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## Hepatic lipid homeostasis by peroxisome proliferator-activated receptor gamma 2<sup>★</sup>

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### Abstract

Peroxisome proliferator-activated receptor gamma (PPAR $\gamma$  or PPARG) is a ligand-activated transcription factor belonging to the nuclear hormone receptor superfamily. It plays a master role in the differentiation and proliferation of adipose tissues. It has two major isoforms, PPAR $\gamma$ 1 and PPAR $\gamma$ 2, encoded from a single gene using two separate promoters and alternative splicing. Among them, PPAR $\gamma$ 2 is most abundantly expressed in adipocytes and plays major adipogenic and lipogenic roles in the tissue. Furthermore, it has been shown that PPAR $\gamma$ 2 is also expressed in the liver, specifically in hepatocytes, and its expression level positively correlates with fat accumulation induced by pathological conditions such as obesity and diabetes. Knockout of the hepatic *Pparg* gene ameliorates hepatic steatosis induced by diet or genetic manipulations. Transcriptional activation of *Pparg* in the liver induces the adipogenic program to store fatty acids in lipid droplets as observed in adipocytes. Understanding how the hepatic *Pparg* gene expression is regulated will help develop preventative and therapeutic treatments for non-alcoholic fatty liver disease (NAFLD). Due to the potential adverse effect of hepatic *Pparg* gene deletion on peripheral tissue functions, therapeutic interventions that target PPAR $\gamma$  for fatty liver diseases require fine-tuning of this gene's expression and transcriptional activity.

### Keywords

Non-alcoholic fatty liver disease (NAFLD); High fat diet (HFD); Adipogenesis; Gene expression; Peroxisome proliferator-activated receptor; gamma (PPAR $\gamma$ )

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Authors' contributions

Y.K. Lee wrote the manuscript and prepared figures. J.E. Park, M. Lee, and J.P. Hardwick reviewed the manuscript.

Conflict of interest

The authors declare that they have no conflict of interest.

## 1. Introduction

The liver is a major organ that controls whole body lipid homeostasis by regulating lipid uptake from the circulatory system, as well as *de novo* synthesis and delivery of the synthesized lipids in the form of very low-density lipoprotein (VLDL) to peripheral tissues.<sup>1</sup> Though the liver controls whole body lipid homeostasis, the white adipose tissue is considered to be the major organ for storing extra lipids. Therefore, the liver plays the aforementioned specific roles to maintain and regulate homeostatic lipid fluxes in normal conditions and is not destined to store fat for storage purposes. However, under pathophysiological conditions such as obesity and diabetes, unbalanced lipid flux in the liver results in fat accumulation. Fat accumulation is the initial and prerequisite step for the progression to the more serious non-alcoholic fatty liver disease (NAFLD), which includes non-alcoholic steatohepatitis (NASH), fibrosis, cirrhosis, and hepatocellular carcinoma.<sup>2,3</sup> Especially, NAFLD has become an epidemic problem worldwide in recent years. Therefore, understanding the underlying molecular mechanisms of hepatic fat accumulation will be a stepping stone for potential therapeutic and preventative approaches to control the progression of NAFLD.<sup>4</sup>

The two regulatory components in hepatic lipogenesis are the transcription factors, sterol regulatory element-binding protein (SREBP) and carbohydrate responsive element-binding protein (ChREBP), which are specifically activated by insulin and glucose, respectively, through distinctive activation mechanisms.<sup>5</sup> In this review, we will discuss another transcription regulator called peroxisome proliferator-activated receptor gamma (PPAR $\gamma$  or PPARG) and its role in hepatic fat accumulation in pathophysiological conditions, especially diet-induced obesity.

## 2. Cloning and structure of PPAR $\gamma$

Peroxisome proliferator-activated receptor (PPAR) belongs to the nuclear hormone receptor superfamily, which is a group of ligand-activated transcription factors classified by the similarity in their protein structure, and is involved in adipogenesis.<sup>6-8</sup> PPAR $\alpha$  is the first PPAR cloned by low stringent hybridization using a mixture of oligonucleotides derived from a highly conserved region in the deoxyribonucleic acid (DNA) binding domain of several nuclear hormone receptors.<sup>9</sup> PPAR $\alpha$  is specifically activated by peroxisome proliferators and fatty acid (FA) derivatives. Two direct AGGTCA repeats separated by a single nucleotide (DR1) were identified as a specific DNA binding sequence of PPAR $\alpha$  in the promoters of the genes encoding rat acyl-CoA oxidase and 3-ketoacyl-CoA thiolase, conferring a strong FA oxidation activity on the receptor.<sup>10</sup> PPAR $\gamma$  was originally isolated from *Xenopus* and subsequently from mouse using a similar homology cloning strategy.<sup>11,12</sup> The encoded mouse PPAR $\gamma$  protein has 83% homology in the DNA-binding domains and 70% homology in the ligand binding domains with the mouse PPAR $\alpha$  protein. Due to the structural homology, PPAR $\gamma$  can activate PPAR $\alpha$  target gene promoters in response to peroxisome proliferators.<sup>12</sup> Like many other nuclear hormone receptors, PPAR $\gamma$  forms a heterodimer with retinoid X receptor (RXR) to bind to the consensus DR1 sequence in target gene promoters.<sup>10,13</sup> Another isoform of PPAR $\gamma$ , termed PPAR $\gamma$ 2, has been identified in a mouse adipocyte cDNA library when searching for adipocyte differentiation factor(s) that

bind to the adipocyte protein 2 (aP2) enhancer region; this isoform encodes 30 additional amino acids amino-terminal to the first ATG of the earlier PPAR $\gamma$ , termed PPAR $\gamma$ 1.<sup>13</sup> In humans, PPAR $\gamma$ 2 contains 28 additional amino acids at the N-terminal side of the ATG compared with PPAR $\gamma$ 1.<sup>14</sup> PPAR $\gamma$ 2 is considered the predominant form in adipose tissues and it is mainly involved in adipocyte formation. A laborious approach identified the mouse PPAR $\gamma$  genomic DNA structure, revealing two separate 5' promoters controlling the expression of the two major isoforms (Fig. 1).<sup>15</sup> The genomic structure of the human gene is very similar to the mouse gene. Two different promoters regulated the expression of the two isoforms via alternative splicing as identified in the mouse gene.<sup>16</sup> The separate regulatory systems produce different mRNA expression patterns of the two isoforms in mammals. Both *PPARG1* and *PPARG2* mRNAs are abundantly expressed in white adipose tissues and in lower levels in skeletal muscles.<sup>17</sup> However, the *PPARG2* mRNA expression is limited to the above two tissues, whereas *PPARG1* mRNA has been observed in many other tissues such as heart, liver and spleen. Furthermore, the levels of *PPARG2* mRNA in adipocytes and liver, two major tissues in lipid homeostasis, positively correlate with obesity and high fat diet (HFD) feeding in humans and mice, whereas the *PPARG1* mRNA levels do not change under these pathophysiological and nutritional conditions.<sup>17–19</sup> These findings strongly suggest that PPAR $\gamma$ 2 should be the target for therapeutic and preventative approaches for metabolic disorders associated with obesity.

A variety of long chain FA and peroxisome proliferators including the fibrate class of hypolipidemic drugs were reported to activate PPAR $\gamma$  to various degrees.<sup>12,21–23</sup> Thiazolidinediones (TZDs), a group of anti-diabetic drugs for type 2 diabetes, as specific PPAR $\gamma$  agonists, were a breakthrough for the field of diabetes.<sup>24</sup> Even though troglitazone was removed from the market due to hepatotoxicity, TZDs have become important tools that induce physiological functions of PPAR $\gamma$  in glucose and lipid metabolism.<sup>7,25–28</sup>

### 3. Adipogenic role of PPAR $\gamma$

Compared with PPAR $\gamma$ 1, PPAR $\gamma$ 2 is a potent transcription activator and adipogenic factor, because of its additional amino acids at the N-terminus.<sup>29,30</sup> Knockdown of PPAR $\gamma$  in adipose tissues using the Cre-lox system led to impairment in the formation of white and brown adipocytes, emphasizing its essential roles in adipogenesis and hepatic fat accumulation.<sup>26,31</sup> Accordingly, when PPAR $\gamma$  was selectively knocked down in adipocytes of adult mice by an inducible Cre-lox system, the mature PPAR $\gamma$ -null white and brown adipocytes died within a few days and were replaced by newly formed, normal PPAR $\gamma$ -positive adipocytes.<sup>32</sup> However, these animals, with adipocyte-specific *PPAR\gamma* knockout, derived from an *aP2* promoter-driven Cre system, demonstrated controversial insulin sensitivity phenotypes owing to non-adipocyte deletions due to a broad tissue expression pattern of Cre recombinase driven by the promoter.<sup>33,34</sup> These studies also demonstrated that gene encoding adiponectin (*Adipoq*) promoter-driven Cre system exhibited a more selective adipocyte-specific expression. The adipocyte-specific PPAR $\gamma$  null mice, which were generated by the *Adipoq*-Cre system, exhibited more significant lipoatrophy, insulin resistance and hepatomegaly, confirming a critical role of adipocyte PPAR $\gamma$  in fat cell formation and whole body metabolic homeostasis, which strongly agrees phenotypically with other mouse models of lipoatrophy.<sup>35–38</sup> One of the common phenotypes of all these

animals with adipocyte-specific deletion of PPAR $\gamma$  is an increase in hepatic triglyceride (TG) accumulation, which is accompanied by a dramatic increase in the expression of hepatic PPAR $\gamma$ .<sup>35</sup> Hepatic steatosis may be a consequence of increased hepatic FA influx due to lack of adipocytes for TG storage and/or the enhanced adipogenic program by upregulated PPAR $\gamma$  expression. In accordance with these observations, many mouse models of obesity and diabetes developing fatty livers are associated with higher expression of PPAR $\gamma$ .<sup>27,36,37,39–43</sup> More specifically, hepatocyte-specific PPAR $\gamma$  expression appears to be responsible for the fat accumulation. Albumin promoter driven Cre recombinase (Alb-Cre), which was mainly expressed in hepatocytes (though expression in cholangiocytes has also been reported, the expression of *Pparg* in the tissue has not been described), mediated hepatocyte-specific deletion of *Pparg*, which rescued steatotic phenotypes in various animal models.<sup>27,37,43–45</sup> Especially, because the hepatocyte-specific Alb-Cre deletion markedly diminished the expression of *Pparg2*, but not *Pparg1*, PPAR $\gamma$ 2 appears to be the major isoform in hepatocytes that contributes to fat accumulation.<sup>37</sup> Consistent with these observations, many studies have reported that only the expression of *Pparg2*, not *Pparg1*, was significantly increased in the livers of animal models of obesity and hepatic steatosis, even though its expression was low in normal conditions.<sup>18,19,46,47</sup> Moreover, Westerbacka *et al.*<sup>48</sup> have reported a strong correlation between hepatic fat accumulation and increased expression of *PPARG2* in human subjects. In addition, over-expression of PPAR $\gamma$ 1 or PPAR $\gamma$ 2 in hepatocytes led to the development of fatty liver.<sup>47,49</sup> Interestingly, PPAR $\gamma$  overexpression was also accompanied by increased transcription of several inflammatory marker genes, suggesting a possible association between PPAR $\gamma$ -mediated fat accumulation and NASH development.<sup>47</sup> This observation exhibited a stark contrast to the antagonism between the proinflammatory cytokine, tumor necrosis factor alpha (TNF $\alpha$ ), and PPAR $\gamma$  in adipocytes.<sup>50–52</sup> Kupffer cells (KCs), resident liver macrophages, are important components for eliminating and detoxifying microorganisms, endotoxins and xenobiotics, which are directed from the gut. KCs constitute approximately 15% of the total liver cell population accounting for 80%–90% of the tissue macro-phages.<sup>53,54</sup> Paradoxically, when KCs are activated to protect the host from invasion of these toxic materials, they release cytokines, chemokines, and reactive oxygen species, which eventually adversely affected the liver function. An earlier study has emphasized a crucial role of KCs in the development of hepatic steatosis and insulin resistance, as depletion of KCs by gadolinium chloride (GdCl<sub>3</sub>) treatment protected rats from these metabolic disorders, which were induced by a high fat and high sucrose diet.<sup>54</sup> A crucial component for the KCs' role appears to be TNF $\alpha$ , a major proinflammatory cytokine released by macrophages. Bone marrow transplant from TNF $\alpha$  null donor animals or treatment with anti-TNF $\alpha$  antibodies improved NAFLD in diet-induced or genetically modified animal models.<sup>54–56</sup> The expression of *Pparg* has been detected in macrophages and its functional role as a negative regulator of macrophage activation and cytokine production was identified.<sup>57,58</sup> This regulation is mediated through inhibition of the transcription factors, activator protein 1 (AP1), signal transducer and activator of transcription (STAT) and nuclear factor- $\kappa$  B (NF- $\kappa$ B), which are the major regulators of macrophage activation and TNF $\alpha$  synthesis. These important functions of PPAR $\gamma$  in KC activation and the role of KCs in hepatic steatosis links KC specific PPAR $\gamma$  to the development of hepatic steatosis. In animal studies, macrophage-specific *Pparg* gene knockout using the Cre-lox system indeed lowered TG accumulation upon HFD feeding

compared with control mice. However, in this study reduction in TG accumulation was more evident in hepatocyte-specific *Pparg* knockout animals, suggesting that hepatocyte-specific PPAR $\gamma$  is the major contributor to TG accumulation.<sup>43</sup> Hepatic stellate cells (HSCs) play an important role in the development of NAFLD as they are the major cells producing collagen, which is responsible for fibrosis when activated.<sup>59</sup> Though PPAR $\gamma$  is expressed in HSCs and is involved in inhibition of HSC proliferation and activation, the role of stellate PPAR $\gamma$  in hepatic steatosis has not been directly addressed.<sup>60–62</sup> Moreover, activation of HSCs is not associated with hepatic fat accumulation, at least in a subset of human patients with NAFLD.<sup>59</sup> Nonetheless, the role of stellate PPAR $\gamma$  appears to be beneficial for liver function, *i.e.*, PPAR $\gamma$  activation inhibits HSC activation and fibrogenesis, and, reciprocally, HSC activation negatively regulates its own PPAR $\gamma$  expression.<sup>59,62</sup>

#### 4. Lipid homeostasis regulated by hepatic PPAR $\gamma$

As anticipated from its adipogenic role in white adipocytes, overexpression of PPAR $\gamma$ 1 or PPAR $\gamma$ 2 significantly induced fat accumulation in the liver. Interestingly, in the case of PPAR $\gamma$ 1 overexpression, significant fat accumulation was observed only in *PPAR $\alpha$*  knockout liver, where FA oxidation was disrupted, while adenovirus-mediated overexpression of PPAR $\gamma$ 2 increased hepatic fat accumulation in wide type (WT) mice fed chow within 7 days post adenovirus injection.<sup>47,49</sup> Because the two PPAR $\gamma$  isoforms share the same DNA binding specificity, the difference in fat accumulation efficacy must result from the difference in their transcription activity, as PPAR $\gamma$ 2 has 5–10-fold greater transcription activity than PPAR $\gamma$ 1.<sup>29</sup> On the contrary, reduction in the expression of PPAR $\gamma$ 2, mediated by short hairpin interfering RNA (shRNA), lowered the hepatic TG levels in mice fed HFD for 4 weeks.<sup>47</sup> In this study, Yamazaki *et al.*<sup>47</sup> have analyzed the mRNA levels of genes involved in lipogenesis including *Pparg* and *Srebp1c* at different time points after HFD feedings. Though *Srebp1c* activation is strongly regulated by well-recognized posttranslational steps, the mRNA level of *Pparg2* rose before that of *Srebp1c* at 4 weeks of HFD feeding containing butter (high in saturated fats), similarly to their target genes: cluster of differentiation 36 (*CD36*) and adipose differentiation-related protein (*Adrp*), and fatty acid synthase (*Fasn*).<sup>63–66</sup> In most of the mouse studies with HFD feeding, PPAR $\gamma$  was the early-induced lipogenic transcription factor in the liver.<sup>42,65</sup> A controversial result has been reported in another HFD feeding experiment where the mRNA levels of *Srebp1c* rose from 1 day after the HFD feeding.<sup>67</sup> This different observation may result from different sources of saturated fat in the diets; the latter study used HFD containing coconut oil, while the former studies used HFD containing butter or lard. The saturated fats in coconut oil are mostly 12 carbon lauric acids, while butter and lard contains C-16 palmitic acids as the major saturated fatty acid (SFA) components, which better represents the overnutrition cause of human fatty liver.

##### 4.1. Downstream target genes of PPAR $\gamma$

Many target genes of PPAR $\gamma$  have been reported in adipocyte studies.<sup>13,68,69</sup> These include *Fabp4/aP2*, *Cebpa/C/EBP $\alpha$* , *Cfd/Adipsin*, *CD36* and lipoprotein lipase (*LpL*), which play important roles in adipogenesis and lipogenesis. Expression of these genes was also strongly induced by PPAR $\gamma$  overexpression in *PPAR $\alpha$* -deficient liver, suggesting that PPAR $\gamma$ -

mediated hepatic steatosis is caused by the conserved adipogenic properties of the transcription factor.<sup>49</sup> These results were corroborated by results obtained from WT mouse liver transduced with an adenoviral vector containing PPAR $\gamma$  and from a hepatic AML-12 cell line stably expressing PPAR $\gamma$ .<sup>47,70</sup> On the contrary, reduction in hepatic *Pparg* gene expression mediated by Alb-Cre driven-Floxed gene deletion or by acute delivery of adenoviruses containing shRNA decreased the expression of these adipogenic and lipogenic target genes, and reduced fat accumulation in obese mouse models.<sup>27,37,47</sup> Interestingly, while the mRNA level of *Srebp1c* was not reduced in PPAR $\gamma$ -deficient livers, its target genes such as *Fasn*, acetyl-CoA carboxylase (*Acc*) and stearoyl-Coenzyme A desaturase 1 (*Scd-1*) were effectively downregulated. These observations suggest that PPAR $\gamma$  synergistically activates these lipogenic genes possibly in association with activated SREBP1 or by inducing SREBP1 cleavage to activate these genes indirectly.<sup>71</sup> To identify the direct transcription targets of hepatic PPAR $\gamma$ , Matsusue *et al.*<sup>72</sup> analyzed RNA isolated from livers of *ob/ob* and PPAR $\gamma$  deficient *ob/ob* mice using a subtractive cloning strategy. The subtractive screening identified the fat-specific protein 27 (*Fsp27*)/*Cidec* gene as one of the direct PPAR $\gamma$  targets containing a peroxisome proliferator response element (PPRE) in its proximal promoter region. The study focused on FSP27, which belongs to the cell death-inducing DFFA-like effector (CIDE) family and contributes to energy storage in white adipose tissues through the formation of large lipid droplets.<sup>73,74</sup> FSP27 overexpression mediated by adenoviruses containing *Fsp27* increased hepatic fat accumulation in the *ob/ob-PPARG/Cre*<sup>+</sup> mice, while *Fsp27* knockdown by adenoviruses expressing shRNA targeting the gene reduced hepatic fat accumulation in the *ob/ob* mice, indicating that FSP27 is a downstream PPAR $\gamma$  target responsible for hepatic fat accumulation in mice. Induction of *Fsp27* expression has also been observed in an earlier study on hepatic steatosis by PPAR $\gamma$  overexpression.<sup>49</sup> It seems clear that increased PPAR $\gamma$  expression in the liver directly or indirectly activates various genes involved not only in lipogenesis, but also in adipogenesis, thereby promoting hepatic steatosis. It has been reported that the genes involved in uptake, intracellular trafficking, esterification and storage of FAs such as *Cd36*, *Fabp4/aP2*, monoacylglycerol O-acyltransferase 1 (*Mogat1*), *Plin2/Adrp* and *Fsp27* are direct targets of PPAR $\gamma$ .<sup>63,75</sup> However, lipogenic genes such as *Fasn*, *Scd-1* and *Acc* have not been proven as direct targets of PPAR $\gamma$ , yet. The upregulation of these genes by PPAR $\gamma$  overexpression may be mediated through SREBP1C, a direct regulator of these genes, which can be activated transcriptionally or through proteolytic cleavage.<sup>71,76</sup> Thus, the direct role of PPAR $\gamma$  in the liver lipid homeostasis is to enhance FAs, either from the diet or from lipolysis of white adipose tissues, up-take them from circulation and store them in lipid droplets. Several mechanistic pathways have been implicated in hepatic lipid homeostasis: FA uptake, *de novo* FA synthesis, FA oxidation, and FA export via VLDL secretion.<sup>77</sup> Dominant esterification of dietary FAs into TGs rather than esterification of newly synthesized FAs highly contributes to the hepatic fat accumulation by HFD feeding, which has been demonstrated by mass isotopomer distribution analysis following [1-<sup>13</sup>C] acetate infusion into experimental mice.<sup>78</sup> This observation signifies an important role of PPAR $\gamma$  in the development of fatty liver induced by HFD.

#### 4.2. Upstream regulators of *Pparg2* gene expression

It is clear that overexpression of hepatic PPAR $\gamma$  leads to fat accumulation through transcriptional activation of genes responsible for lipid uptake and storage. Unraveling how *Pparg* expression is regulated is key to discovering therapeutic and preventative approaches for NAFLD. A recent study on PPAR $\gamma$ 2 upregulation by HFD feeding adequately illustrated the linkage between PPAR $\gamma$ 2 activation and diet-induced hepatic fat accumulation.<sup>79</sup> The study using ghrelin receptor knockout mice and exogenous ghrelin infusion has demonstrated that ghrelin, a gastric hormone released during fasting, triggered the activation of mammalian target of rapamycin (mTOR) signaling and *Pparg2* mRNA expression in the liver, thereby inducing lipid accumulation. The highly specific PPAR $\gamma$  antagonist, GW9962, blocked ghrelin-induced TG accumulation and lipogenic gene expression in cultured hepatocytes, confirming that PPAR $\gamma$  is the downstream target responsible for ghrelin-induced lipid accumulation. In conjunction with the finding that HFD induces expansion of ghrelin-producing cells, ghrelin signaling is an important mediator that links HFD feeding and PPAR $\gamma$ 2-induced hepatic steatosis; however, the responsible transcription factor has not been identified or suggested in that study.<sup>80</sup> The idea that mTOR signaling induces PPAR $\gamma$ 2 activation is also strongly supported by the rapid induction of *Pparg2* expression by insulin in adipose tissues.<sup>81</sup> In another elaborate study, AP1 was identified as a direct regulator of *Pparg2* transcription.<sup>82</sup> AP1 is a dimeric transcription factor that forms homodimers or heterodimers with various basic leucine zipper proteins such as the JUN proto-oncogene (JUN), FOS proto-oncogene (FOS), MAF bZIP transcription factor (MAF) and activating transcription factor (ATF) subfamilies, and is involved in cell survival and proliferation in response to physiological stimuli and environmental insults.<sup>83</sup> Using individual *API* monomer gene gain- and loss-of-function mouse models, and transient transfection reporter assays, Hasenfuss *et al.* have identified that Fra1/Jun or Fra2/Jun heterodimers repressed *Pparg2* gene transcription and hepatic lipid accumulation, while Fos/Jun dimers induced them. Though the study established AP1 as a direct regulator of *Pparg2* and hepatic lipid homeostasis, the extracellular signaling pathways leading to the formation of specific heterodimers of AP1 proteins remain to be revealed. Several upstream regulators of *Pparg2* associated with hepatic steatosis have been identified. Retinoic acid signaling activates the novel transcription repressor, hes family bHLH transcription factor 6 (HES6), which represses hepatocyte nuclear factor 4 $\alpha$  transcription activity on the *Pparg2* promoter.<sup>84–86</sup> It is worth noting that HES1, a direct target of cyclic adenosine monophosphate (cAMP) response element binding protein, is directly implicated in the repression of *Pparg1* gene expression during fasting-induced breakdown of hepatic lipids.<sup>87</sup> Though it has not been studied in the setting of hepatic steatosis, progesterone has also been reported to directly induce *Pparg2* expression through progesterone receptor in ovaries and macrophages.<sup>88,89</sup>

#### 4.3. Two faces of hepatic PPAR $\gamma$ in lipid metabolism

A line of reports presented in this review suggests that PPAR $\gamma$  overexpression in the liver induced by HFD feeding or pathophysiological stresses leads to lipid accumulation, which is the initiation step in the development of NAFLD (Fig. 2). Blocking *Pparg* gene expression in the liver of HFD-fed mice reduced not only lipid accumulation, but also the expression of inflammatory genes, which is an indication of NASH progression.<sup>47</sup> This observation was strongly supported by a study using HFD-fed *Fra1*-liver-specific transgenic mice with low

*Pparg2* gene expression, where inflammatory marker genes' expression and serum alanine aminotransferase (ALT) levels were significantly downregulated, compared with the control counterparts.<sup>82</sup> These observations strongly suggest that the induction of hepatic PPAR $\gamma$ 2 expression is linked to NASH development.

Considering its direct role in TG synthesis and lipid droplet formation, PPAR $\gamma$  may have a protective role against lipotoxicity mediated by free fatty acids (FFAs) and their derivatives.<sup>90</sup> Especially, the promotion of TG synthesis is considered a protective pathway against SFA insults.<sup>91</sup> While unsaturated FAs are readily incorporated into inert TGs, excess SFAs remain largely unesterified.<sup>92</sup> These excess free SFAs are rapidly incorporated into saturated phospholipid species that can be integrated into the endoplasmic reticulum (ER) membrane bilayers.<sup>93</sup> Because the ER membrane contains unsaturated phosphatidylcholine as the major phospholipid component, incorporation of saturated phospholipids into the membrane results in the loss of membrane fluidity and dissociation of protein folding chaperones, *i.e.*, protein disulfide isomerase and GRP78, from the membrane, which may trigger the unfolded protein response and ER stress, a well-documented etiology of NAFLD.<sup>93–96</sup> As Listenberger *et al.* have reported, promotion of TG synthesis and lipid droplet formation should protect the liver from damage induced by dietary SFAs. When whole body deletion of *Pparg2* was introduced in *ob/ob* mice, their liver contained more ceramides, well-known mediators of NASH development, compared with the control *ob/ob* mice.<sup>97,98</sup> However, because that study focused on  $\beta$ -cell dysfunction by lipotoxicity, the liver phenotypes were not examined. Nonetheless, this observation indicates that ablation of hepatic *Pparg* may result in adverse effects on other peripheral tissues, which were also manifested in the liver-specific *Pparg* knockout *ob/ob* mice.<sup>27</sup> In NAFLD induced by a methionine-choline deficient (MCD) diet, adenovirus-mediated hepatic PPAR $\gamma$  overexpression protected the liver from fibrotic NASH.<sup>99</sup> Earlier manifestations of mitochondrial membrane stiffening and down-regulation of key genes in TG synthesis in the liver of mice fed an MCD diet may explain the protection by PPAR $\gamma$  in this setting.<sup>100,101</sup>

## 5. Conclusions

Many reports point out that HFD consumption strongly induces PPAR $\gamma$ 2 expression thereby activating downstream target genes' expression to facilitate FA uptake, intracellular trafficking, TG synthesis and lipid droplets formation (Fig. 2). This leads to TG accumulation in the liver, an initial prerequisite step in the proposed two-hit theory of NAFLD.<sup>2,3</sup> Hepatic PPAR $\gamma$ 2 expression is maintained at a low level in normal conditions, which allows the liver to deliver newly synthesized and/or dietary FAs in the form of VLDL to other peripheral tissues as an energy source. The induction of hepatic PPAR $\gamma$ 2 expression upon HFD feeding appears to protect peripheral tissues from lipotoxicity by promoting a program to store excess FFAs in the form of TGs. This would be a normal process for combating against constant fat flux in the circulation. However, ablation of hepatic PPAR $\gamma$  reduced not only fat accumulation, but also inflammatory genes' expression and serum ALT levels, which are the signs of NASH development. Therefore, lowering hepatic PPAR $\gamma$  expression is one of the strategies for preventing NAFLD progression. To elucidate the possible linkage between HFD-induced *Pparg2* expression and ghrelin signaling or stress activated AP1 transcription factor, further studies are warranted. Furthermore, clarifying the



link between HFD feeding and hepatic *Pparg2* gene expression will help develop therapeutic and preventative approaches for treating NAFLD. Developing selective PPAR $\gamma$  modulators that can fine-tune its transcriptional activity is another field that requires additional attention.

102

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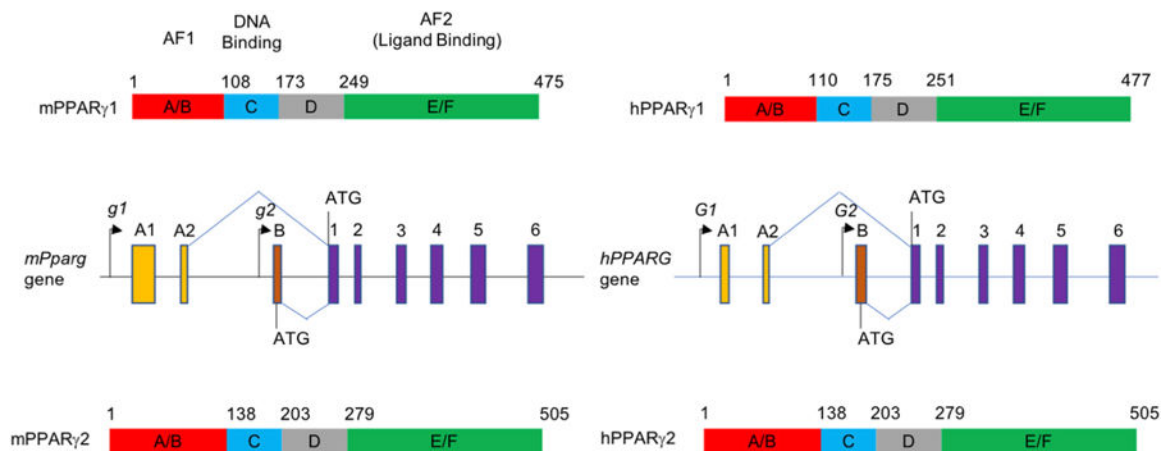
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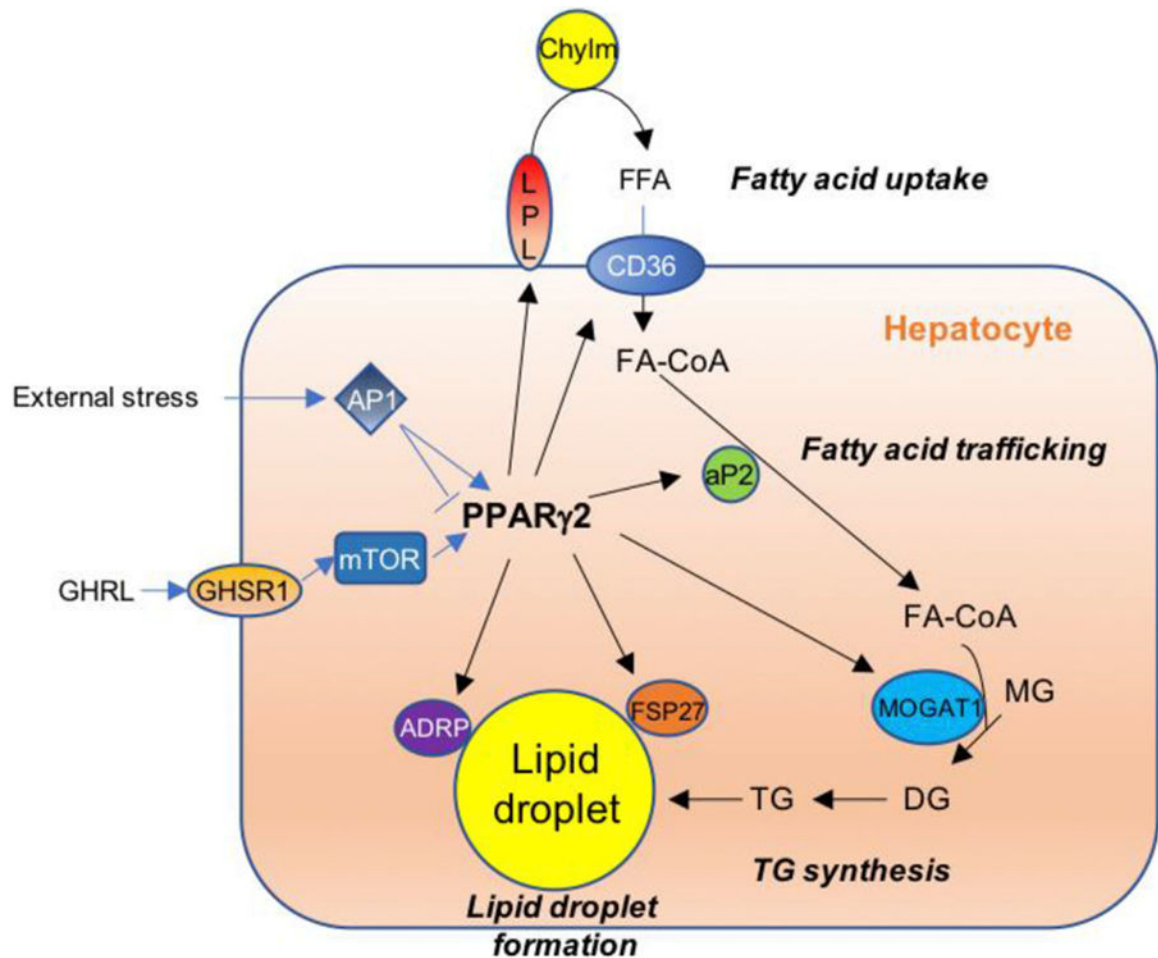
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**Fig. 1. Gene and protein structures of mouse and human PPAR $\gamma$  isoforms.**

Genomic structures of mouse *Pparg1* and *Pparg2* (middle left), and human *PPARG1* and *PPARG2* (middle right) are depicted, based on the earlier reports.<sup>15,16</sup> Purple solid rectangles are common exons for *Pparg1* and *Pparg2* isoforms. Orange (A1 and A2) and brown rectangles (B) are specific for *Pparg1* and *Pparg2* isoforms, respectively. PPAR $\gamma$ 1 protein structures are shown at the top and PPAR $\gamma$ 2 structures are presented at the bottom. The functional domains of mouse and human PPAR $\gamma$ s are based on sequence alignment reported in an earlier review.<sup>20</sup> Abbreviations: PPAR $\gamma$ , peroxisome proliferator-activated receptor gamma; AF, activation function.



**Fig. 2. Upstream regulators and downstream targets of PPAR $\gamma$ 2-mediated hepatic lipid homeostasis.**

Increased ghrelin by chronic HFD consumption induces *Pparg2* gene expression through mTOR signaling. Similarly, external stresses (*i.e.*, nutritional stress) induce or inhibit *Pparg2* transcription via AP1 depending on the specific heterodimer formation. Increased PPAR $\gamma$ 2 activates downstream target genes such as *LPL* and *CD36* for FA uptake, *aP2* for intracellular FA trafficking, *MOGAT1* for synthesis of diacylglycerol, and *ADRP* and *FSP27* for lipid droplet accumulation. These targets are not major genes in hepatic TG synthesis during normal conditions. However, when PPAR $\gamma$ 2 expression is increased by HFD feeding, these target genes contribute to lipid accumulation in the liver. Abbreviations: PPAR $\gamma$ 2, peroxisome proliferator-activated receptor gamma 2; Chylm, chylomicron remnants; FFA, free fatty acids; FA-CoA, fatty acyl-Coenzyme A; MG, monoacylglycerol; DG, diacylglycerol; TG, triacylglycerol; GHRL, ghrelin; GHSR1, ghrelin receptor; LPL, lipoprotein lipase; CD36, cluster of differentiation 36; aP2, adipocyte protein 2; AP1, activator protein 1; mTOR, mammalian target of rapamycin; ADRP, adipose differentiation-related protein; FSP27, fat specific protein 27; MOGAT1, monoacylglycerol O-acyltransferase 1.