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PPAR γ in human and mouse physiology

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Summary

The peroxisome proliferator activated receptor gamma (PPAR γ) is a member in the nuclear receptor superfamily which mediates part of the regulatory effects of dietary fatty acids on gene expression. As PPAR γ also coordinates adipocyte differentiation, it is an important component in storing the excess nutritional energy as fat. Our genes have evolved into maximizing energy storage, and PPAR γ has a central role in the mismatch between our genes and our affluent western society which results in a broad range of metabolic disturbances, collectively known as the metabolic syndrome. A flurry of human and mouse studies has shed new light on the mechanisms how the commonly used insulin sensitizer drugs and PPAR γ activators, thiazolidinediones, act, and which of their physiological effects are dependent of PPAR γ . It is now evident that the full activation of PPAR γ is less advantageous than targeted modulation of its activity. Furthermore, new roles for PPAR γ signaling have been discovered in inflammation, bone morphogenesis, endothelial function, cancer, longevity, and atherosclerosis, to mention a few. Here we draw together and discuss these recent advances in the research into PPAR γ biology.

Keywords

PPAR γ ; mouse models; human genetic variants; longevity; bone homeostasis; metabolism

Introduction

Peroxisome proliferator-activated receptor-gamma (PPAR γ , NR1C3) belongs to a nuclear receptor superfamily of transcription factors. It is mainly known to regulate adipocyte differentiation and fatty-acid uptake and storage (reviewed in [1-3]). The two distinct isoforms of PPAR γ protein, PPAR γ 1 and PPAR γ 2, originate from one PPAR γ gene through the use of separate promoters and 5' exons (Fig. 1), and differ by the presence of an extra 28 (human) – 30 (mouse) amino acids at the NH₂-terminal end of PPAR γ 2 [4-10]. This extension of the ligand-independent activation domain makes PPAR γ 2 a better transcriptional activator relative to PPAR γ 1 [11]. Not only the protein structure of PPAR γ 1 and 2 is different but both isoforms show also a distinct expression pattern. PPAR γ 2 expression is mainly limited to the adipose tissue whereas PPAR γ 1 is ubiquitously expressed [12,13]. The transcriptional activity of PPAR γ is controlled by the promiscuous binding of small lipophilic ligands into the ligand-binding pocket. Although a natural compound exhibiting specific, high-affinity binding

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characteristics remains unidentified, endogenous polyunsaturated fatty acids and eicosanoids, derived from nutrition or metabolic pathways, have been recognized as ligands for PPAR γ [14-16]. In addition, many synthetic compounds, most particularly the thiazolidinediones (TZDs), are potent PPAR γ agonists (reviewed in [17,18]).

Human metabolism is evolutionarily equipped to cope with pre-agricultural cycles of feast and famine, and physical activity and rest. Because of the rapid emergence of the modern westernized life-style, exposing people to chronically elevated levels of natural PPAR γ ligands and positive energy balance, our genetic makeup has become ill adapted to cope with our lifestyle [19-21]. The continual PPAR γ activation promotes adipogenesis and fatty-acid storage, and eventually obesity and associated metabolic diseases such as hyperlipidemia, insulin resistance, type 2 diabetes mellitus (T2DM) and cardiovascular diseases including hypertension, which constitute a heavy social and economic burden. Among the most potent current treatment strategies for T2DM are the TZDs which exert their antidiabetic effects by sensitizing the body to insulin's action. However, the clinical use of these full PPAR γ agonists is limited by weight gain due to increased adiposity, fluid retention, and heart failure in up to 15% of patients [22-24]. In addition, despite their fairly wide use, the long-term adverse effects of TZDs are not very well known, and they may increase the risk for osteoporosis [25,26] and colon cancer [27,28].

In this review we summarize the studies that have shed new light on the role of PPAR γ in energy homeostasis not only in the main metabolic tissues i.e. adipose tissue, liver and skeletal muscle, but also in other tissues. The reviewed studies also emphasize that insulin sensitization can be achieved without concomitant increase in fat deposition by modulating PPAR γ activity. In addition to obesity, altered PPAR γ activity, elicited by our westernized lifestyle, has potentially influenced bone homeostasis, longevity, cardiovascular and kidney function and cancer risk, as recent literature supports a significant role for PPAR γ in these processes. Furthermore, animal models with altered PPAR γ activity have elucidated the distinct roles of PPAR γ in various tissues, as well as PPAR γ -dependent and independent actions of TZDs therein. We can introduce here only a fraction of the existing information on this nuclear factor, and will thus mostly concentrate on the lessons learned from the study of various natural or engineered genetic variants of PPAR γ that have altered PPAR γ activity.

Human PPAR γ genetic variants

The vital role of PPAR γ in adipogenesis began to emerge more than a decade ago [12] and has remained undisputed since. Both of the processes central in adipogenesis, namely preadipocyte differentiation and fatty acid storage in mature adipocytes, are controlled by PPAR γ , and particularly the PPAR γ 2 isoform (reviewed in [2,3,20,21]). Genetic association studies in humans underscore the role for PPAR γ in adipogenesis as well as the complexity of PPAR γ biology. One of the first links was the discovery that PPAR γ locus on chromosome 3p25-p24 associates with obesity in Pima Indians [29]. To date, dozens of reports have revealed associations of genetic variation and population risk to T2DM or related conditions, as summarized in Table 1 for Ppar γ . The most widely reproduced association is that with the PPAR γ 2 gene polymorphism Pro12Ala (Fig. 1B) [30,31] which has been suggested to induce a modest impairment of transcriptional activation due to decreased DNA-binding affinity [31,32]. The original reports describing a significantly reduced risk of T2DM in the normal-weight carriers of the Ala12 allele [30,31] have subsequently been confirmed by many independent studies, as reviewed in [2], and by recent meta-analyses [33-35]. For example, a meta-analysis compiling over 25,000 cases of diabetes unequivocally confirmed the association between the PPAR γ Pro12 allele and T2DM, and suggested that patients who carry the Pro12 allele have a 1.27-fold higher risk for developing T2DM than Ala12 carriers [33]. This seemingly modest effect translates into a staggering 25% population-attributable risk

because of the high frequency of the Pro12 allele (up to ~80-100%), especially in Japanese and European populations [33].

Genes do not work in a vacuum, but react to e.g. environmental stimuli. Clear demonstration of this, in the context of PPAR γ , is the apparently paradoxical linkage of the Ala12 allele to higher body mass index (BMI) in obese (BMI \geq 27) subjects [34]. Thus, pre-existing obesity may be required for the Ala12 allele to cause further increase in obesity, whereas in lean subjects the effect is either lacking [34] or opposite [31,36]. Furthermore, the phenotypic effects of PPAR γ Pro12Ala variant, also other than those on BMI and T2DM, have been shown to be modulated by the superimposition of environmental factors like obesity, physical activity, and the dietary fatty acid composition [37-40]. For example, Ala12 allele causes an increase in muscle glucose uptake only in lean carriers and not in obese [37]. The Pro12Ala variant in itself has also been associated with such additional phenotypes as longevity, cognitive decline, atherosclerosis, hypertension, birth weight, myocardial infarction and cancer which may provide further insight into the function of this variant in vivo [41-48]. Taken together, current evidence supports a role for PPAR γ at the interface between the environment and the control of metabolism [40,49].

Genes not only react to environmental signals, but also interact with each other. As most human metabolic disorders are clearly polygenic in nature, recently the combined effects of PPAR γ mutations and variants of other genes have been investigated. For example, Pro12Ala variant has been shown to interactively influence insulin sensitivity and body composition with the A-376C variant of fatty acid binding protein 4 (FABP4) gene [50], representing a synergistic (1+1>2) interaction where the combined effect is more than what would be expected from simply adding up the individual effects. On the other hand, only additive (1+1=2) interaction was found among three common T2DM risk alleles (Lys23 of KCNJ11, Pro12 of PPAR γ , and the T allele at rs7903146 of TCF7L2) [51]. There is also evidence for a subtractive (1-1=0) interaction, albeit within one gene, as two variants of PPAR γ , Pro12Ala and C-681G were recently reported to have an opposite effect on growth in British school children [52]. Similarly, the C1431T variant (a.k.a. His477His) can negate the beneficial effects of the Pro12Ala variant on T2DM [53]. Furthermore, the effect of Pro12Ala polymorphism may be restricted to certain ethnic groups, as suggested for Caucasian subpopulations by a recent meta-analysis of pre-diabetic traits in about 32,000 nondiabetic subjects [35]. Interestingly, genetic background has also had a profound effect in certain mouse models with altered PPAR γ activity, as discussed below. The above genetic interaction studies clearly indicate that the genetic makeup of an organism adds to the complex nature of PPAR γ biology.

In contrast to the relatively mild effects of the common Pro12Ala variant, rare dominant negative and loss-of-function mutations affecting the ligand-binding domain of PPAR γ have been identified in patients afflicted with partial lipodystrophy (loss of fat from the limbs and gluteal region), hepatic steatosis, dyslipidemia, severe insulin resistance, diabetes and hypertension. These and other currently described functional or otherwise important human PPAR γ variants are depicted in Figure 1B. The first identified loss-of-function mutations were 185Stop [54], Val290Met (also called V318M) [55], Arg425Cys (also R397C) [56], and Pro467Leu (also called P495L) [55,57]. Apart from 185Stop, which results in a truncated protein, the rest of these mutant receptors retain ability to bind target DNA but exhibit severely reduced transcriptional activation via diminished capacity to recruit cofactors [55,58]. A very recent report described five new mutations, three of which (Cys114Arg, Cys131Tyr and Cys162Trp) prevent PPAR γ from binding to the target DNA while the other two lead to missense (Arg357X) or truncated (315Stop) proteins [59]. Heterozygous carriers of these new mutations are severely insulin resistant and hepatosteatotic, and display partial lipodystrophy; some of the patients are also hypertensive [59]. Although these studies provide direct genetic evidence of a link between PPAR γ action and the regulation of mammalian glucose

homeostasis, it remains uncertain whether the profound effects on insulin resistance observed in these individuals is only a manifestation of reduced adipose tissue mass or whether other direct effects of PPAR γ action on insulin signaling are impaired. Recent evidence, however, suggests that dysfunction rather than relative lack of the adipose tissue may be more significant [49].

Contrasting the loss-of-function mutations, a rare Pro115Gln substitution is a gain-of-function mutation which renders PPAR γ constitutively active and results in extreme obesity while, paradoxically, normal insulin sensitivity prevails [60]. On the other hand, Phe388Leu (also F360L) [61], Tyr355X [62] and a PPAR γ promoter 4 variant A-14G [63] represent cases of haploinsufficiency where the affected allele reduces PPAR γ function without interfering with the wild-type PPAR γ protein. However, patients carrying these variants still exhibit the stereotypical partial lipodystrophy, fatty liver, severe insulin resistance if not T2DM and hyperlipidemia. Additional human PPAR γ variants include a common silent His477His polymorphism in PPAR γ exon 6 (also called C1431T, C161T of exon 6, or CAC478CAT), associated originally with altered leptin levels, higher BMI and lower bone mineral density [64-66], and later with increased myocardial infarction risk [67] as well as with potential protection from atherosclerotic lipid alterations [68]; a C-2821T variant in the PPAR γ 2 promoter, associating with whole-body insulin action and hepatic insulin sensitivity, likely via altered binding on the overlapping E2-box, a binding consensus site for e.g. myogenin differentiation 1 (MyoD) [69]; a C-681G variant in the promoter of the shorter form of PPAR γ 1 (also called PPAR γ 3), associating with increased body size and plasma LDL levels, via reduced binding of signal transducer and activator of transcription 5B (STAT5B) onto the PPAR γ promoter [70]; and a C-689T variant in the PPAR γ 2 promoter, associating again with increased body weight and plasma LDL levels [71]. Recently also intronic PPAR γ variants, associating with body size, BMI and glucose levels, have been identified [72].

Mouse genetic variants

PPAR γ exerts pleiotropic functions in a wide range of tissues and in processes beyond metabolism. Genetic manipulations in the mouse offer excellent opportunities to unravel the complex physiological effects of altered PPAR γ activity in a well-controlled genetic background and environmental setting. First came the generation of a conventional PPAR γ deficient mice which, unfortunately, die in utero due to major placental and cardiac defects. Although a single PPAR γ ^{-/-} animal was rescued by tetraploid aggregation, it survived the severe lipodystrophy for only a few days [73]. The lipodystrophy of the rescued PPAR γ ^{-/-} mouse, together with the characterization of mice chimeric for PPAR γ ^{-/-} ES cells [74], showed the importance of PPAR γ in adipose tissue development in vivo. Next, the physiological function of PPAR γ in mice was studied in the heterozygous PPAR γ ^{+/-} mice. These heterozygous PPAR γ knock-out mice are a difficult model to understand, as both resistance [75] and susceptibility [76] to high-fat diet induced obesity and subsequent insulin resistance have been reported; for thorough discussion about the potential reasons, see [76]. To overcome the embryonic lethality of the germ-line PPAR γ deficient mice, tissue-specific deletions of PPAR γ have been generated subsequently in mice to help to elucidate the tissue specific activities of PPAR γ [77] (summarized in Table 2 for main metabolic tissues as targets, and in Table 3 for other tissues).

PPAR γ in adipose tissue

The essential role of PPAR γ in adipogenesis was revealed by inactivation of both PPAR γ 1 and PPAR γ 2 in the adipose tissue [78-80]. Moreover, the vital role of adipose tissue per se was exemplified by the significant mortality rate (>40%) of the severely lipodystrophic WAT-specific hypomorphic PPAR γ 1 and PPAR γ 2 knockdown mice (PPAR γ ^{hyp/hyp}) [78]. When an

aP2-driven Cre recombinase transgene was used to ablate PPAR γ 1 and PPAR γ 2 from the mature adipocytes, a more moderate reduction of adipose mass was observed, which was accompanied by hyperlipidemia, liver steatosis, and protection from high-fat diet induced increase in adiposity [79,80]. Interestingly, the surviving adult PPAR $\gamma^{\text{hyp/hyp}}$ mice did not have liver steatosis or dyslipidemia due to efficient oxidation of excess lipids in the muscle by PPAR α and PPAR β/δ -driven pathways [78]. Intriguingly, all three adipose PPAR γ -deficient models had close to normal glucose tolerance [78-80]. The importance of PPAR γ in the survival of mature adipocytes was high-lighted by yet another independent ablation of total PPAR γ function in adipocytes, this time in a temporally controlled manner in adult mice [81].

To gain more insight to the relative roles of PPAR γ 1 and 2, mice with selective disruption of the more adipogenic and adipose-tissue restricted PPAR γ 2 isoform have been generated. However, these studies have provided somewhat confusing results. On C57Bl/6 genetic background, ablation of PPAR γ 2 resulted in diminished adipose tissue (WAT) mass, decreased insulin sensitivity and reduced adipocyte differentiation in vitro. In addition, it provided protection against high-fat diet induced weight gain [82]. In contrast, on a 129 background, PPAR γ 2-deficiency led to insulin resistance without affecting adiposity in vivo, even on high-fat diet, although in vitro a defect in fat cell differentiation was clear [83]. Despite the differences in adiposity and insulin sensitivity/resistance in these two models, likely due to the different genetic backgrounds of the mice in the two studies, the authors of both papers linked the phenotype to reduced levels of plasma adiponectin [82,83]. Moreover, the fact that there still was fat in the PPAR γ 2-deficient mice indicates that also PPAR γ 1 is able to initiate at least some adipocyte differentiation.

PPAR γ in skeletal muscle

Although PPAR γ is predominantly expressed in adipose tissue, also skeletal muscle expresses it at low levels. Furthermore, muscle is an important tissue in glucose and fuel homeostasis. Considering the large relative mass of muscle in the body, even a small change in PPAR γ activity might have significant metabolic effects. However, the role of PPAR γ in the muscle is fairly minor according to the two independent reports, albeit with essentially opposite results, of muscle-specific PPAR γ knock-out mouse models [84,85]. The report published first [84] described muscle-specific PPAR γ knock-out mice with normal glucose homeostasis and insulin levels, but with reduced hepatic insulin sensitivity which was attributed to the increased WAT mass. The inability of PPAR γ -deficient muscle to effectively use lipids as fuel explained the shunt of lipids to the adipocytes and thus the resulting adiposity. Since the beneficial effects of TZDs on glucose homeostasis prevailed in the absence of muscle PPAR γ , it was concluded that the insulin-sensitizing effects of TZDs are independent of muscle PPAR γ [84]. These findings are consistent with the observations in the PPAR $\gamma^{\text{hyp/hyp}}$ mouse model where adipose tissue PPAR γ expression was shown to be crucial for the insulin-sensitizing effects of TZDs, as TZD treatment ameliorated only the glucose intolerance but not the insulin resistance of these mice [78]. In contrast to the first report, the second study [85] showed that muscle-specific PPAR γ -deficient mice develop severe muscle insulin resistance, leading to hyperinsulinemia, glucose intolerance and hypertriglyceridemia. Since TZD treatment failed to enhance insulin-stimulated glucose disposal into PPAR γ -deficient muscle, suggesting a lack of improvement in muscle insulin sensitivity, it was concluded that muscle PPAR γ is the direct target of TZD actions [85]. According to most studies, however, it seems that PPAR γ in the muscle is more responsible for coordinating the use of energy rather than directly controlling glucose homeostasis or responses to insulin [78,79,84,86,87]. Thus it is likely that the insulin-sensitizing effects of PPAR γ are predominantly mediated by WAT. Therefore, in addition to the role as master regulator of adipogenesis in vivo, PPAR γ in the WAT also directs glucose and lipid homeostasis.

The role of PPAR γ in the adipocytes differentiation is well established. Interestingly, PPAR γ seems to have a role also in muscle differentiation, at least in vitro. A recent study by Singh et al [88] shows that correct regulation of PPAR γ activity is vital for proper C2C12 myocyte differentiation as both 25-30% increase and similar decrease in PPAR γ protein levels resulted in virtually complete inhibition of myocyte differentiation. However, it seems that in the in vivo setting there are compensatory mechanisms at play since none of the muscle specific or heterozygous whole-body PPAR γ knock-out models have been described with muscular dystrophy.

PPAR γ in the liver

Like skeletal muscle, also the liver expresses low levels of PPAR γ . Again, consistent with the adipose tissue and muscle-specific PPAR γ knock-out models, also the liver-specific ablation of PPAR γ leads to impaired lipid balance. Lack of PPAR γ in the livers of two separate mouse models with pre-existing liver steatosis (leptin-deficient *ob/ob* or lipodystrophic A-ZIP/F-1 mice) protected the mice from the development of fatty liver by reducing liver triglyceride content [86,87]. However, it also led to elevated serum levels of FFA and lipoprotein as well as insulin resistance, illustrating PPAR γ 's role in liver lipogenesis. PPAR γ in the liver was shown to be critical for the ability of TZDs to lower triglycerides and glucose in conditions of lipodystrophy. Indeed, in the absence of WAT, liver PPAR γ regulates both fat and glucose homeostasis [86], but in the presence of WAT, the impact of PPAR γ in the liver on glucose homeostasis is minimal.

An interesting alternative, especially useful for overexpression studies, is the systemic adenoviral delivery of a transgene, typically resulting in liver-specific expression. Using this methodology, in conjunction with PPAR α -deficiency, the independent role of PPAR γ 1 in the liver has been elucidated [89,90]. In contrast to the lack of PPAR γ , overexpression of PPAR γ 1 in the mouse liver leads to hepatic steatosis not only in the absence of PPAR α but also to some degree in wild-type mice via a mechanism involving transcriptional activation of genes linked to adipogenesis, some of which are novel as PPAR γ target genes [89,90]. Using classical transgenesis, the artificial Leu468Ala/Glu471Ala double variant of PPAR γ has also been expressed in the mouse liver [91]. This model, resulting in suppression of both PPAR α and PPAR γ target genes, revealed potentially distinct roles for PPAR α and PPAR γ in fasting and high-fat diet induced hepatic steatosis.

The PPAR γ -deficient mouse models specific to the three main metabolic tissues have helped us to realize that when PPAR γ is absent in any of them, whole-body lipid homeostasis and insulin sensitivity are significantly altered. This is a fascinating observation considering that PPAR γ expression levels vary greatly among these tissues. The resulting repartitioning of lipids that occurs in these mouse models has also unveiled the presence of a complex network of cross-talk between the liver, adipose and muscle that is essential to the maintenance of energy balance. This balance is in part achieved by the adaptation of PPAR γ in the non-targeted tissues and by the other PPAR isoforms, PPAR α and β/δ , which enhance fatty acid oxidation to minimize hyperlipidemia and the consequential insulin resistance.

PPAR γ in pancreas

Based on the evidence from rat and human pancreatic islets, PPAR γ is expressed by the beta-cells [92,93]. However, in contrast to adipose tissue, muscle and liver, the deletion of PPAR γ in pancreatic beta-cells did not result in metabolic phenotype. Instead, it high-lighted the antiproliferative role of PPAR γ because on chow diet these mice had a 2-fold increase in pancreatic islet size. Opposite to this, on a high-fat diet the normal expansion of beta-cell mass was markedly blunted in the absence of PPAR γ [94]. Another study, using high-fat fed PPAR $\gamma^{+/-}$ mice, identified a role for PPAR γ in insulin secretion and triglyceride partitioning

into the islets upon high-fat feeding, leading to protective effects against lipotoxicity [95]. However, the importance of these findings, when it comes to translating them to human biology, may be reduced by the fact that PPAR γ gene expression in mouse islets [95] is very low compared to human (and rat) islets [92,93]. This difference in PPAR γ expression in the pancreas is also evident in the SymAtlas gene expression data sets for mouse and human (<http://symatlas.gnf.org/SymAtlas/>).

PPAR γ in the macrophages

As the role of PPAR γ in atherosclerosis, in which macrophages are integral players, is covered by another review in this issue of BBA, we present and discuss here only those studies utilizing mice with macrophage-specific PPAR γ inactivation. PPAR γ has a similar function in macrophages and adipocytes as it modulates lipid homeostasis in both cell types via regulation of genes including e.g. lipoprotein lipase and CD36. Studies using macrophage-specific PPAR γ -deficient mice have identified a definite antiatherogenic role for PPAR γ as in these mice lipid homeostasis in the arterial wall is significantly impaired and the development of atherosclerosis enhanced [96-98]. Mechanism behind the antiatherogenic properties of PPAR γ involves stimulation of cholesterol efflux from macrophages into the plasma (reduced in knock-out mice) and inhibition of monocyte recruitment into the developing atherosclerotic lesion, the latter suggested by increased CC chemokine receptor 2 gene expression [97]. Interestingly, macrophage-specific ablation of PPAR γ results in exaggerated insulin resistance upon high-fat feeding, suggesting that macrophage PPAR γ has a protective role in obesity [99]. Indeed, an intriguing link between macrophages, inflammation, adipose tissue and T2DM has recently emerged [100-102]. In obesity, the adipose tissue is continually under metabolic stress, leading to the activation of stress and inflammatory pathways, which in turn result in macrophage accumulation within the adipose tissue. Subsequently, adipocytes release cytokines, adipokines and free fatty acids, which may cause insulin resistance not only locally but also in the liver and/or skeletal muscle. Further research is needed to discover how macrophage PPAR γ fits into the developing picture on the role of adipose-macrophages in insulin resistance.

PPAR γ in cardiovascular system

In an attempt to elucidate the mechanisms by which PPAR γ ligands ameliorate hypertension in humans, the role of PPAR γ in vascular endothelial cells has been investigated using tissue-specific PPAR γ -deficient mice (PPAR γ E-null) [103]. These mice did not have apparent developmental, reproductive or biochemical abnormalities, nor changes in systolic blood pressure or heart rate on chow diet. However, upon a challenge with high-fat diet, an increase in both blood pressure and heart rate was evident in the PPAR γ E-null mice, whereas only the heart rate was affected upon salt-loading [103]. Although treating the mice with rosiglitazone was clearly effective per se, as indicated by the decreased plasma insulin, it failed to lower the high-fat diet induced hypertension in PPAR γ E-null mice, contrary to the effect in wild type mice. Even in the absence of mechanistic data, this study demonstrates the central role for PPAR γ in mediating the antihypertensive effects of rosiglitazone, especially under conditions partly simulating human type 2 diabetes.

Due to the presence of PPAR γ in cardiac muscle, combined with the fact that at super-clinical doses TZDs cause cardiac hypertrophy, the role of PPAR γ in the heart has been investigated [104,105]. Initial observation on PPAR $\gamma^{+/-}$ mice was that under pressure-overloaded conditions the heterozygous PPAR γ -deficiency leads to cardiac hypertrophy, and that pioglitazone surprisingly provides either full (wild type) or partial protection (PPAR $\gamma^{+/-}$) against the condition, suggesting that pioglitazone action is mostly PPAR γ -dependent [104]. In a more recent study [105], also the selective absence of PPAR γ in the heart muscle resulted

in cardiac hypertrophy, similar to that caused by rosiglitazone, but systolic function was retained. The study of Duan et al [105] also provides deeper mechanistic insight by showing that the promotion of cardiac hypertrophy by rosiglitazone and cardiac-specific PPAR γ -deficiency are mediated by different mechanisms, as evidenced by the differential effects on gene expression, NF- κ B activity and the activation of the members of MAPK pathways. In this respect, the most noteworthy observation was the PPAR γ -independent effect of rosiglitazone on Erk1/2 activation [105]. This study is yet another demonstration of the potential that the PPAR γ cell type-specific knock-out models provide for discerning the PPAR γ -dependence of e.g. pharmacological interventions.

Taken together, these studies emphasize the importance of PPAR γ in the maintenance of cardiac and vascular function and shed light on the PPAR γ -dependent and independent mechanisms of TZD action in this organ system.

PPAR γ in kidney

Edema and fluid retention are common and serious side effects of TZD treatment. Since PPAR γ is a significant target for TZDs and it is expressed in the collecting ducts of the kidneys, the specific involvement of PPAR γ in fluid metabolism has been recently elucidated by two groups using mice with collecting duct-specific ablation of PPAR γ [106,107]. Both studies show a critical role for PPAR γ in systemic fluid retention through the regulation of renal sodium transport, and that the adverse effects of TZD in fluid metabolism are indeed PPAR γ -dependent. *Scnn1g*, a gene encoding for the gamma subunit of the epithelial Na⁺ channel (ENaC) was identified as a critical PPAR γ target gene in the control of fluid metabolism [107].

PPAR γ in the lung

PPAR γ expression has been detected in the lung, in particular the airway epithelium [108]. A specific role for PPAR γ in lung maturation was recently revealed by Simon et al [109] using mice where PPAR γ deletion was initiated specifically in conducting airway epithelium at late fetal to early postnatal stage. Physiological consequences of the PPAR γ deletion in the airway epithelium include a persistent, but not progressive enlargement of airspaces in adult mice, which together with other phenotypic changes in the lungs point to a role for PPAR γ in postnatal lung maturation [109]. Gene expression studies corroborated the physiological phenotype and suggested a role for PPAR γ in differentiation as well as lipid metabolism in the lung. Although these mice were kept in pathogen-free conditions, to exclude inflammation as a confounding factor [109], it is likely that these mice are susceptible to inflammation as PPAR γ is a recognized regulator of inflammatory response. For example, it has been shown that PPAR γ , together with PPAR α , down-regulates several immune system parameters in a murine model of human asthma [110,111]. Thus, not only PPAR γ but also PPAR α should be targeted for the best therapeutic effect when combating the allergic or inflammatory reactions within the airways.

PPAR γ in mammary epithelium, B- and T-cells, and in ovarian cells

Cui et al generated separate knock-out lineages where PPAR γ was inactivated either in mammary epithelial cells during pregnancy and lactation (WAP-Cre) or in mammary epithelial cells, salivary gland, B- and T-cells, oocytes, granulosa cells and megacaryocytes (MMTV-Cre) [112]. Their results show that PPAR γ is not necessary for mammary development nor function, nor does its absence lead to increased tumorigenesis in this tissue. Also B- and T-cell development is normal in the absence of PPAR γ . However, the lack of PPAR γ in ovarian cells, including oocytes, granulosa cells and corpora lutea, but not in the uterus, resulted in impaired female fertility, possibly due to disturbances in implantation. This points to a role for

PPAR γ in female reproduction, in line with other recent research (reviewed in [113]). In fact, also sperm has been shown to express PPAR γ [114], and it will be interesting to see if PPAR γ has a significant role also in male reproduction.

PPAR γ in the gastrointestinal tract

In the mouse intestine, PPAR γ regulates cell growth and differentiation. In addition, PPAR γ is highly expressed in the (epithelium of) colon and cecum [28,115]. This suggests that PPAR γ has potential for colon cancer association. However, the available evidence continues to be conflicting in whether PPAR γ acts as a promoter or inhibitor in intestinal tumorigenesis, let alone in general. Administration of PPAR γ ligands, i.e. PPAR γ activation, increases tumorigenesis in C57BL/6J-APC^{Min/+} mice which are predisposed to intestinal neoplasia [27,28]. However, increased susceptibility to colon cancer has been shown to result also from heterozygous PPAR γ -deficiency in a chemical model of tumorigenesis induced by azoxymethane administration [116]. Furthermore, when the intestinal PPAR γ was fully or partly inactivated on the same C57BL/6J-APC^{Min/+} background as above, spontaneous tumorigenesis was significantly enhanced in the colon, and in female mice also in the small intestine, suggesting an antitumorigenic role for PPAR γ in the gastrointestinal tract [117]. Intestinal PPAR γ may also have a sex-specific developmental role, as some female embryonic lethality was reported. The above studies seem to suggest that an optimal level of intestinal PPAR γ may exist from which any significant deviation will promote tumorigenesis. In fact, the suggested requirement for a balanced PPAR γ activity in intestinal tumorigenesis resembles the effects of PPAR γ in muscle cell differentiation (see above) [88]. In addition, the cellular context of PPAR γ cofactors (e.g. APC (see above) and retinoblastoma protein [118]) seems to influence tumorigenesis.

Another independently generated intestine-specific PPAR γ knock-out model [119] demonstrated the importance of PPAR γ as a protective agent against experimental inflammatory bowel disease (IBD), as mice lacking PPAR γ in the colon epithelium had increased susceptibility to dextran sodium sulphate (DSS) induced IBD and cytokine gene expression. This model recapitulates earlier results where heterozygous whole-body loss of PPAR γ also rendered the mice more susceptible to experimental IBD [120]. Furthermore, the involvement of PPAR γ in the anti-inflammatory effects of 5-aminosalicylic acid, which is a drug widely used to treat the human IBD, has been recently shown in PPAR γ ^{+/-} mice where the drug protected only the wild type mice from IBD [121]. On the other hand, the anti-inflammatory effect of rosiglitazone in experimental IBD seems to be independent of PPAR γ , as the colon-specific PPAR γ knock-out mice benefited from the treatment similarly to wild-types [119]; this is in contradiction to the PPAR γ -dependent anti-inflammatory role of rosiglitazone in macrophages [122].

Taken together, these results are in line with the suggested role of PPAR γ as an anti-inflammatory agent. Furthermore, they suggest that the anti-inflammatory function of TZDs may act via different routes in the colon epithelium from that in macrophages. Although the tumorigenesis-related and anti-inflammatory effects of PPAR γ have been clarified, to a degree, by the above studies, possible systemic effects of intestinal PPAR γ remain unclear as metabolic phenotyping is lacking in the intestinal-specific PPAR γ knock-out mice.

PPAR γ in the epidermis

PPAR γ activation stimulates keratinocyte differentiation and reduces inflammatory response in the skin. Using dermal-specific PPAR γ knock-out mice, it has been possible to demonstrate that the dermal effects of TZDs on keratinocyte differentiation are indeed PPAR γ -dependent but the effects on inflammation seem independent of PPAR γ [123]. In basal conditions,

however, all the key functions of the epidermis were normal in these mice and the only observed phenotypic effects were a patchy hair loss upon aging and a slight epidermal hyperplasia.

PPAR γ in the neural tissues

High-level PPAR γ expression has been detected in the mouse embryonal brain and neural stem cells, but in the adult brain in general PPAR γ expression is very low [124]. The data of Wada et al [124] demonstrate a role for PPAR γ in the developing brain where it promotes differentiation as the embryonal neural stem cells from heterozygous PPAR γ knock-out mice have decreased growth rates. In addition, PPAR γ agonists stimulate the growth of neural stem cells whereas antagonists cause apoptosis [124].

There is also a role for PPAR γ in the inflammatory diseases of the brain, as heterozygous PPAR γ knock-out mice have an exacerbated response in an experimental allergic encephalomyelitis model, which is a Th1 cell-mediated inflammatory demyelinating autoimmune disease resembling multiple sclerosis [125,126].

PPAR γ and bone homeostasis

Physical activity is a prerequisite for food procurement, food is a prerequisite for energy storage, and stored energy is a prerequisite for physical activity. Because of this inextricable linkage, it is plausible that concomitant with the role PPAR γ has in fuel storage and use, it also regulates bone mass to provide the structural strength required in procuring the next meal. Further link between energy storage and bone arises from the fact that both adipocytes, whose differentiation PPAR γ promotes, and osteoblasts differentiate from the same mesenchymal progenitor cells. On the other hand, osteoclasts, mediating bone resorption, originate from hematopoietic precursors [127]. The initial suggestion that PPAR γ might influence bone development and homeostasis came from an investigation of 404 Japanese menopausal women carrying a silent His477His variant of PPAR γ which associated with mildly decreased bone mineral density (BMD) [65]. Although this association has been recently challenged by the lack thereof in otherwise comparable 263 Korean women [128], other evidence is aplenty and irrefutable. For example, natural and synthetic PPAR γ agonists hinder bone formation in mice [129-131]. On the other hands, heterozygous PPAR γ -deficient mice have enhanced osteoblastogenesis resulting in increased bone mass [132]. Similarly, the specific absence of PPAR γ in fat robustly increases bone mass as it favors osteogenic rather than adipogenic differentiation of mesenchymal precursor cells [26]. The absence of PPAR γ in adipocytes also limits their capacity to secrete antiosteogenic-signaling factors, including leptin, further enhancing the bone phenotype [26]. In addition, the strongly enhanced bone mass consequentially reduces the bone marrow cavity volume and suppressed hematopoiesis which is, however, compensated for by extramedullary hematopoiesis in the spleen [26]. Moreover, PPAR γ haploinsufficiency (PPAR $\gamma^{+/-}$) in vitro promotes osteoblastogenesis but does not affect osteoclast differentiation [25], further strengthening the evidence for the antiosteogenic role of PPAR γ .

If these data obtained in the mouse models can be extrapolated to humans, inhibition of PPAR γ activity could be an interesting strategy to combat osteoporosis. It also warrants careful monitoring of T2DM patients treated with PPAR γ agonists to detect the eventual development of osteoporosis. The most favorable pharmacological approaches to combat diabetes and osteoporosis via PPAR γ -targeting would be those that segregate the positive effects on insulin resistance from the adverse effects on e.g. osteoporosis and cancer.

PPAR γ and longevity

Obesity is accompanied by insulin resistance, hyperlipidemia and T2DM which are risk factors for many other diseases that are likely to shorten lifespan. On the other hand, also lipodystrophy is known to shorten lifespan and it results in complications surprisingly similar to those seen in obesity, both in mice and humans (reviewed in [133,134]). Conversely, caloric restriction promotes longevity and is accompanied by reduced fat mass and improved insulin sensitivity (reviewed in [135,136]). Indeed, decrease in adipose mass and alterations in the insulin/IGF-1 signaling pathway are consistently implicated as critical in mediating the extension of lifespan, as exemplified by the prolonged life of the fat-specific insulin receptor knock-out mice [137]. Among the recently identified mediators of insulin signaling are the Forkhead box 'Other' (FOXO) proteins (reviewed in [138]). Fittingly, the modulation of FOXO expression specifically in the adipose tissue of *Drosophila* or *C. elegans* is sufficient to mediate FOXO's effects on life span [139-141]. However, also the inhibition of PPAR γ can explain the beneficial effects of caloric restriction on longevity. SIRT1, the mammalian ortholog of silent information regulator Sir2, is a NAD⁺-regulated protein deacetylase and a transcriptional inhibitor associating strongly with longevity. SIRT1 represses PPAR γ and hence genes controlling fat storage by docking to the PPAR γ corepressors NCoR and SMRT [142]. In Sirt1^{+/-} mice, release of fatty acids from white adipocytes upon fasting is reduced, supporting Sirt1 mediated PPAR γ inactivation as part of the molecular pathway connecting caloric restriction to life extension in mammals [142]. However, this model does not account for how SIRT1 mediates increased insulin sensitivity under long-term caloric restriction if it represses PPAR γ . The insulin sensitizing effect of SIRT1 is, on the other hand, more likely linked to enhanced mitochondrial activity and energy expenditure as recently demonstrated [143]. Consistent with the Sirt1^{+/-} mouse model, however, is the fact that the human Pro12Ala PPAR γ variant with reduced function also associates with increased longevity [42]. Nonetheless, at present it remains unclear precisely how PPAR γ influences aging and by what mechanism.

Human PPAR γ mutations in the mouse

Mouse models carrying specific PPAR γ mutations have been generated to further refine the information gained from the whole-body and tissue-specific deletions of PPAR γ . First such model was the knock-in of alanine at position 112 (S112A) which prevents serine phosphorylation and renders PPAR γ constitutively active, thus resembling but not replicating the human Pro115Gln mutation [144]. In mice this mutation preserves insulin sensitivity during diet-induced obesity due to undersized adipocytes, and elevated serum adiponectin and reduced FFA levels. This suggests that modulation in the phosphorylation state of PPAR γ may serve as a pharmacological target for insulin sensitization free of weight gain. Another synthetic PPAR γ variant reconstituted in mouse is the Leu466Ala variant, which in vitro is a strong dominant-negative mutant with altered coactivator (absent) and corepressor (enhanced) recruitment characteristics [145]. While this variant is lethal when homozygous, in heterozygous mice it remarkably reproduces the phenotype of adipose tissue-specific PPAR γ knock-out mice [79,80] as the mice exhibit lipodystrophy and hepatosteatosis on chow diet, and insulin resistance on high-fat diet [146]. In addition, Leu466Ala female mice become hypertensive upon high-fat feeding [146], whereas in mice deficient of PPAR γ in vasculature, high-fat diet induces hypertension in both males and females [103]. Unfortunately, published data is lacking on the hypertensive status of the adipose-specific PPAR γ knock-outs.

Also the de facto human genetic variants of PPAR γ are starting to find their way into mice. Similarly to Leu466Ala, the homozygous Pro465Leu PPAR γ mutant (P467L or P495L in humans) (Fig. 1B) proved lethal [147,148]. In heterozygous state both independent versions of Pro465Leu mutant mice had, surprisingly, normal insulin sensitivity on chow diet. This is in stark contrast to the severe insulin resistance described in Pro467Leu humans [55,57].

Although the mutation in the adjacent Leu466 did lead to lipodystrophy (see above), the authors of Pro465Leu mice raised a question of how well the results obtained from PPAR γ mutant mouse models actually translate to human physiology [147]. However, similarities between humans and mice with this mutation also exist, including the redistribution of fat depots [147,148], hypertension [148] and impairment in the postprandial lipid clearance [147]. Furthermore, when bred to hyperphagic *ob/ob* genetic background, severe insulin resistance and other metabolic disturbances became evident [147]. In mice, thermogenic capacity is also diminished due to Pro465Leu PPAR γ genotype, and the brown adipocyte recruitment within the WAT is decreased [149].

Together with the vasculature-specific PPAR γ -deficient mice [103], exhibiting hypertension in the absence of lipodystrophy or insulin resistance, the Pro465Leu mice [148] provide evidence against the dogma that hypertension is a consequence of the insulin resistance in the wake of PPAR γ deficiency and lipodystrophy [150]. The uncoupling between lipodystrophy, insulin resistance and hypertension implies direct modulation of blood pressure by PPAR γ , possibly through regulating the reninangiotensin system activity in adipose tissue [148,150]. Furthermore, this hypothesis provides an explanation for the decrease in blood pressure observed with TZD treatment and emphasizes the continued value of using natural mutations and targeted gene deficiency models to understand receptor function and pharmacology [151,152].

Conclusions and perspectives

The phenotypic effects of human PPAR γ variants and various mouse models with modified PPAR γ expression levels unequivocally demonstrate the highly complex nature of PPAR γ biology. Despite occasionally confusing results, accumulating evidence confirms the critical role for PPAR γ in adipogenesis, maintenance of glucose and lipid metabolism, bone homeostasis, and control of inflammation and blood pressure. The specific roles for PPAR γ in each tissue are also emerging, as adipogenesis is regulated by PPAR γ of the adipose, an inflammatory role for PPAR γ is evident at least in intestinal epithelium and the brain, hypertension due to high-fat diet is modulated by endothelial PPAR γ , and fluid retention is controlled by PPAR γ of the kidney collecting ducts. On the other hand, concerted efforts of PPAR γ in adipose tissue, liver, muscle and possibly also the macrophage are required to maintain normal insulin sensitivity. However, PPAR γ is not working alone, as many of the above roles are partly complementary to those of PPAR α , implicated in inflammation and fatty acid oxidation in the liver and other tissues, and the less studied, ubiquitously expressed PPAR δ , also implicated in the control of inflammation as well as fat homeostasis (for review, see e.g. [153]). Taken together, in light of the adverse side effects of full PPAR γ agonists, future pharmacological strategies for treatment of T2DM, metabolic syndrome and other related conditions will undoubtedly benefit both from compounds that modulate PPAR γ specifically in a tissue-selective fashion [154] and compounds targeting more widely the PPAR family [155-157].

The improvement in longevity during human evolution has occurred because efficient energy conservation and storage has allowed survival through periods of famine whereas an enhanced innate immune response has protected from infections, uncontrolled cell proliferation and cancers. The fact that PPAR γ has been implicated in several of these biological processes, as reviewed above, and in particular in adipogenesis and glucose homeostasis, suggests that PPAR γ plays an active role in age-related pathophysiology. It is certain that the investigation of PPAR γ has already impacted on many scientific fields e.g. by revealing significant roles for PPAR γ in several tissues, and not only in those directly related to fat storage. This trend is likely to continue, long into the future.

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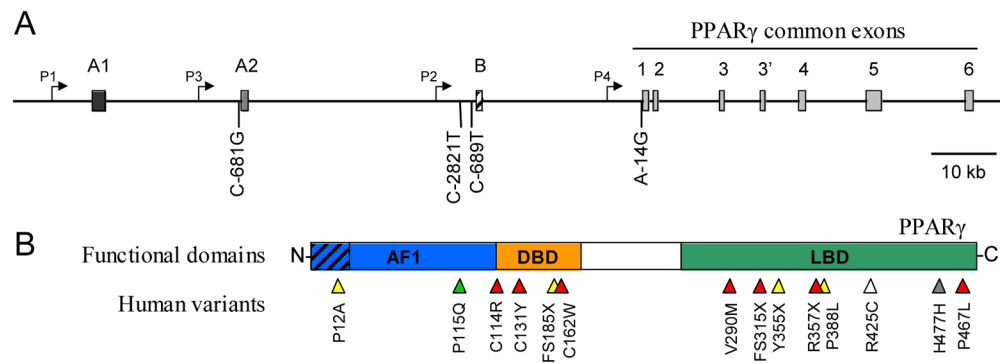
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**Figure 1.**

Human PPAR γ genetic variants. **A:** Genomic structure of the human PPAR γ gene (>150 kb) with thus far described promoter mutants below the structural scheme. Exons are presented as boxes with identification above. Exons A1 and A2 are non-coding, while B encodes for the N-terminal addition in PPAR γ 2 which is missing in PPAR γ 1. The exon sizes are exaggerated for clarity. Note the recently identified additional exon in the intron 3 which contains an in-frame stop codon and the use of which results in a truncated protein (Kim et al, *Biochem. Biophys. Res. Commun.* 347 (2006) 698-706). Promoters are indicated by angled arrows. Numbering for the promoter mutants is relative to the transcriptional initiation site for each promoter. **B:** Functional structure of PPAR γ protein with currently identified human PPAR γ functional variants. Hatched section at the N-terminal end indicates the 28 amino acids specific for PPAR γ 2. AF1, ligand independent activation domain 1; DBD, DNA binding domain; LBD, ligand binding domain. PPAR γ mutations are shown as arrowheads along the structural regions, color indicating the type of mutation as follows: green, gain of function; yellow, partial loss of function; red, loss of function, dominant-negative; grey, silent variant; white, unknown. Note that the amino acid numbering of the variants follows that of the originating publications, and thus some refer to PPAR γ 1, some PPAR γ 2. H477H is not likely to be a functional variant, but it is included here due to the fair number of papers associating it with various disease states.

Table 1

A summary of human PPAR γ genetic variants and their main characteristics.

Variant	Main characteristics and phenotypic effects	References
<i>Common polymorphisms</i>		
Pro12Ala	Specific to PPAR γ 2 isoform; ethnicity-dependent frequency \leq 20%. Ala variant less active, protects from T2DM and weight gain in lean subjects, but with opposite effect in obese subjects. Effects on longevity, cognition, atherosclerosis, HT, birth weight, MI and cancer. Phenotypic effects modulated by environmental and genetic factors. Silent, single nucleotide polymorphism; frequency \sim 14-20%. Associated with leptin levels, BMI, bone density, MI, and atherotic lipid changes.	[30,31,33-36,53] [41-48] [37-40,49]
His477His		[64-68]
<i>Dominant-negative, loss-of-function mutations</i>		
Pro467Leu	Mutant proteins that inhibit also the wild type protein.	[54-59]
Val290Met	Either lack DNA or cofactor binding capacity.	
Cys114Arg	Severe insulin resistance or full diabetes, fatty liver, partial lipodystrophy, dyslipidemia, and often also HT.	
Cys131Tyr		
Cys162Trp		
315Sstop		
Arg357X		
<i>Haploinsufficient mutations</i>		
Arg425Cys	Result in non-functional or missing protein without effect on the wild type variant.	[54,56,61,62]
Phe388Leu	Severe insulin resistance or full diabetes, fatty liver, partial lipodystrophy, dyslipidemia, and often also HT, i.e. the same as for dominant-negative variants.	
Tyr355X		
185Sstop		
<i>Gain-of-function mutations</i>		
Pro115Gln	Constitutively active.	[60]
<i>Promoter variants</i>		
P2 C-689T	Carriers extremely obese, but paradoxically with normal insulin sensitivity.	
P2 C-2821T	Associates with increased body weight and LDL levels; mechanism unknown.	[71]
P3 C-681G	Associates with whole-body and hepatic insulin action; affects MyoD binding (?)	[69]
P4 A-14G	Associates with large body size and LDL levels; affects STAT5B binding.	[70]
	Partial lipodystrophy, metabolic syndrome, no HT; reduced promoter activity.	[63]

Notes: Frequencies are given only for the common polymorphisms as the rest are typically very rare, each found only in a hand-full of subjects. Reference list for the Pro12Ala variant is far from complete, e.g. several studies on the other variants also include this variant. T2DM, type 2 diabetes mellitus; HT, hypertension; MI, myocardial infarction; BMI, body mass index; MyoD, myogenin differentiation 1; STAT5B, signal transducer and activator of transcription 5B.

Table 2

A comparison of PPAR γ knockout models specific to metabolic tissues.

Targeted tissue (type of knock-out)	Adiposity	Plasma profile	Adipokine production	Liver steatosis	Insulin resistance	Other phenotype
Adipose [26,78-83] (hypomorph)[26,78]; w/ aP2-Cre[79,80]; aP2-Cre-ERT2[81]; PPAR γ 2-KO[82,83])	Congenital lipodystrophy[78] Progressive lipodystrophy[79, 81] Moderate lipodystrophy[82] Normal adiposity [83]	↑Glc & ↑Ins[78,83] Normal Glc & Ins[79,82] ↑TG, ↑FFA[78,79] ↓TG[81] Normal TG & Chol[82] or FFA[83]	↓Leptin[78,79,82] ↑Leptin[83] ↓Adiponectin[26,78-80,82, 83]	Normal liver TG[78,82,83] Steatosis[79]	Yes[78,79,82, 83]	↑Bone mass[26]
Muscle [84,85] (w/ MCK-Cre)	↑Adipose mass[84] (↓)Adipose mass [85]	Normal Glc, Ins, TG & FFA[84] Normal Glc, ↑Ins, ↑TG & ↑FFA[85]	Normal leptin[84] ↑Leptin & ↓Adiponectin[85]	Normal liver TG[84] Steatosis[85]	Yes[84,85]	Severely impaired HGP [84] Impaired HGP[85]
Liver [86,87] (w/ Alb-Cre)	Progressive obesity [86] Normal[87]	↑Glc, ↑Ins, ↑TG[86] Normal Glc[87]	↑Leptin & ↓Adiponectin[86]	Normal liver TG[86,87]	Yes[86] No[87]	
Pancreas [94] (w/ Insulin-Cre)	Normal	Normal	ND	Normal liver TG	No	Pancreatic islet expansion on chow diet, but blunted response to high-fat diet Increased atherosclerosis in recipients of PPAR γ ^{-/-} macrophages[96,97]
Macrophage [96-98] (chimeras [#] [96], w/ Mx-Cre [*] [98]; Lyzs-Cre[97])	ND	↓apoE, ↓LDL-cholesterol[98]	ND	ND	ND	

The different mouse models have various age and diet-dependent responses, thus for simplicity the above descriptions are for the adult phenotype in the postprandial state on a chow diet unless otherwise indicated. ND, not determined; Glc, glucose; Ins, insulin; TG, triglycerides; FFA, free fatty acids; MCK, muscle creatine kinase; HGP, hepatic glucose production; Alb, albumin; Mx, myxovirus resistance 1, interferon-inducible protein; Lyzs, lysozyme; apoE, apolipoprotein E; LDL, low density lipoprotein.

[#] Derived from PPAR γ ^{-/-} ES-cells, >90% of all macrophages PPAR γ ^{-/-}.

^{*} The use of Mx-Cre also leads to PPAR γ deficient liver.

Table 3A comparison of PPAR γ knockout models specific to other tissues.

Targeted tissue (Cre promoter)	Main phenotypic characteristics
Vasculature, endothelial cells (Tie2)[103]	Normal plasma profile Blood pressure normal on chow, increased on high-fat diet Hypertension unresponsive to rosiglitazone on high-fat diet
Heart, cardiomyocytes (α MHC)[105]	Normal body weight and plasma glucose Cardiac hypertrophy but normal (or slightly improved) systolic function
Kidney, collecting ducts (Aq2)[106,107]	Protection from thiazolidinedione-induced edema
Lung, conducting airway epithelium (CC10)[109]	Impaired lung maturation (non-progressive condition)
Mammary epithelium (WAP, MMTV)[112]	Normal mammary function No differences in tumorigenesis
B- and T-cells, and ovaries (MMTV)[112]	Normal B- and T-cell production Partial to complete infertility (due to impaired implantation?)
Intestine (Villin)[117] (on ApcMin/+ background)	Normal body weight Enhanced intestinal tumorigenesis (some gender differences)
Colon, epidermal cells (Villin)[119]	Sensitization to experimental inflammatory bowel disease with similar relative protection by rosiglitazone
Epidermis (K14)[123]	Normal skin function

α MHC, alpha myosin heavy chain; Aq2, aquaporin 2; WAP, whey acidic protein; MMTV, mouse mammary tumor virus; Apc, adenomatosis polyposis coli; K14, keratin 14.