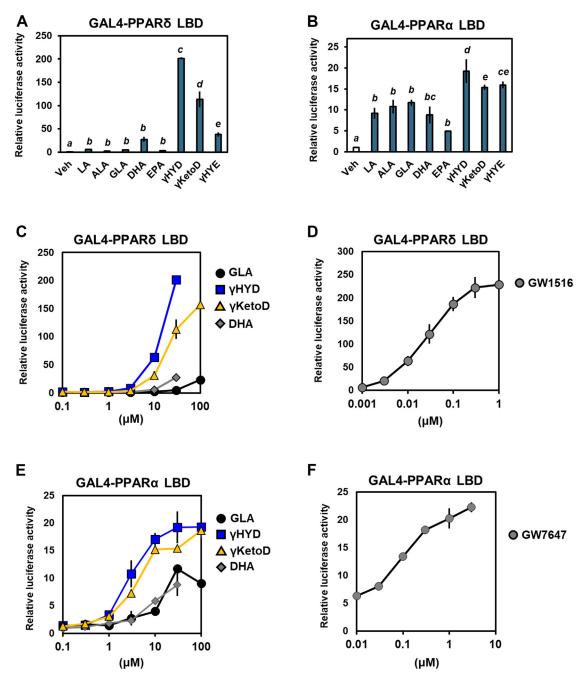


Figure 2. GLA-derived fatty acids are potential naturally occurring PPARS activators. *A* and *B*, effects of GLA metabolites and PUFAs on PPARs in GAL4receptor luciferase assays. HEK293 cells were cotransfected with the GAL4-PPARs LBD expression plasmids and a luciferase reporter gene and treated with 30 µM fatty acids. *C–F*, comparative dose-response relationships of PPARS (*C* and *D*) and PPARa (*E* and *F*). EC₅₀s were calculated using the results in (*C–F*), as shown in Table 1. Data represent means ± SEM (n = 3), and Tukey's test was used for analysis. Different letters indicate significant differences between groups (p < 0.05). PUFA, polyunsaturated fatty acid; PPAR, peroxisome proliferator-activated receptor; GLA, γ -linolenic acid; LBD, ligand-binding domain.

20.3 μ M, respectively, Table 1]. These activation efficacies were much higher than that of GLA (EC₅₀ = 509 μ M), indicating that γ HYD and γ KetoD are potential activators of PPAR δ .

GLA-derived fatty acids regulate the recruitment of coactivators and corepressors

We performed mammalian two-hybrid assays to determine the mechanism underlying the activation of PPARs by GLA derivatives. NRs, including PPARs, interact with corepressors, such as NCoR without ligands. Upon ligand binding, NRs release the corepressors and recruit coactivators such as SRC-1, inducing transcription (17). Expression plasmids for GAL4-SRC-1 contain GAL4 and the receptor-interacting domain of the coactivator SRC-1 and VP16-PPARs, which contain PPARs and the transactivation domain of the herpes virus VP16 protein and were used. As reported previously, PPAR activation by specific agonists increased the ligand-dependent

Table 1 EC50 values of GLA-derived fatty acids in relation to PPARδ (A) and PPARα (B)

Ligand/fatty acids	EC ₅₀ (µM)
A. GAL4-PPARδ LBD	
GW1516	0.025
DHA	44.559
GLA	509.000
γHYD	10.585
γKetoD	20.324
B. GAL4-PPARα LBD	
GW7647	0.106
DHA	9.324
GLA	11.003
γHYD	2.842
γKetoD	4.136

Values were calculated from luciferase activity using a Quest Graph EC50 Calculator.

recruitment of SRC-1 to PPARs (Fig. 3, A and B). Additionally, γ HYD, γ KetoD, and γ HYE but not GLA induced coactivator-recruitment to PPARs. Importantly, these data are consistent with the activation of PPARs (Fig. 1B). Similar to the SRC-1–related results, γ HYD, γ KetoD, and γ HYE reduced the interaction between PPARs and corepressor NCoR (Fig. 3, C and D). Thus, GLA-derived fatty acids activate PPARs through the association/dissociation of coactivators and corepressors.

GLA metabolites are PPAR_δ ligands

GLA-derived fatty acids bind directly to human PPARS

To identify the mechanism underlying the activation of PPAR δ by GLA-derived fatty acids, we performed a [¹⁴C] DHA competitive ligand-binding assay describing the displacement of ligands from receptors with recombinant human PPAR8 LBD protein produced by a bacterial expression system (Figs. 4, A and B and S2). PPAR& LBD or glutathione-Stransferase (GST) recombinant protein was incubated with both [14C] DHA and nonradioactive competitors including GLA derivatives. A competitive inhibition of [¹⁴C] DHA binding was analyzed as a direct binding to PPARS LBD (see Experimental procedures). Similar to the DHA-related results, GLA derivatives (γ HYD, γ KetoD, and γ HYE) displaced [¹⁴C] DHA binding to PPARS LBD competitively (Fig. 4C). Consistent with transactivation, the only weak competition was observed with GLA, which activates PPARs moderately, and no competition was observed with GST protein. These results suggest that GLA-derived fatty acids bind directly to human PPARδ.

Next, we performed a docking simulation using AutoDock Vina (38) to construct binding models of human PPAR δ LBD with GLA-derived fatty acids. Consistent with a previous study (39), human PPAR δ bound to a ligand (DHA)

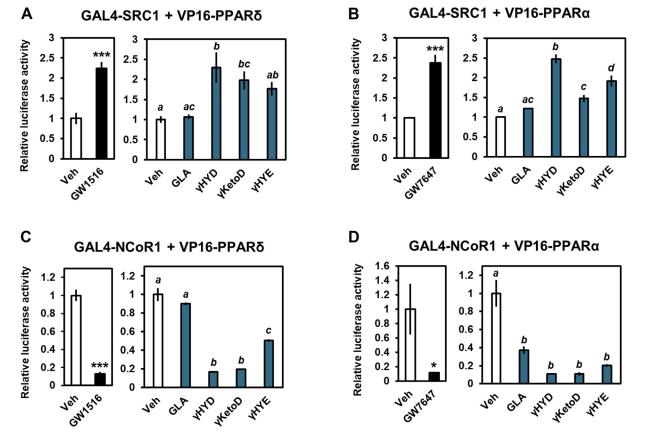


Figure 3. GLA-derived fatty acids regulate coactivator/corepressor exchange. *A* and *B*, mammalian two-hybrid assay of PPARs and the coactivator SRC-1. HEK293 cells were cotransfected with VP16-PPARδ (*A*) or VP16-PPARa (*B*). *C* and *D*, mammalian two-hybrid assay of PPARs and the corepressor NCoR. HEK293 cells were cotransfected with VP16-PPARδ (*C*) or VP16-PPARa (*D*). The ligands used were 100 nM GW1516 (PPARδ agonist), 1 μ M GW7647 (PPARa agonist), or 30 μ M fatty acids. Data represent means ± SEM (n = 3), and Student's *t* test or Tukey's test was used for analysis. **p* < 0.05 and ****p* < 0.001 or different letters indicate significant differences between groups (*p* < 0.05). Veh, vehicle; GLA, γ-linolenic acid; NCoR, nuclear receptor corepressor; SRC-1, steroid receptor coactivator-1; PPAR, peroxisome proliferator-activated receptor.

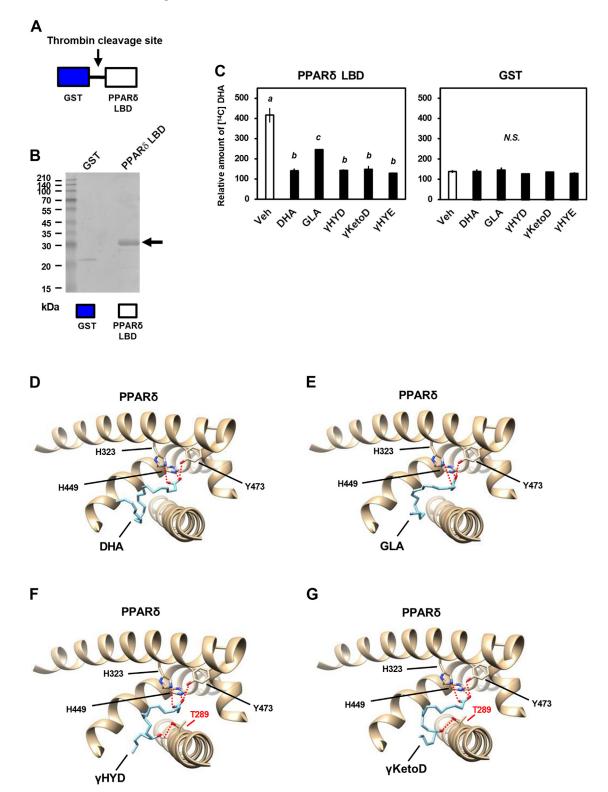


Figure 4. Binding of GLA-derived fatty acids to PPAR6. *A*, a construction of GST-human PPAR6 LBD protein. *B*, purified human PPAR6 LBD recombinant protein used in the binding assay was analyzed using Coomassie Brilliant Blue staining. *C*, competitive binding of GLA-derived fatty acids to purified human PPAR6 LBD proteins in the presence of 100 nM [14 C] DHA and 1 μ M nonlabeled fatty acids. (*D*–*G*), binding model of DHA (*D*), GLA (*E*), γ HYD (*F*), and γ KetoD (*G*) to human PPAR6 (PDB: 3gwxA), as analyzed using AutoDock Vina. Data represent means \pm SEM (n = 3), and Tukey's test was used for analysis. Different letters indicate significant differences between groups (*p* < 0.05). CBB, Coomassie Brilliant Blue; PPAR, peroxisome proliferator-activated receptor; GLA, γ -linolenic acid; DHA, docosahexaenoic acid; LBD, ligand-binding domain; γ HYD, 13-hydroxy-*cis*-6,*cis*-9-octadecadienoic acid; γ KetoD, 13-oxo-*cis*-6,*cis*-9-octadecadienoic acid.



GLA metabolites are PPAR_δ ligands

through hydrogen bonds with polar residues (H323, H449, and Y473) (Fig. 4D). Furthermore, the docking results showed that both GLA and GLA-derived fatty acids also associate with these polar residues (Fig. 4, E-G). Interestingly, the additional polar residue (T289) formed hydrogen bonds selectively with GLA-derived fatty acids but not GLA (Fig. 4, F and G). H323, H449, and Y473 were associated with the carboxy-terminus of fatty acids, whereas T289 donated a hydrogen bond to C13 of yHYD or yKetoD. T289 of human PPARS is conserved among mammals and this threonine residue is replaced by serine in PPAR α and PPAR γ (Fig. S3), the activations of which were not affected by the saturation of GLA. These results suggest that saturation at C13 of GLA by lactic acid bacteria may serve to donate hydrogen bonds to T289 of PPARS and stabilize receptorligand docking, in a subtype-selective manner.

Human intestinal PPAR δ is activated by GLA metabolites

In studies of human intestinal biology, human intestinal epithelial organoids are considered powerful tools because they represent structure and functions *in vivo*. To investigate the physiological role of GLA-derived fatty acids in human tissues, we used human-induced pluripotent stem cell–derived intestinal organoids (40). First, we confirmed that endogenous PPAR δ gene expression was indistinguishable between human intestinal organoids and differentiated Caco-2 cells, that is, the human cell line which expresses endogenous PPAR δ (Fig. S4*A*) (41, 42). In addition, PPAR δ protein levels in human intestinal organoids are comparable to mouse tissues where PPAR δ is highly expressed (Fig. S4*B*). Treatment with the PPAR δ agonist GW1516 upregulated the mRNA expression of target genes in the organoids (*i.e., CPT1A, HMGCS2, PDK4*, and *ASCL1*; Fig. 5*A*). In agreement with the GW1516-based results, the

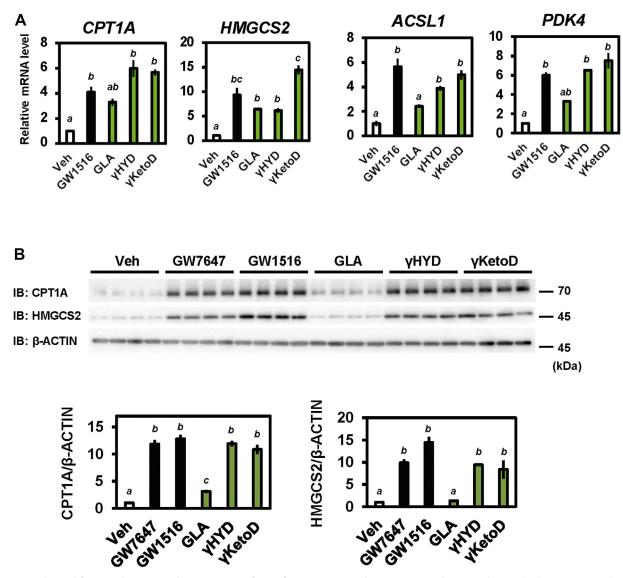


Figure 5. GLA-derived fatty acids increase the expression of PPAR6 target genes in human intestinal organoids. *A* and *B*, human intestinal organoids were treated with 1 μ M GW1516 (PPAR6 agonist) or 30 μ M GLA-derived fatty acids for 24 h. Relative mRNA levels were determined using RT-qPCR (*A*). CPT1A, HMGCS2, and β -ACTIN protein levels were measured using Western blotting (*B*). Data represent means ± SEM (n = 3 or 4), and Tukey's test was used for analysis. Different letters indicate significant differences between groups (p < 0.05). IB, immunoblotting; Veh, vehicle. PPAR, peroxisome proliferator-activated receptor; CPT1A, carnitine palmitoyltransferase 1A; HMGCS2, 3-hydroxy-3-methylglutaryl-CoA synthase 2; ACSL1, Acyl-CoA Synthetase Long Chain Family Member 1; PDK4, pyruvate dehydrogenase kinase 4; GLA, γ -linolenic acid.



GLA metabolites are PPAR_δ ligands

expression of PPARδ target genes was increased significantly by treatment with GLA-derived fatty acids relative to treatment with GLA (Fig. 5*A*). Similar results occurred when primary intestine tissue-derived human organoids were used (Fig. S4*C*). In addition, protein expression levels of CPT1A and HMGCS2 were significantly increased (Fig. 5*B*). These findings indicate that GLA-derived fatty acids activate PPARδ in human intestinal epithelial cells.

GLA-derived fatty acids reduce lipid accumulation in human intestinal organoids

Because activation of PPAR δ leads to fat burning through induction of fatty acid β -oxidation-related target genes, we

examined the regulation of lipid metabolism by GLA derivatives in human intestinal organoids. Activation of fatty acid β -oxidation in living cells was detected using the fluorescence dye FAOBlue (43). Consistent with the observed increase in mRNA levels, the PPAR δ agonist and GLA-derived fatty acids but not GLA significantly increased the activity of fatty acid β oxidation (Fig. 6, *A* and *B*). Next, we analyzed intracellular triglyceride accumulation using BODIPY staining of neutral lipid. Consistent with the activities of fatty acid β -oxidation, intracellular triglyceride levels were reduced in the presence of GLA-derived fatty acids (Fig. 6*C*). Quantitative analysis revealed that GLA-derived fatty acids but not GLA significantly reduced intracellular triglyceride levels and the PPAR δ

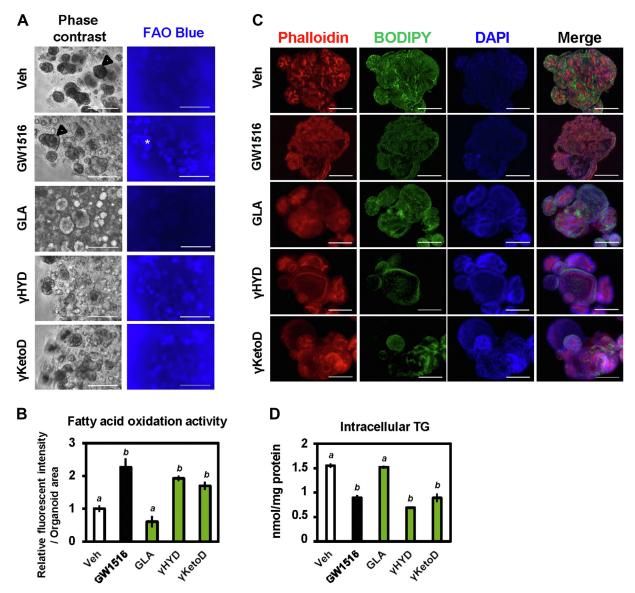


Figure 6. GLA-derived fatty acids promote fatty acid β-oxidation and reduce lipid accumulation in human intestinal organoids. *A* and *B*, fluorescence detection of fatty acid β-oxidation activity in living organoids using FAOBule. Organoids were incubated with 30 µM FAOBlue at 37 °C for 30 min. The scale bar represents 500 µm (*A*). Relative fluorescence intensities were determined and normalized to the organoid surface area (*B*). *C*, triglyceride accumulation in human intestinal organoids was analyzed using BODIPY staining. Organoids were stained with Phalloidin (*red*: F-actin), BODIPY 493/503 (*green*: lipid droplets), and DAPI (*blue*: nucleus). The scale bar represents 200 µm. *D*, quantification of intracellular triglyceride. Organoids pottereated with 500 µM Goleic acid for 48 h were then treated with 1 µM GW1516 (PPARδ agonist) and 30 µM GLA-derived fatty acids for 24 h. Fluorescence imaging and fluorescence intensity were analyzed using a BZ-X800 analyzer (Keyence). Data are means ± SEM (n = 3), and Tukey's test was used for analysis. Different letters indicate significant differences between groups (*p* < 0.05). PPAR, peroxisome proliferator-activated receptor; GLA, γ-linolenic acid.



agonist (Fig. 6D). The PPAR δ agonist and GLA-derived fatty acids do not affect cell viability (Fig. S5). Thus, GLA-derived fatty acids may reduce lipid accumulation through activation of fatty acid β -oxidation in human intestinal epithelial cells.

Discussion

Human gut microbiota produces numerous molecules through the metabolism of dietary components, such as dietary fibers, bile acids, and amino acids. These microbiotaderived metabolites play crucial roles in regulating host metabolism (44, 45). SCFAs, one of the major microbiotaderived metabolites, are produced via the fermentation of dietary fibers and are the most well-studied metabolites in host-microbiota interactions by which host energy metabolism is regulated through the activation of SCFA-sensing GPCRs (e.g., GPR41 and GPR43) (8, 10). Some bacteria metabolize LCFAs, especially PUFAs, to generate hydroxy fatty acids, oxo fatty acids, conjugated fatty acids, and partially saturated *trans*-fatty acids (13, 14). The biological signal of LCFAs is mainly mediated through membrane LCFA-sensing GPCRs (e.g., GPR40 and GPR120) and nuclear fatty acid receptor PPARs. Previous studies showed that microbiotaderived PUFAs stimulate GPCRs and PPARs (33, 35, 46-48). Although intestinal GPCRs for microbiota-derived LCFAs in the intestine have been reported, nuclear mediators have yet to be identified. Fatty acids and fatty acid-derived molecules such as eicosanoids and endocannabinoids regulate the activities of PPARs and other NRs including retinoid X receptor, hepatocyte nuclear factor- 4α , retinoic acid receptor, and liver X receptor (49-51). These NRs are highly expressed in the intestine (19), suggesting they are potential mediators of microbiota-derived fatty acid derivatives. The present study showed that GLA and GLA metabolites activate PPARs, especially PPARα and PPARδ, selectively. Fatty acids activate all PPARs as dietary ligands. Endogenous ligands for PPARa (1-palmitoyl-2-oleoyl-sn-glycerol-3-phosphocholine) and PPARy (15-deoxy- $\Delta^{12,14}$ -prostaglandin J₂) have been reported (36, 52-54); prostacyclin and carbaprostacyclin were reported as endogenous ligands for PPARS (55, 56), although they also activated other PPARs. Our study found that GLA metabolites activate PPAR δ potently and to a greater extent than that achieved by other fatty acids. Lactic acid bacteria-derived fatty acids are present in the intestine, the primary site of fatty acid absorption. Although bacterial fatty acid metabolites exists lower levels than original compounds, these metabolites produced by lactic acid bacteria were detected in the intestine (13, 46), implying that substantial levels of these metabolites are present in host tissues. These findings suggest that lactic acid bacteria-derived GLA metabolites function as ligands for PPARδ.

Similar to a previous study (57), our data showed that GLA preferentially activates PPAR α and PPAR δ rather than PPAR γ . Consistent with another study (39), our docking simulation indicated that γ HYD and γ KetoD are capable of binding to human PPAR δ through hydrogen bonds between the fatty acids and the polar residues of human PPAR δ (His323, His449,

and Tyr473), which are located in arm I of the LBD. The binding ability of fatty acids to PPAR δ is generally proportional to the length of their hydrocarbon chains, indicating the strength of hydrophobic interactions (57). However, in the current study, yHYD and yKetoD, both C18 fatty acids, showed comparable ligand-binding abilities to that of the C22 fatty acid DHA (Fig. 4B). Our docking model showed that yHYD and yKetoD but not GLA formed additional hydrogen bonds with Thr289. GLA saturation selectively activates PPARδ transactivation but not other PPARs (Fig. 1B). Saturations of LA (HYD, KetoD, and HYE) and ALA (aHYD) are also effective (Fig. 1B), suggesting that fatty acid saturation may be a common mechanism underlying the PPARS activation. His323, His449, and Tyr473 of human PPAR8 were important residues in hydrogen bonding with other fatty acids (39). These amino acid residues and Thr289 are located in arm I of the LBD, indicating the helix 12, which contributes to the ligand-dependent recruitment of the coactivator complex. Although the LBD of PPARs share 60%-70% sequence identity (58), Thr289 of human PPAR δ is not conserved and replaced with the serine residue in PPARa and PPARy (Fig. S3). Threonine and serine are similar amino acids with polar uncharged side chains, and the serine residues of PPARα (Ser280) and PPARy (Ser289) are reported to contribute to bind other fatty acids (39). Because the ligand-binding assays of PPAR α and PPARy was not performed, further studies are required to determine how the threonine residue selectively contributes to the binding and the activation of PPARδ by GLA metabolites. In this study, the mammalian two-hybrid assay using GAL4coactivator/corepressor and VP16-NRs was used to detect a recruitment of coactivator/corepressor to NRs in response to ligands or fatty acids. Because this model relies on the VP16 transactivation domain of a yeast protein for activity, further experiments including chromatin immunoprecipitation assay should be required to verify an endogenous interaction between them.

PPAR δ is reported to play an important role as a regulator in lipid metabolism in multiple tissues, including the liver and skeletal muscle, through the regulation of fatty acid β-oxidation-related gene expression. In addition, intestinal PPAR8 protects against diet-induced obesity and dyslipidemia (27). Cardiovascular disease is a major cause of death in worldwide, and postprandial hyperlipidemia is an important risk factor for cardiovascular disease (59). An absorbed dietary lipid is assembled into a chylomicron in the intestine for secretion into the lymph system in the postprandial state. Excess dietary lipids are temporally stored as cytosolic lipid droplets (CLDs) (60). In obese mice, intestinal CLDs are enlarged. They contain the distinctive expression profile of CLD-localized proteins, suggesting that the changes mentioned above prevent absorbed lipids from being mobilized and utilized effectively (61-63). In clinical and experimental studies, PUFA intake improves postprandial hyperlipidemia (64, 65). In the present study, GLA metabolites reduced triglyceride accumulation in human intestinal epithelial cells by activating fatty acid β-oxidation. Lipid transport by fatty acid transport proteins (FABP1 and FABP2) is critical for fatty acid catabolism in

enterocytes. FABP1 is involved in fatty acid oxidation in the intestine, whereas FABP2 directs fatty acids to triacylglyceride synthesis (66). Consistent with these studies, we found that the expression of FABP1 but not FABP2 was increased by GLA metabolites (Fig. S4*D*), suggesting that these metabolites direct fatty acids to degradation in the intestine. Interestingly, GLA metabolites also increased the expression of PPARδ target genes in human hepatocytes (Fig. S6), indicating improved lipid metabolism in multiple tissues through PPARδ activation.

Organoids are recognized as *in vitro* organ models with highly physiological characteristics (67). Human intestinal cell lines, such as Caco-2 cells, lack some important pathways, including lipoprotein metabolism, observed *in vivo* (68, 69). In addition, PPARs exhibit marked species differences in response to ligand activation (70, 71). We found that GLA-derived fatty acids activate PPAR δ and reduce lipid accumulation in human intestinal organoids. Considering these findings with evidence that microbiota-derived metabolites are present in the intestine, we suggest that GLA metabolites could improve lipid metabolism *via* PPAR δ activation in the human intestine. Although intestinal organoids possess high physiological properties, *in vivo* study may need to describe whether GLA metabolites are *bona fide* physiological ligands for PPAR δ .

In conclusion, the GLA-derived fatty acids, γ HYD and γ KetoD, produced by lactic acid bacteria are ligands for PPAR δ . GLA saturation selectively enhances PPAR δ transactivation through an additional hydrogen bond between Thr289 and fatty acids. Moreover, the GLA-derived fatty acids reduce CLD levels in human intestinal epithelial cells (Fig. 7). These findings will likely contribute to the development of effective preventative treatments for metabolic disorders, including obesity, because the aforementioned fatty acid metabolites exhibited high bioactivity in reducing lipid storage in human intestinal epithelial cells.

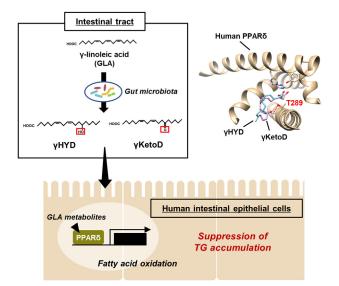


Figure 7. Models of the mechanism by which lactic acid bacteriaderived GLA metabolites activate PPARδ and modulate lipid metabolism in human intestine. GLA, γ-linolenic acid; PPARδ, peroxisome proliferator-activated receptor delta.

Experimental procedures

Materials

Lactic acid bacteria–derived fatty acids were produced as described previously (Fig. S1 and Table S1) (13). GW7647 and GW1516 were purchased from Sigma–Aldrich. The following antibodies were purchased from commercial sources: anti-HMGCS2 and anti-CPT1A (ab137043 and ab128568); anti- β -actin (A5441). All other chemicals of analytical grade were purchased from Sigma–Aldrich, FUJIFILM Wako Pure Chemical, or nakalai tesque.

Animals

C57BL/6J mice were purchased from Nihon Crea. Mice were housed with a 12:12-h light–dark cycle and provided free access to water and standard diet (Labo MR Stock; Nosan Corporation Bio-Department). All animal experiments were conducted according to the guidelines of the Animal Usage Committee of the University of Tokyo. The experiments using animal studies were approved by the Animal Usage Committee of The University of Tokyo.

Cell culture

HEK293 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum, 100 units/ml penicillin, and 100 µg/ml streptomycin. As described previously, human intestinal organoid cultures and passages were conducted (40). Briefly, organoids were cultured with a 25% L-WRNH-conditioned medium embedded in Matrigel Matrix (Corning). The entire medium was changed every 2 to 3 days, and passages were performed every 5 to 6 days. Following passages, cell dissociation was performed using TrypLE express (Corning) at a general ratio of 1:8 embedded in Matrigel Matrix on a Nunclon Delta 4-well dish (Thermo Scientific). All cells were cultured at 37 °C in a 5% CO₂ atmosphere. The experiments using primary human organoids complied with the Declaration of Helsinki and were approved by the human ethical committee of The University of Tokyo and Osaka University. All tissues were sampled with informed consent.

Cotransfection and luciferase assay

HEK293 cells were plated in 96-well plates (Greiner Bio-One) and cultured on DMEM medium supplemented with 10% charcoal-treated fetal bovine serum, 100 units/ml penicillin, and 100 µg/ml streptomycin for 24 h. After that, they were transfected with 50 ng of one of the reporter plasmids, 40 ng of one of each of the expression plasmids, and 10 ng of pCMV- β -Gal (an expression plasmid for β -galactosidase) using the calcium phosphate method. At 24 h after transfection, vehicle, fatty acids, or ligands were added. After incubation for an additional 24 h, luciferase activity was measured using a SpectraMax M2 (Molecular Devices). Luciferase activities were normalized to β -galactosidase activities. Plasmids were generous gifts from Dr Makoto Makishima (GAL4-SRC1 and GAL4-NCoR), Dr David Mangelsdorf and Dr Steven Kliewer



(pCMX, pCMX-GAL4-NR LBD, TK-MH100×4-luc, pCMX TK-PPREx3-luc, and TK-luc), and Dr Kazuhiko Umesono (pCMX-PPARδ).

RNA isolation and real-time quantitative PCR

Total RNA was extracted from cells or organoids using ISOGEN (Nippon gene) per the manufacturer's instructions. cDNA was synthesized and amplified from total RNA using a High-Capacity cDNA Reverse Transcription Kits (Applied Biosystems). Real-time quantitative PCR was performed using an Applied Biosystems StepOnePlus Real-Time PCR System (Thermo Fisher Scientific) and FastStart Universal SYBR Green Master (Roche Applied Science) per the manufacturer's protocols. All relative mRNA expression levels were normalized to that of *18S*. Primer sequences are listed in Table S2.

Western blot analysis

Cells or organoids were treated as described in the figure legends. After treatment, protein extraction was prepared using a cell suspension in RIPA buffer [50 mM Tris-HCl (pH 8.0), 1 mM EDTA, 150 mM NaCl, 1% NP-40, and 0.25% sodium deoxycholate] supplemented with protease inhibitors. All samples were treated with 6× Laemmli buffer [1 mM Tris-HCl (pH 6.8), 30% glycerol, 10% SDS, 600 mM DTT, and 0.03% bromophenol blue]. The protein samples were analyzed by SDS-PAGE followed by immunoblotting with the indicated antibodies and visualized by Amersham Bioscience ECL Western Blotting Detection Reagent (GE Healthcare Life Sciences) or Immobilon Western Chemiluminescent HRP Substrate (Merck Millipore).

Recombinant protein expression and purification

Human PPARδ LBD (140-442) construct was cloned into a pGEX-4T1 vector (GE Healthcare Life Sciences) at the restriction enzyme site of SmaI and XhoI. The protein was expressed in Eschericia coli BL21 (DE3) pLys cells (Novagen) as a C-terminal fusion to a GST tag with a thrombin cleavage site. A single colony was cultured in 2 ml of LB media supplemented with 20 µg/ml of ampicillin and 30 µg/ml of chloramphenicol at 37 °C and 200 rpm for 18 h. The preculture was then transferred to 1 l of LB media until the A600 reached 0.6 to 0.8. IPTG was added to produce a final concentration of 0.4 mM, and expression was continued at 24 °C and 150 rpm for 18 h. Cells were collected using centrifugation, and pellets were resuspended in lysis buffer comprising 50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 5 mM DTT, 1 mM EDTA, and 10% glycerol before sonication was performed. The supernatant was then collected using centrifugation at 100,000g and 4 °C for 70 min, after which it was loaded onto GST Accept (nacalai tesque) and equilibrated using the lysis buffer. Subsequently, the column was washed using five column volumes of the lysis buffer and thrombin cleavage buffer comprising 20 mM Tri-HCl (pH 8.4), 150 mM NaCl, 2.5 mM CaCl2, and 1 mM DTT, respectively. The GST tag was removed via digestion using biotinylated thrombin (Merck) for 18 h at 4 °C. The

biotinylated thrombin was removed using Dynabeads M-280 streptavidin (Veritas). The purity of the target proteins was verified using SDS-PAGE.

Ligand-binding assay

A ligand-binding assay was performed as described previously with minor modifications (72). Briefly, purified recombinant human PPAR δ LBD protein was incubated with 100 nM (10 Ci/mmol) [¹⁴C] DHA in GP buffer (137 mM NaCl, 8.1 mM Na₂HPO₄, 2.68 mM KCl, 1.47 mM KH₂PO₄, 1% sodium azide, and 0.1% gelatin) overnight at 4 °C with or without various competitors (1 μ M), including DHA and GLA-derived fatty acids. Unbound ligands were removed by adsorption to 3% dextran-coated charcoal, and the supernatant was collected. The PPAR δ -bound [¹⁴C] DHA was measured using a scintillation counter (PerkinElmer).

Docking simulation

A docking simulation was performed using the AutoDock Vina computational program (38) to predict the binding models of human PPAR δ LBD protein with GLA-derived fatty acids. The PPAR δ LBD segment of the PPAR δ X-ray crystallography structure (PDB: 3GWX, 2AWH, 2BAW, and 2B50) was obtained and used as a receptor.

Fluorescence detection of fatty acid β -oxidation

Fatty acid β -oxidation activity in living cells was detected using FAOBlue (Funakoshi) (43) per the manufacturer's instructions. Human intestinal organoids pretreated with 500 μ M of oleic acid for 48 h were then treated with 1 μ M GW1516 (PPAR δ agonist) or 30 μ M GLA-derived fatty acids together with oleic acid for 24 h. Embedded human intestinal organoids were incubated with 30 μ M FAOBlue at 37 °C for 30 min. The fluorescence signal derived from fatty acid β -oxidation activity was detected using fluorescence microscopy (BZ-X800, Keyence).

Intracellular triglyceride measurements

Intracellular triglyceride was measured as described previously (73). Briefly, human intestinal organoids pretreated with 500 μ M of oleic acid for 48 h were then treated with 1 μ M GW1516 (PPAR δ agonist) or 30 μ M GLA-derived fatty acids together with oleic acid for 24 h. Organoids were harvested using Cell Recovery Solution (Corning) from Matrigel. Intracellular triglyceride was extracted using hexane in 2-propanol (3:2, v/v), and its levels were determined using the Triglyceride Assay Kit Quantification (abcam) and normalized to the levels of total cellular protein, per the manufacturer's instructions.

Neutral lipid staining

Human intestinal organoids were harvested using Cell Recovery Solution (Corning) from Matrigel. The organoids were treated with a blocking solution (3% bovine serum albumin solution in PBS). They were then fixed and permeabilized

using Fixation/Permeabilization Kit (BD Biosciences), after which they were stained with BODIPY 493/503 (Thermo Fischer Scientific), Alexa Fluor 568 Phalloidin (Thermo Fischer Scientific), and DAPI (Dojindo) according to the manufacturers' instructions. BODIPY, Phalloidin, and DAPI were used to counterstain neutral lipids, F-actin, and DNA, respectively.

Statistical analysis

All data are presented as the mean \pm SEM. Data were analyzed statistically using one-way ANOVA followed by Tukey's post hoc test or Dunnet's test. Statistical differences were considered significant at p < 0.05.

Data availability

All data are contained within the article.

Supporting information—This article contains supporting information.

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Abbreviations—The abbreviations used are: ALA, α-linolenic acid; CLD, cytosolic lipid droplet; DHA, docosahexaenoic acid; GLA, γlinolenic acid; GPCR, G protein–coupled receptor; LA, linoleic acid; LBD, ligand-binding domain; LCFA, long-chain fatty acid; NCoR, nuclear receptor corepressor; NR, Nuclear hormone receptor; PPARδ, peroxisome proliferator-activated receptor delta; PPRE, peroxisome proliferator-response element; PUFA, polyunsaturated fatty acid; SCFA, short-chain fatty acid; SRC-1, steroid receptor coactivator-l; γHYD, 13-hydroxy-*cis*-6,*cis*-9-octadecadienoic acid; γHYE, 10,13-dihydroxy-*cis*-6-octadecenoic acid; γKetoD, 13-oxo*cis*-6,*cis*-9-octadecadienoic acid.

References

- Vrieze, A., Van Nood, E., Holleman, F., Salojärvi, J., Kootte, R. S., Bartelsman, J. F., *et al.* (2012) Transfer of intestinal microbiota from lean donors increases insulin sensitivity in individuals with metabolic syndrome. *Gastroenterology* 143, 913–916.e917
- Walker, A. W., Ince, J., Duncan, S. H., Webster, L. M., Holtrop, G., Ze, X., et al. (2011) Dominant and diet-responsive groups of bacteria within the human colonic microbiota. *ISME J.* 5, 220–230
- Eckburg, P. B., Bik, E. M., Bernstein, C. N., Purdom, E., Dethlefsen, L., Sargent, M., *et al.* (2005) Diversity of the human intestinal microbial flora. *Science* 308, 1635–1638
- Gerritsen, J., Smidt, H., Rijkers, G. T., and de Vos, W. M. (2011) Intestinal microbiota in human health and disease: the impact of probiotics. *Genes Nutr.* 6, 209–240
- Ley, R. E., Turnbaugh, P. J., Klein, S., and Gordon, J. I. (2006) Microbial ecology: human gut microbes associated with obesity. *Nature* 444, 1022–1023
- Turnbaugh, P. J., Ley, R. E., Mahowald, M. A., Magrini, V., Mardis, E. R., and Gordon, J. I. (2006) An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* 444, 1027–1031
- Keenan, M. J., Zhou, J., Hegsted, M., Pelkman, C., Durham, H. A., Coulon, D. B., *et al.* (2015) Role of resistant starch in improving gut health, adiposity, and insulin resistance. *Adv. Nutr.* 6, 198–205
- Kaczmarczyk, M. M., Miller, M. J., and Freund, G. G. (2012) The health benefits of dietary fiber: beyond the usual suspects of type 2 diabetes mellitus, cardiovascular disease and colon cancer. *Metabolism* 61, 1058–1066
- Lu, Y., Fan, C., Li, P., Chang, X., and Qi, K. (2016) Short chain fatty acids prevent high-fat-diet-induced obesity in mice by regulating G proteincoupled receptors and gut microbiota. *Sci. Rep.* 6, 37589
- 10. Kimura, I., Inoue, D., Maeda, T., Hara, T., Ichimura, A., Miyauchi, S., et al. (2011) Short-chain fatty acids and ketones directly regulate sympathetic nervous system via G protein-coupled receptor 41 (GPR41). Proc. Natl. Acad. Sci. U. S. A. 108, 8030–8035
- Kimura, I., Ozawa, K., Inoue, D., Imamura, T., Kimura, K., Maeda, T., et al. (2013) The gut microbiota suppresses insulin-mediated fat accumulation via the short-chain fatty acid receptor GPR43. Nat. Commun. 4, 1829
- Hara, T., Kashihara, D., Ichimura, A., Kimura, I., Tsujimoto, G., and Hirasawa, A. (2014) Role of free fatty acid receptors in the regulation of energy metabolism. *Biochim. Biophys. Acta* 1841, 1292–1300
- Kishino, S., Takeuchi, M., Park, S. B., Hirata, A., Kitamura, N., Kunisawa, J., et al. (2013) Polyunsaturated fatty acid saturation by gut lactic acid bacteria affecting host lipid composition. Proc. Natl. Acad. Sci. U. S. A. 110, 17808–17813
- 14. Hirata, A., Kishino, S., Park, S. B., Takeuchi, M., Kitamura, N., and Ogawa, J. (2015) A novel unsaturated fatty acid hydratase toward C16 to C22 fatty acids from Lactobacillus acidophilus. *J. Lipid Res.* 56, 1340–1350
- Committee, N. R. N. (1999) A unified nomenclature system for the nuclear receptor superfamily. *Cell* 97, 161–163
- De Bosscher, K., Desmet, S. J., Clarisse, D., Estébanez-Perpiña, E., and Brunsveld, L. (2020) Nuclear receptor crosstalk - defining the mechanisms for therapeutic innovation. *Nat. Rev. Endocrinol.* 16, 363–377
- Kang, Z., and Fan, R. (2020) PPARα and NCOR/SMRT corepressor network in liver metabolic regulation. *FASEB J.* 34, 8796–8809
- Klepsch, V., Moschen, A. R., Tilg, H., Baier, G., and Hermann-Kleiter, N. (2019) Nuclear receptors regulate intestinal inflammation in the context of IBD. *Front. Immunol.* **10**, 1070
- Bookout, A. L., Jeong, Y., Downes, M., Yu, R. T., Evans, R. M., and Mangelsdorf, D. J. (2006) Anatomical profiling of nuclear receptor expression reveals a hierarchical transcriptional network. *Cell* 126, 789–799



- Schmidt, D. R., and Mangelsdorf, D. J. (2008) Nuclear receptors of the enteric tract: guarding the frontier. *Nutr. Rev.* 66, S88–97
- Evans, R. M., and Mangelsdorf, D. J. (2014) Nuclear receptors, RXR, and the big bang. *Cell* 157, 255–266
- 22. Kersten, S., Desvergne, B., and Wahli, W. (2000) Roles of PPARs in health and disease. *Nature* **405**, 421–424
- Chiarelli, F., and Di Marzio, D. (2008) Peroxisome proliferator-activated receptor-gamma agonists and diabetes: current evidence and future perspectives. *Vasc. Health Risk Manag.* 4, 297–304
- 24. Kliewer, S. A., Forman, B. M., Blumberg, B., Ong, E. S., Borgmeyer, U., Mangelsdorf, D. J., *et al.* (1994) Differential expression and activation of a family of murine peroxisome proliferator-activated receptors. *Proc. Natl. Acad. Sci. U. S. A.* **91**, 7355–7359
- Modica, S., Gofflot, F., Murzilli, S., D'Orazio, A., Salvatore, L., Pellegrini, F., et al. (2010) The intestinal nuclear receptor signature with epithelial localization patterns and expression modulation in tumors. *Gastroenter*ology 138, 636–648
- 26. Girroir, E. E., Hollingshead, H. E., He, P., Zhu, B., Perdew, G. H., and Peters, J. M. (2008) Quantitative expression patterns of peroxisome proliferator-activated receptor-beta/delta (PPARbeta/delta) protein in mice. *Biochem. Biophys. Res. Commun.* 371, 456–461
- Doktorova, M., Zwarts, I., Zutphen, T. V., Dijk, T. H. V., Bloks, V. W., Harkema, L., *et al.* (2017) Intestinal PPARδ protects against diet-induced obesity, insulin resistance and dyslipidemia. *Sci. Rep.* 7, 846
- Vrins, C. L., van der Velde, A. E., van den Oever, K., Levels, J. H., Huet, S., Oude Elferink, R. P., *et al.* (2009) Peroxisome proliferator-activated receptor delta activation leads to increased transintestinal cholesterol efflux. *J. Lipid Res.* 50, 2046–2054
- Brunham, L. R., Kruit, J. K., Iqbal, J., Fievet, C., Timmins, J. M., Pape, T. D., *et al.* (2006) Intestinal ABCA1 directly contributes to HDL biogenesis *in vivo. J. Clin. Invest.* **116**, 1052–1062
- 30. Peters, J. M., Walter, V., Patterson, A. D., and Gonzalez, F. J. (2019) Unraveling the role of peroxisome proliferator-activated receptor-β/δ (PPARβ/δ) expression in colon carcinogenesis. NPJ Precis Oncol. 3, 26
- Giordano Attianese, G. M., and Desvergne, B. (2015) Integrative and systemic approaches for evaluating PPARβ/δ (PPARD) function. *Nucl. Recept Signal.* 13, e001
- 32. Willy, P. J., Umesono, K., Ong, E. S., Evans, R. M., Heyman, R. A., and Mangelsdorf, D. J. (1995) LXR, a nuclear receptor that defines a distinct retinoid response pathway. *Genes Dev.* 9, 1033–1045
- 33. Goto, T., Kim, Y. I., Furuzono, T., Takahashi, N., Yamakuni, K., Yang, H. E., *et al.* (2015) 10-oxo-12(Z)-octadecenoic acid, a linoleic acid metabolite produced by gut lactic acid bacteria, potently activates PPARγ and stimulates adipogenesis. *Biochem. Biophys. Res. Commun.* 459, 597–603
- 34. Nagatake, T., Kishino, S., Urano, E., Murakami, H., Kitamura, N., Konishi, K., *et al.* (2022) Intestinal microbe-dependent ω3 lipid metabolite αKetoA prevents inflammatory diseases in mice and cynomolgus macaques. *Mucosal Immunol.* 15, 289–300
- 35. Ohue-Kitano, R., Yasuoka, Y., Goto, T., Kitamura, N., Park, S. B., Kishino, S., *et al.* (2018) α-Linolenic acid-derived metabolites from gut lactic acid bacteria induce differentiation of anti-inflammatory M2 macrophages through G protein-coupled receptor 40. *FASEB J.* 32, 304–318
- 36. Forman, B. M., Chen, J., and Evans, R. M. (1997) Hypolipidemic drugs, polyunsaturated fatty acids, and eicosanoids are ligands for peroxisome proliferator-activated receptors alpha and delta. *Proc. Natl. Acad. Sci. U. S. A.* 94, 4312–4317
- 37. Krey, G., Braissant, O., L'Horset, F., Kalkhoven, E., Perroud, M., Parker, M. G., et al. (1997) Fatty acids, eicosanoids, and hypolipidemic agents identified as ligands of peroxisome proliferator-activated receptors by coactivator-dependent receptor ligand assay. *Mol. Endocrinol.* 11, 779–791
- Trott, O., and Olson, A. J. (2010) AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. *J. Comput. Chem.* **31**, 455–461
- 39. Fyffe, S. A., Alphey, M. S., Buetow, L., Smith, T. K., Ferguson, M. A., Sørensen, M. D., *et al.* (2006) Recombinant human PPAR-beta/delta ligand-binding domain is locked in an activated conformation by endogenous fatty acids. *J. Mol. Biol.* 356, 1005–1013

- 40. Takahashi, Y., Sato, S., Kurashima, Y., Yamamoto, T., Kurokawa, S., Yuki, Y., *et al.* (2018) A refined culture system for human induced pluripotent stem cell-derived intestinal epithelial organoids. *Stem Cell Rep.* 10, 314–328
- Mathur, S. N., Watt, K. R., and Field, F. J. (2007) Regulation of intestinal NPC1L1 expression by dietary fish oil and docosahexaenoic acid. *J. Lipid Res.* 48, 395–404
- 42. van der Veen, J. N., Kruit, J. K., Havinga, R., Baller, J. F., Chimini, G., Lestavel, S., *et al.* (2005) Reduced cholesterol absorption upon PPARdelta activation coincides with decreased intestinal expression of NPC1L1. *J. Lipid Res.* 46, 526–534
- Uchinomiya, S., Matsunaga, N., Kamoda, K., Kawagoe, R., Tsuruta, A., Ohdo, S., *et al.* (2020) Fluorescence detection of metabolic activity of the fatty acid beta oxidation pathway in living cells. *Chem. Commun. (Camb)* 56, 3023–3026
- Sonnenburg, J. L., and Bäckhed, F. (2016) Diet-microbiota interactions as moderators of human metabolism. *Nature* 535, 56–64
- McCarville, J. L., Chen, G. Y., Cuevas, V. D., Troha, K., and Ayres, J. S. (2020) Microbiota metabolites in health and disease. *Annu. Rev. Immunol.* 38, 147–170
- 46. Miyamoto, J., Igarashi, M., Watanabe, K., Karaki, S. I., Mukouyama, H., Kishino, S., *et al.* (2019) Gut microbiota confers host resistance to obesity by metabolizing dietary polyunsaturated fatty acids. *Nat. Commun.* 10, 4007
- Miyamoto, J., Mizukure, T., Park, S. B., Kishino, S., Kimura, I., Hirano, K., *et al.* (2015) A gut microbial metabolite of linoleic acid, 10-hydroxy*cis*-12-octadecenoic acid, ameliorates intestinal epithelial barrier impairment partially *via* GPR40-MEK-ERK pathway. *J. Biol. Chem.* 290, 2902–2918
- 48. Hira, T., Ogasawara, S., Yahagi, A., Kamachi, M., Li, J., Nishimura, S., et al. (2018) Novel mechanism of fatty acid sensing in enteroendocrine cells: specific structures in oxo-fatty acids produced by gut bacteria are responsible for CCK secretion in STC-1 cells via GPR40. Mol. Nutr. Food Res. 62, e1800146
- Sampath, H., and Ntambi, J. M. (2005) Polyunsaturated fatty acid regulation of genes of lipid metabolism. *Annu. Rev. Nutr.* 25, 317–340
- 50. de Urquiza, A. M., Liu, S., Sjöberg, M., Zetterström, R. H., Griffiths, W., Sjövall, J., et al. (2000) Docosahexaenoic acid, a ligand for the retinoid X receptor in mouse brain. *Science* 290, 2140–2144
- Levi, L., Wang, Z., Doud, M. K., Hazen, S. L., and Noy, N. (2015) Saturated fatty acids regulate retinoic acid signalling and suppress tumorigenesis by targeting fatty acid-binding protein 5. *Nat. Commun.* 6, 8794
- 52. Chakravarthy, M. V., Lodhi, I. J., Yin, L., Malapaka, R. R., Xu, H. E., Turk, J., et al. (2009) Identification of a physiologically relevant endogenous ligand for PPARalpha in liver. Cell 138, 476–488
- 53. Kliewer, S. A., Lenhard, J. M., Willson, T. M., Patel, I., Morris, D. C., and Lehmann, J. M. (1995) A prostaglandin J2 metabolite binds peroxisome proliferator-activated receptor gamma and promotes adipocyte differentiation. *Cell* 83, 813–819
- 54. Forman, B. M., Tontonoz, P., Chen, J., Brun, R. P., Spiegelman, B. M., and Evans, R. M. (1995) 15-Deoxy-delta 12, 14-prostaglandin J2 is a ligand for the adipocyte determination factor PPAR gamma. *Cell* 83, 803–812
- 55. Lim, H., Gupta, R. A., Ma, W. G., Paria, B. C., Moller, D. E., Morrow, J. D., et al. (1999) Cyclo-oxygenase-2-derived prostacyclin mediates embryo implantation in the mouse via PPARdelta. Genes Dev. 13, 1561–1574
- Hatae, T., Wada, M., Yokoyama, C., Shimonishi, M., and Tanabe, T. (2001) Prostacyclin-dependent apoptosis mediated by PPAR delta. *J. Biol. Chem.* 276, 46260–46267
- 57. Xu, H. E., Lambert, M. H., Montana, V. G., Parks, D. J., Blanchard, S. G., Brown, P. J., et al. (1999) Molecular recognition of fatty acids by peroxisome proliferator-activated receptors. *Mol. Cell* 3, 397–403
- Khuchua, Z., Glukhov, A. I., Strauss, A. W., and Javadov, S. (2018) Elucidating the beneficial role of PPAR agonists in cardiac diseases. *Int. J. Mol. Sci.* 19, 3464
- 59. Nordestgaard, B. G., Benn, M., Schnohr, P., and Tybjaerg-Hansen, A. (2007) Nonfasting triglycerides and risk of myocardial infarction, ischemic heart disease, and death in men and women. *JAMA* 298, 299–308



- Xiao, C., Stahel, P., and Lewis, G. F. (2019) Regulation of chylomicron secretion: focus on post-assembly mechanisms. *Cell Mol. Gastroenterol. Hepatol.* 7, 487–501
- Zembroski, A. S., D'Aquila, T., and Buhman, K. K. (2021) Characterization of cytoplasmic lipid droplets in each region of the small intestine of lean and diet-induced obese mice in response to dietary fat. *Am. J. Physiol. Gastrointest. Liver Physiol.* **321**, G75–G86
- 62. D'Aquila, T., Zembroski, A. S., and Buhman, K. K. (2019) Diet induced obesity alters intestinal cytoplasmic lipid droplet morphology and proteome in the postprandial response to dietary fat. *Front. Physiol.* 10, 180
- 63. Bouchoux, J., Beilstein, F., Pauquai, T., Guerrera, I. C., Chateau, D., Ly, N., et al. (2011) The proteome of cytosolic lipid droplets isolated from differentiated Caco-2/TC7 enterocytes reveals cell-specific characteristics. *Biol. Cell* 103, 499–517
- 64. Drouin-Chartier, J. P., Tremblay, A. J., Lépine, M. C., Lemelin, V., Lamarche, B., and Couture, P. (2018) Substitution of dietary ω-6 polyunsaturated fatty acids for saturated fatty acids decreases LDL apolipoprotein B-100 production rate in men with dyslipidemia associated with insulin resistance: a randomized controlled trial. *Am. J. Clin. Nutr.* 107, 26–34
- Fernandez, M. L., and West, K. L. (2005) Mechanisms by which dietary fatty acids modulate plasma lipids. J. Nutr. 135, 2075–2078
- 66. Lagakos, W. S., Gajda, A. M., Agellon, L., Binas, B., Choi, V., Mandap, B., et al. (2011) Different functions of intestinal and liver-type fatty acidbinding proteins in intestine and in whole body energy homeostasis. *Am. J. Physiol. Gastrointest. Liver Physiol.* 300, G803–G814

- 67. Rossi, G., Manfrin, A., and Lutolf, M. P. (2018) Progress and potential in organoid research. *Nat. Rev. Genet.* **19**, 671–687
- Levy, E., Mehran, M., and Seidman, E. (1995) Caco-2 cells as a model for intestinal lipoprotein synthesis and secretion. *FASEB J.* 9, 626–635
- 69. Takahashi, Y., Noguchi, M., Inoue, Y., Sato, S., Shimizu, M., Kojima, H., et al. (2022) Organoid-derived intestinal epithelial cells are a suitable model for preclinical toxicology and pharmacokinetic studies. *iScience* 25, 104542
- 70. Lawrence, J. W., Li, Y., Chen, S., DeLuca, J. G., Berger, J. P., Umbenhauer, D. R., *et al.* (2001) Differential gene regulation in human *versus* rodent hepatocytes by peroxisome proliferator-activated receptor (PPAR) alpha. PPAR alpha fails to induce peroxisome proliferation-associated genes in human cells independently of the level of receptor expresson. *J. Biol. Chem.* 276, 31521–31527
- Neels, J. G., and Grimaldi, P. A. (2014) Physiological functions of peroxisome proliferator-activated receptor β. *Physiol. Rev.* 94, 795–858
- Umetani, M., Domoto, H., Gormley, A. K., Yuhanna, I. S., Cummins, C. L., Javitt, N. B., *et al.* (2007) 27-Hydroxycholesterol is an endogenous SERM that inhibits the cardiovascular effects of estrogen. *Nat. Med.* 13, 1185–1192
- 73. Sasaki, T., Watanabe, Y., Kuboyama, A., Oikawa, A., Shimizu, M., Yamauchi, Y., *et al.* (2021) Muscle-specific TGR5 overexpression improves glucose clearance in glucose-intolerant mice. *J. Biol. Chem.* 296, 100131

