

PPAR gamma, bioactive lipids, and cancer progression

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1. ABSTRACT

In this article we review the evolution of cancer research involving PPARgamma, including mechanisms, target genes, and clinical applications. For the last thirteen years, the effects of PPARgamma activity on tumor biology have been studied intensely. Most of this research has focused upon the potential for employing agonists of this nuclear receptor in cancer treatment. As a monotherapy such agonists have shown little success in clinical trials,

while they have shown promise as components of combination treatments both in culture and in animal models. Other investigations have explored a possible role for PPARgamma as a tumor suppressor, and as an inducer of differentiation of cancer stem cells. Whereas early studies have yielded variable conclusions regarding the prevalence of PPARgamma mutations in cancer, the protein level of this receptor has been more recently identified as a significant prognostic marker. We predict that indicators of PPARgamma activity may also serve as predictive markers for tailoring treatments.

2. INTRODUCTION

PPARgamma is a member of the peroxisome proliferator activated receptor (PPAR) family, a subfamily of the nuclear receptor superfamily. The name derives from the fact that the first identified member, mPPAR, was observed to respond to a group of hepatocarcinogens that up-regulate the proliferation of peroxisomes (1). The gamma variant was first cloned from a *Xenopus* cDNA library, along with the alpha and beta variants (2). In the same study, all three receptors were observed to increase the activity of the acyl coenzyme A oxidase promoter, evidencing a role in the regulation of beta-oxidation. The same year, a sequence identified on the acyl coenzyme A oxidase promoter that bound to one of the PPARs was found to be indispensable for this induction and was, thus, termed a “peroxisome proliferator response element” (PPRE) (3). A number of additional genes containing active PPREs in their promoters have since been characterized, and most of these are similarly involved in lipid metabolism (4). Not long after the discovery of the three PPAR variants, a murine version of the gamma variant (mPPARgamma1) was cloned (5). This was followed by a second murine form (mPPARgamma2) which, through a screening of several genes, was discovered to be part of an mRXR heterodimer known to be necessary for the transcription of aP2, a lipoprotein expressed only in adipocytes (6). Accordingly, the same study found mPPARgamma2 mRNA expression to be at least 20 fold higher in murine adipose tissue than in several other organs. mPPARgamma2 was, thus, believed to be involved in adipocyte differentiation. Indeed, it was later shown that murine fibroblasts could be differentiated into adipocytes *in vitro* through retroviral expression of mPPARgamma2 (7).

PPARgamma1 and PPARgamma2, which arise from separate promoters on the same gene, are also present in humans (8). The PPARgamma2 form contains 28 extra N-terminal amino acids that increase the ligand independence of its activity (9). At least two dominant-negative isoforms of PPARgamma have also been identified, emerging through the inclusion of introns with stop codons. Among these are gammaORF4, which ends in the fourth intron (10), and PPARgamma1_{tr}, which ends in the third intron (11). Both of these lose their activity through exclusion of the C-terminal ligand-binding domain, a common alternative splicing strategy for deactivating members of the nuclear receptor superfamily (12). Other transcripts also arise from distinct promoters, but it is currently understood that the proteins they encode are not unique. A third promoter, for example, results in mRNA transcript PPARgamma3, which yields PPARgamma1 after translation (13). Two additional promoters are known to produce mRNA transcripts PPARgamma4 and PPARgamma6 (14, 15), which both also presumably yield PPARgamma1 after translation (15), although any data verifying this have not been published.

Tissue localization experiments on the active forms of PPARgamma have found that the PPARgamma1 form is expressed ubiquitously at the mRNA level, whereas

PPARgamma2 is expressed primarily in adipocytes like its murine homologue (16). The same experiments have also found that the mRNA level of PPARgamma2 in adipose tissue is positively associated with obesity and can be down-regulated through caloric restriction. Shortly after PPARgamma's role in adipocyte differentiation was characterized, the thiazolidinedione (TZD) drug troglitazone was discovered to be a potent ligand (17). Currently, PPARgamma is understood to be the primary mediator of TZDs' ability to reverse insulin resistance in patients with type II diabetes (18). PPARgamma is also believed to play a role in suppressing the development of atherosclerosis (19). More recently, PPARgamma has been characterized *in vitro* as an antagonist of the differentiation of mesenchymal stem cells into osteoblasts, while PPARgamma antagonists have been proposed for use as therapeutic enhancers of osteogenesis in patients with osteoporosis (20).

Shortly after PPARgamma's role in adipocyte differentiation was characterized, differentiation and growth inhibition effects were demonstrated in cell lines from several types of cancer, both *in vitro* and in xenografts (21-24). For the last decade much research has, therefore, focused upon characterizing the role of this receptor in cancer biology, as well as the potential for exploiting its agonists as clinical treatments. Early studies, however, collectively failed to establish either mutations of PPARgamma or changes in PPARgamma mRNA level as prevalent events in tumorigenesis (25-27). Additionally, speculation emerged that the anticarcinogenic effects elicited by synthetic agonists are independent of this receptor's activity (28, 29). Clinical trials also failed to demonstrate the effectiveness of such agonists as a monotherapy for cancer treatment, a fact which fueled a search for combination treatments to enhance their effects (30). Other researchers directed their focus toward developing optimized compounds derived from thiazolidinediones, with or without PPARgamma activation activity (31). Within the last 2-3 years, a significant shift in the understanding of PPARgamma's role in tumor biology has occurred; studies employing immunohistochemistry staining have shown that the alteration of PPARgamma protein level is, in fact, significantly correlated with both tumor progression and patient prognosis in several types of carcinomas. An understanding of PPARgamma's activity, as well as the post-genomic regulation of this activity, therefore, holds much promise for both the development of future treatments and the classification of tumors.

3. HISTORY OF CANCER RESEARCH INVOLVING PPARgamma

3.1. Characterization of the anti-carcinogenic effects of PPARgamma agonists

3.1.1. Early experiments with troglitazone

PPARgamma's potential tumor suppressive role was first explored when the same research group that characterized its role in adipocyte differentiation demonstrated that a human liposarcoma cell line could be re-differentiated through treatment with the PPARgamma agonist troglitazone (22). The following year, the same

research group confirmed similar effects in carcinoma cell lines from colon cancer and breast cancer (23, 24), while another group repeated them in prostate cancer (21). Differentiation was observed in each of these studies; however, the type of differentiation and the methods of measurement varied. The colon cancer group observed re-differentiation into normal colon mucosa through both an increase in carcinoembryonic antigen staining (immunohistochemistry) and changes in the expression profile of several mRNAs associated with malignancy (northern blot). The breast cancer study observed suppression of both K19 and Muc-1, while changes in gene expression usually observed during adipocyte differentiation were absent. The prostate cancer group observed differentiation through several markers including a decrease in PSA. This group then carried out a morphological analysis of TEM images from the treated cells. Interestingly, the cytoplasmic volume increased, along with the number and volume of vacuoles. Many of these cells contained vacuoles large enough to displace the nuclei as in adipocytes; however, unlike the storage vacuoles of such cells, they did not stain positively for lipids. Growth inhibition was also observed in each of these studies, and the timescale for this effect was much longer than for a cytotoxic agent. The colon cancer study measured growth after 7 days of continuous culturing, while the prostate cancer study examined colony formation on soft agar. In xenografts of highly malignant PC-3 (prostate cancer) cells in immuno-compromised mice, continuous treatment with troglitazone similarly halted the growth of tumors for about a week before they resumed the growth curve characteristic of the control group (21). It is worth noting that troglitazone, the PPARγ agonist used in all of these experiments, is no longer used clinically in the United States on account of liver toxicity (32).

3.1.2. A growing repertoire of qualitative effects on tumors

As more studies have been performed with other agonists, such as rosiglitazone, ciglitazone, pioglitazone, and edogenous ligands, an increasing number of qualitative effects on tumor biology have since been documented. Among these is the promotion of apoptosis, although this does not occur with all agonists or in all conditions (29). The reasons for this will be discussed in the Mechanisms of PPARγ Activity section. PPARγ agonists may also influence tumors *in vivo* by inhibiting angiogenesis through their activity in endothelial cells (33). In glioblastomas, PPARγ agonists also reportedly block the promotion of the cancer stem cell subpopulation by growth factors *in vitro*, an important effect since this subpopulation is responsible for both metastasis and resistance to chemotherapy (34).

3.2. Characterizing PPARγ activity in tumors

3.2.1. Early attempts to characterize PPARγ activity in tumors

The effects of PPARγ activation in early experiments with troglitazone led researchers to search for a loss of PPARγ expression in both cell lines and clinical samples. In one of the early studies, 4 out of 55 clinical samples of sporadic colon cancer were found to

have either missense or nonsense mutations, all of which resulted in a loss of PPARγ activity (25). Another study found non-intragenic hemizygous deletions of PPARγ in 8 of 38 prostate tumor samples and noted a reduction of PPARγ protein levels in a few of these samples relative to the normal prostate tissue (26). A following study, however, failed to find either mutations or losses of expression at the mRNA level in both cell lines and clinical samples from several types of cancer including carcinomas of the colon, breast, lung and prostate; gliomas; osteosarcomas; myelodysplastic syndrome; and several leukemias (27). When compared with patient prognosis, however, a clear correlation emerged as PPARγ mRNA transcript levels were found to be a favorable indicator in lung carcinomas (35). Only within the last 2-3 years have reliable correlations linking markers of PPARγ activity to patient prognosis been constructed for other cancers.

3.2.2. Recent immunohistochemistry correlations

While most clinicopathological correlations involving PPARγ appear to be inconclusive at the DNA/RNA level, those involving immunohistochemistry (IHC) data have been much more informative. In breast cancer, for example, the level of PPARγ staining in clinical tumor samples is strongly positively correlated with the patients' survival ($p < 0.001$), with a higher independent predictive value than tumor size, axillary lymph node status, TNM stage, Histologic grade, ER, or Ki-67 in a combined model (36). Likewise, in colon cancer overall survival is significantly higher in patients whose tumors demonstrate higher PPARγ staining (37). Similar findings have also been demonstrated in mobile tongue squamous cell carcinoma (38). As for prostate cancer, IHC staining is detectable in the nuclei of tumor cells in clinical samples, whereas it is absent in the adjacent, non-malignant epithelial tissue; however, the expression level is highly inversely correlated with PSA level (39). This would suggest that in prostate cancer PPARγ functions as an inducible tumor suppressor triggered by malignancy, while its expression is down-regulated during tumor progression. A direct survival correlation, however, was not constructed in this study. In pancreatic cancer the expression of PPARγ is *inversely* associated with patients' survival time (40). Most likely, PPARγ exerts similar tumor-suppressive activity in these tumors, while this activity is down-regulated through mechanisms independent of changes in its protein level.

3.2.3. Expression of dominant negative splice variants

Studies examining the alternative splicing of PPARγ have yielded results consistent with a tumor suppressive role in all tumor types studied. In one such study, mRNA transcripts encoding the dominant negative splice variant gammaORF4 were expressed in 16 of 25 clinical specimens of sporadic colorectal cancer at high levels relative to the adjacent nonmalignant tissue (10). It is unknown, however, whether the protein expression profile mirrored that of the mRNA. Shortly after this study, another group identified PPARγ1_{tr} (another dominant-negative splice variant) and noted its expression in the cell lines K562 (myelogenous leukemia), THP-1

(monocytic leukemia), A549 (alveolar adenocarcinoma), and HeLa (cervical cancer) (11). Expression of this splice variant was later detected in 8 of 9 clinical lung tumor samples at the protein level, whereas it was absent in the adjacent nonmalignant tissue (41). Importantly, there is no conclusive evidence that the expression level of either dominant negative isoform in clinical samples was sufficient to significantly reduce wild-type PPARγ activity. Several hypothesized mechanisms for the repression of nuclear receptors by their respective dominant-negative splice variants have been reviewed by others and may lead to a method for conclusively confirming their suppression of PPARγ activity *in vivo* (12).

3.3. Animal models

3.3.1. Early controversy over PPARγ's influence in colorectal cancer

Given the complexity of clinicopathological data regarding PPARγ, observations drawn from controlled experiments using animal models should be more informative. Such studies examining PPARγ's role in colorectal cancer, however, have yielded mixed results, although more recent evidence appears to support a tumor suppressive role. In two nearly identical early studies, long-term treatment of APC (+/-) mice with PPARγ agonists increased the frequency of spontaneous polyps in the colon (42, 43). Saez and colleagues used troglitazone exclusively, while the others used both troglitazone and rosiglitazone. In a subsequent model, however, treatment of mice with the PPARγ agonist pioglitazone was able to reduce the number of spontaneous tumors induced by dimethylhydrazine (44). Taken together without further evidence, these studies might have suggested that PPARγ activation generally suppresses tumorigenesis in tumors driven by random mutations, whereas it contributes to malignancy when coupled to an APC mutation. Subsequent studies, however, have rejected this conclusion. Another group of researchers using APC (+/-) mice replaced PPARγ agonists with intestine-specific PPARγ haploinsufficiency and found that this increased the rate of tumor formation (45), although a previous theoretically redundant experiment had failed to observe this difference (46). In yet another study employing the agonist MCC-555 in APC (+/-) mice, PPARγ activation reduced the rate of tumor-formation (32). Other studies employing animal models have established the efficacy of PPARγ-specific agonists in suppressing colitis, an established risk factor for colorectal cancer (47-49). Rosiglitazone has also been approved as a clinical treatment for colitis, although it has not become a mainstream treatment because of adverse effects on the cardiovascular system (50). Even more recently, a diet rich in conjugated linoleic acid (another PPARγ ligand) has been shown to suppress tumor formation (in addition to colitis) in mice during long-term azoxymethane treatment, an effect which is abrogated by PPARγ deficiency (50).

3.3.2. Animal models for carcinomas, aside from colon cancer

Studies employing animal models for other types of cancer have similarly characterized PPARγ as a tumor suppressor. The agonists rosiglitazone and fenretinide, for example, have been shown to exert a protective effect in a rat

model for mammary carcinogenesis (51). Similarly, in a gastric carcinoma chemoprevention model, PPARγ (+/-) mice displayed an enhanced generation of tumors during treatment with N-methyl-N-nitrosourea (52). In lung cancer, lung-specific overexpression of PPARγ in transgenic mice reduced the formation of tumors induced by ethyl carbamate treatment (53).

3.4. Epidemiological correlations and clinical trials

Clinical data regarding the effects of PPARγ activation clearly indicate the potential for modulation of PPARγ as a chemopreventive strategy, although an effective treatment using PPARγ agonists against established tumors has not been developed. One study employing data on 87,678 male diabetic patients correlated the use of TZDs (PPARγ ligands) with the risk of developing cancer, finding a risk factor-adjusted 29% reduction in lung cancer for all patients, a 45% reduction in colorectal cancer for African Americans, an insignificant reduction in colorectal cancer for whites, and an *increase* in prostate cancer at 15% ($P=0.03$) for whites and 18% (not statistically significant) for African Americans (54). Unfortunately, the data for this study included patients treated with troglitazone, which can no longer be used clinically and may not accurately reflect the effects of other PPARγ agonists. In an early clinical trial with prostate cancer, long-term treatment with troglitazone prevented the rise of PSA levels, especially for androgen-dependent tumors (26). For more advanced, late stage tumors that are refractory to either chemotherapy or hormone therapy, however, clinical trials using PPARγ agonists alone have shown little success. In one such study, troglitazone treatment of patients with metastatic colorectal cancer resulted in no partial responses (55). In a separate trial, breast cancer patients with either stage IV or stage IIIB tumors also showed no partial responses to troglitazone treatment, although this study was discontinued prematurely because the drug was withdrawn from the market (56). In yet another trial using the PPARγ agonist rosiglitazone to treat recurrent prostate cancer, a small, statistically insignificant increase in survival time was observed relative to a placebo group (57).

3.5. Combination therapies

Subsequent attempts have been made to develop combination therapies in which PPARγ activation synergizes or potentiates other drugs. Since much of the genomic activity of PPARγ is achieved through a heterodimer with RXRα, treatment strategies employing agonists for both receptors have been proposed (58). A phase I trial using this approach, however, failed to demonstrate any partial responses in a group of patients with refractory solid tumors (59). The most widely accepted explanation for this failure will be discussed in the PPARγ-RXR part of the Mechanisms of PPARγ Activity section.

Another promising combination treatment strategy is co-administration with conventional chemotherapy drugs (30). Treatments combining rosiglitazone with the platinum-based drug carboplatin, for

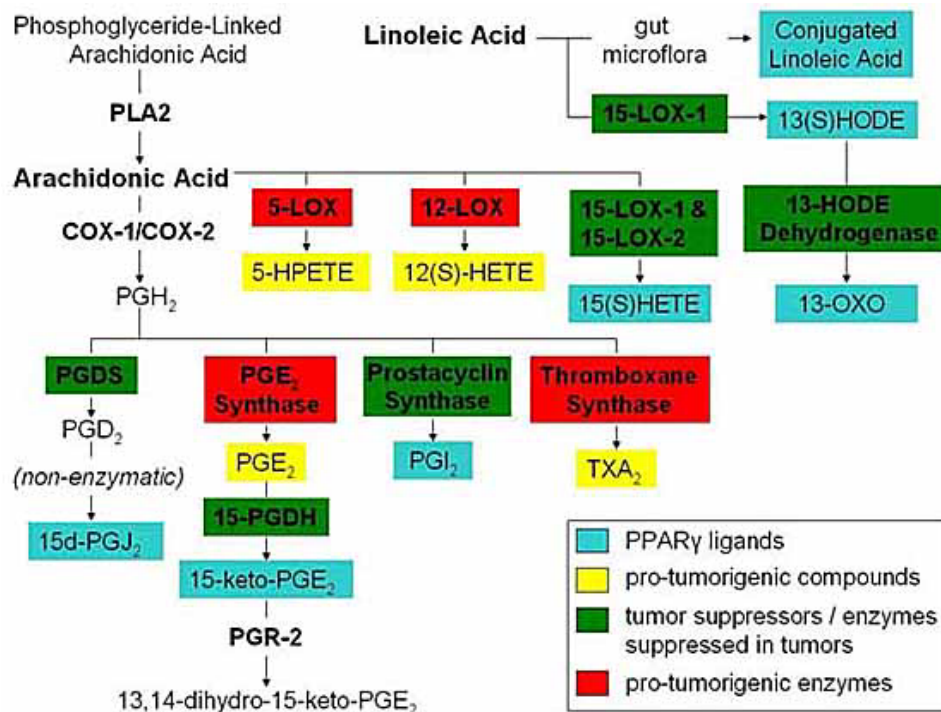


Figure 1. Naturally occurring PPARgamma ligands arising from the metabolism of arachidonic acid and linoleic acid are shown. Several of the enzymes in these pathways are associated with tumorigenesis, and some of them have well described tumor-suppressive functions.

example, result in a marked improvement over either individual compound both in cell lines and in vivo in a murine model with KRAS-induced tumors (60, 61). Cisplatin also shows synergistic combination effects with rosiglitazone in DMBA-induced murine mammary tumors (62), and with troglitazone in a mesothelioma cell line (63). A similar combination effect occurs between rosiglitazone and 5-fluorouracil in colon cancer and liver cancer cell lines (64, 65). 15d-PGJ₂, an endogenous PPARgamma ligand, also reportedly acts synergistically with docetaxel in lung cancer cell lines (66). Antagonism, however, likely occurs for compounds removed from the cell by the ATP cassette transporter ABCG2, since PPARgamma-RXR directly transactivates this gene (67). Such drugs include irinotecan (68), daunorubicin, doxorubicin, and mitoxantrone (69). Among these, doxorubicin is antagonized by rosiglitazone in HT-29 cells (70), while, to our knowledge, no report exists regarding combination effects between specific PPARgamma agonists and the remaining compounds from this group. The agonists ciglitazone and rosiglitazone have also been reported to antagonize gamma radiation-induced cell death in Caco2 cells in vitro by up-regulating Hsp70 (71). Additional proposals for combination treatments have been reviewed by others (30). Many more of these approaches will likely emerge as the mechanisms of PPARgamma activity are further elucidated.

4. REGULATION OF PPARgamma

4.1. Ligands

4.1.1. Lipoxygenase products

PPARgamma is activated by several known endogenous ligands emerging from the metabolism of arachadonic

acid and linoleic acid. A map of these pathways is shown in Figure 1.

Among the ligands represented are the lipoxygenase products 13 (S)HODE (produced from linoleic acid by 15-LOX-1) and 15 (S)HETE (produced from arachidonic acid by both 15-LOX-1 and 15-LOX-2, although 15-LOX-2 catalyzes this reaction much more efficiently) (72). Induction of 15-LOX-1 activity has actually been shown to mediate the promotion of apoptosis by non-steroidal anti-inflammatory drugs (NSAIDs) in certain tumor cell lines and to occur independently of COX-2 inhibition (73, 74). Although this finding was originally demonstrated only in colon cancer cell lines, it has been repeated in cell lines from both esophageal cancer and gastric cancer (75, 76). Supposedly, apoptosis is achieved through the activity of 13 (S)HODE because, unlike 15 (S)HETE, its level is induced by these treatments, while inhibition of 15-LOX-1 reverses this effect (73, 74). Additional compounds produced either in parallel to these products by 15-LOX-1 or downstream of them, however, may account for this effect. 13 (S)HODE is, in fact, degraded by 13-HODE dehydrogenase to form 13-oxooctadecadienoic acid (13-OXO) (77), another PPARgamma ligand (78). Seeing as the expression of 13-HODE dehydrogenase is reportedly reduced in colon cancer samples relative to nonmalignant tissue (79), 13-OXO likely influences additional mechanisms. In contrast to its role as a ligand, 13 (S)HODE can also *suppress* PPARgamma activity through a poorly understood, context-dependent MAPK activation (80). Because a pro-

tumorigenic effect has been demonstrated for 15-LOX-1 in PC-3 cells, it has been hypothesized that this activity reverses its role in prostate cancer, causing it to enhance, rather than suppress, tumorigenesis (81). Importantly, the role of 15-LOX-1 has not been firmly established in prostate cancer.

15 (S)HETE is believed to play a less significant role in activating PPARγ, at least in colorectal cancer (73, 74). While the ability of 13 (S)HODE and 15 (S)HETE to activate PPARγ at concentrations of 5 μM appears to be roughly comparable (82), the endogenous concentration of 13 (S)HODE has been determined to be about 4-5 times that of 15 (S)HETE in clinical samples from both colorectal tumors and paired non-malignant epithelium (83). Roughly the same ratio has been reported for mice lungs, both for non-malignant tissue and for tumors generated through treatment with 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (84). This difference has been attributed to a much higher availability of linoleic acid than arachidonic acid in the diet (83). A decrease of 13 (S)HODE production has also been observed in clinical colorectal tumor samples relative to paired nonmalignant epithelium samples, whereas no discernable difference has been observed with respect to the concentration of 15 (S)HETE, suggesting that 15 (S)HETE plays a less significant role in suppressing these tumors (83). In a lung carcinogenesis model, however, a statistically significant decrease was detected in the levels of both 13 (S)HODE and 15 (S)HETE (84). While the concentration of 15 (S)HETE appears to be low in tumors, it is possible that the downstream metabolites are more prevalent. Among these, both 15-oxo-EETE and 5-oxo-15 (S)-OH-EETE have been characterized as PPARγ ligands, although extremely high concentrations are required for their activity (85). It is unlikely that the local concentrations of these compounds are ever sufficient to activate PPARγ.

Interestingly, in assays measuring the endogenous production of 15 (S)HETE, about 95% of this product is detected in the medium, although the efficiency of its secretion appears to vary between cell lines (72). Such variation may indicate that this process is regulated, in part, by an active transport mechanism. Recently, it has also been demonstrated that 15 (S)HETE preferentially activates PPARβ/δ over PPARγ (86). While the expression and activation of PPARβ/δ are down-regulated by 13 (S)HODE during the induction of 15-LOX-1 in colon cancer cells (where PPARβ/δ activity favors malignant characteristics) (87), activation may occur within neighboring cells that lack 13 (S)HODE. Interestingly, PPARβ/δ activation specifically within stromal cells has been shown to alter cytokine production so as to *reduce* mitogenic paracrine signals when cultured with multiple myeloma cells (88). Although 15 (S)HETE may not play a significant role in the activation of PPARγ in most tumors, it could conceivably exert a similar tumor-suppressive effect through such paracrine signaling.

4.1.2. Prostaglandins

Several arachidonic acid metabolites generated downstream of the COX enzymes can also act as

PPARγ ligands. Among these, 15d-PGJ2 appears to be the most prevalent in the literature, probably because it was the first endogenous ligand discovered for PPARγ (89). Prostacyclin (PGI2), another downstream product of the COXs, is also believed to activate PPARγ as its stable analog iloprost has been shown to activate a PPARγ reporter in both a bronchial epithelial cell line and two lung adenocarcinoma cell lines (53). Furthermore, it has been suggested that this activity mediates prostacyclin's well-established tumor suppressive activity, since knock-down of the IP receptor (a G-protein-coupled receptor for prostacyclin) fails to reduce the protective effect of prostacyclin synthase over-expression (53). The evidence for this, however, is still inconclusive because the effect of PPARγ knockdown on prostacyclin synthase-mediated suppression of tumorigenesis has never been determined. Increased activity of a PPARγ reporter has also been observed upon treatment of 3T3-L1 cells with 15-keto-PGE2, an arachidonic acid product generated through conversion of PGE2 by 15-PGDH (90). This particular ligand is believed to be indispensable for at least a subset of endogenous processes that require PPARγ activation, seeing as exogenous over-expression of the downstream enzyme PGR-2 (which metabolizes 15-keto-PGE2 to form 13,14-dihydro-15-keto-PGE2) blocks hormone-induced differentiation of 3T3-L1 cells into adipocytes (90). On the other hand, the activity of 13,14-dihydro-15-keto-PGE2 may be responsible for this effect, rather than the absence of 15-keto-PGE2.

4.1.3. Importance of arachidonic acid products

Given PPARγ's role in adipocyte differentiation, it is interesting that siRNA-mediated knockdown of phospholipase A2, the initiator of arachidonic acid signaling, is able to block hormone-induced differentiation of 3T3-L1 preadipocytes (91). It is also worth noting that this differentiation is rescued through treatment with the PPARγ agonist troglitazone. These observations provide highly suggestive, circumstantial evidence that at least one of the known PPARγ ligands generated through arachidonic acid metabolism is necessary for endogenous induction of PPARγ activity. This conclusion is also consistent with *in vivo* observations in animal models, although these can be readily explained by at least one other mechanism. In the aforementioned adipocyte-specific PPARγ double knockout study in mice, for example, increases in body weight due to a high fat diet were attenuated relative to a control group, as was the total body fat weight (92). Similarly, adipocyte-specific phospholipase A2 knockout mice had a normal body weight when fed a standard diet, but they failed to develop obesity in response to a high fat diet (93). Although the results of the latter study were consistent with the effects of decreased PPARγ activity, the researchers explained them through an elevation of lipolysis due to decreased PGE2 production. Nonetheless, current evidence appears to support the hypothesis that ligands originating from arachidonic acid metabolism are the principal means of inducing PPARγ activity for most organs *in vivo*, whereas other mechanisms only modulate this activation. In the colon, however, an exception emerges in that natural PPARγ ligands from the diet complement those from

the arachidonic acid pathway. As mentioned previously, dietary supplementation with conjugated linoleic acid, has been shown to reduce colorectal tumorigenesis induced by azoxymethane in mice, presumably through an observed suppression of colitis (a known risk factor for colorectal cancer), whereas this effect is absent in PPARgamma-deficient mice (50).

4.2. Phosphorylation

Phosphorylation of PPARgamma also plays a significant role in its regulation. Not long after PPARgamma's discovery, treatment of NIH3T3 and 293T cells with either EGF or PDGF was shown to down-regulate the activity of PPARgamma, an event which was attributed to MAPK-mediated phosphorylation of PPARgamma1 at Ser82 (94). In breast cancer, it has actually been hypothesized that a loss of PPARgamma activity is achieved entirely through MAPK activation, as evidenced by the fact that the growth inhibition effect of troglitazone treatment in an otherwise resistant cell line can be rescued through the addition of the MAPK inhibitor PD98059 (24). More recent studies have found that this effect can be achieved through phosphorylation of RXR (part of an important heterodimer with PPARgamma) under the same conditions, while it can also be reduced through transfection with an RXR mutant protected against phosphorylation (95, 96). The two mechanisms are, in fact, complementary; several lines of evidence confirming an independent role for the phosphorylation of PPARgamma in modulating its activity have been reviewed (97).

4.3. Corepressors

The activity of PPARgamma is also modulated through interaction with corepressors, either through a repression of PPARgamma activity or through PPARgamma's enhancement of the ability of these corepressors to transrepress other genes (98). PPARgamma's affinity for these proteins can be modulated by numerous factors. For example, most of these corepressors lose their affinity for nuclear receptors when these receptors are activated by their respective ligands (98), while some of these interactions are *enhanced* by ligands. The binding of the corepressor RIP140 to ternary complexes of PPARgamma and RXR, for example, is enhanced by the addition of RXR ligands (99). Additionally, at least one protein is known to block the interaction between PPARgamma and its corepressors. Direct interaction with phosphorylated extracellular signal-related kinase 5 (ERK5) has been observed to increase the activity of PPARgamma1 in reporter assays, presumably by blocking its interaction with the corepressor SMRT (100). Seeing as an elevation of this mitogenic kinase's expression has been observed in prostate tumor samples relative to the corresponding nonmalignant tissue, this type of mechanism could be prevalent in cancer (101). This fact may also explain why a suppression of PPARgamma protein level would be necessary for highly malignant prostate tumors, seeing as ERK5 would reduce the ability of these corepressors to suppress PPARgamma activity.

4.4. Repression of PPRES by other proteins

The genomic activity of PPARgamma can also be blocked through binding of other proteins to PPRES. This behavior has been reported for the estrogen receptor (102). A

similar repression of PPRES has been reported for a thyroid receptor beta mutant observed clinically, in which either a homodimer or heterodimers with either PPARgamma or RXR could bind and repress PPRES (103). Whether such a direct repression of PPRES is common clinically remains to be seen.

4.5. Proteasomal degradation

PPARgamma activity is also regulated through proteasomal degradation. Targeting of PPARgamma to the proteasome occurs through ubiquitylation of the AF-2 segment of its ligand binding domain (104). This process is counterintuitively enhanced by the addition of TZDs, an effect which contrasts with their effect on the activation of PPRES (105). In cancer cell lines, however, the influence of this process often appears to be overcome by a competing mechanism. PC-3 cells, for example, show no change in the protein level of PPARgamma upon treatment with troglitazone (21), while a similar treatment elicits an *increase* in PPARgamma protein in 21MT cells (24).

4.6. Transcriptional regulation

Little is known regarding control of PPARgamma transcription in epithelial cells. The C2H2 zinc finger transcription factor Zac, which is known to play a role in apoptosis, has been reported to activate the transcription of PPARgamma and is expressed in some colon cancer cell lines (106). Additionally, during the well studied process in which NIH-3T3 cells are differentiated into adipocytes through activation of PPARgamma, a positive feedback loop emerges in which PPARgamma and its target gene C/EBPalpha up-regulate the transcription of each other (107). In light of the effect ligands have in promoting PPARgamma degradation (105), this process likely proceeds after a transient induction by endogenous ligands. A similar loop may be active during the treatment of carcinomas with synthetic PPARgamma agonists. Two transcription factors modulated by TGFbeta, Egr-1 and AP1, are also considered to be important regulators of PPARgamma transcription in smooth muscles; however, their importance in epithelial cells has not been established (108). Likewise, the circadian clock transcription factors DBP and E4BP4 have been shown to regulate the PPARgamma6 mRNA transcript level (15), while their role in PPARgamma regulation in epithelial cells and tumors has not been characterized.

5. MECHANISMS OF PPARgamma ACTIVITY

5.1. Is PPARgamma responsible for the antitumor effects of its agonists?

Many researchers have speculated that the anticancer effects elicited by PPARgamma agonists are independent of this receptor's activity. This conclusion was reached in an early study after growth inhibition was elicited by both troglitazone and ciglitazone in PPARgamma (-/-) mouse ES cells (28). Another group of researchers extended this finding to other agonists upon finding that the anticancer effects elicited by troglitazone, ciglitazone, and 15-d-PGJ2 (an endogenous ligand) on several prostate and bladder carcinoma cell lines varied qualitatively (growth inhibition vs. apoptosis), while rosiglitazone and pioglitazone elicited no effects

whatsoever (29). An interpretation of these discrepancies, however, should account for the fact that different agonists can influence independent mechanisms of PPARγ activity. In one study, for example, treatment of a myeloid leukemia cell line with either 15-d-PGJ2 or troglitazone resulted in a repression of STAT3 reporter activity, an effect which was reversed by the PPARγ antagonist GW9662 (109). 15-d-PGJ2, however, caused direct binding of PPARγ to STAT3, whereas troglitazone increased the binding of NCoR to STAT3, presumably through the observed release of this corepressor from PPARγ. Considering that all of the known mechanisms of PPARγ's activity are also context-dependent, much of the variability in the effects of PPARγ ligands is likely caused by an interaction between off-target mechanisms and the activity of PPARγ.

5.2. PPARγ-RXR heterodimer

Among the mechanisms of PPARγ activity, the most prevalent in the literature is that of the PPARγ-RXR heterodimer, which is known to promote the transcription of genes whose promoters contain peroxisome proliferator response elements (PPREs) (98). In adipocytes several genes, such as aPC, are constitutively bound to PPARγ-coactivator complexes, among which PPARγ-RXR is highly prevalent (110). The significance of the activity of this heterodimer in clinical tumors, however, has not been established. This uncertainty stems from the fact that treatments combining ligands for PPARγ and RXR result in an additive or synergistic induction of the dimer's activity (6). In early studies on the effects of PPARγ activation in cancer, this behavior was observed in a liposarcoma cell line (22). Recently, however, the activity of this heterodimer has been shown to be absent in several cancer cell lines due to growth factor-triggered phosphorylation of RXRα, while the synergy between ligands for the two receptors can be restored through either the withdrawal of growth factors or the addition of MAPK inhibitors (95, 96). An elevation of RXRα phosphorylation has actually been observed in clinical colorectal tumor samples relative to nonmalignant epithelial colon tissue (95). Much research has, therefore, focused upon the prospect of developing combination therapies that reduce the phosphorylation of RXR to potentiate the effect of PPARγ agonists (58). Importantly, the activity resulting from PPARγ's interaction with RXR is not restricted to the induction of PPREs. The oncogenic protein beta-Catenin, for example, has been shown to interact with both RXR and PPARγ (111-113). Moreover, treatment of cells with PPARγ ligands during exogenous expression of PPARγ and RXR decreases the ability of beta-Catenin to transactivate its target genes (114). Much of PPARγ's anticancer activity, however, is achieved through mechanisms independent of RXR. This is evident in the antitumor effects elicited by troglitazone in MDA-MB-231 breast cancer cells (115), which lack a detectable level of RXRα expression (116).

5.3. Coactivators

The transcription activity of PPARγ's target genes can also be achieved through complexes containing PPARγ and various coactivators, although the specificity

of the target genes may vary. A complex with PGC-1α, for example, activates the transcription of UCP-1, which is inaccessible to PPARγ-RXR (117). Different coactivators also have different modes of activity. Many of the classical coactivators, such as CBP/p300 and SRC-1, achieve this activity through their histone acetyl transferase (HAT) activity, while others like PGC-1α simply recruit other coactivators to complexes with PPARγ (118). The influence of PPARγ ligands on the activity of these coactivators also varies. In most cases, interaction between PPARγ and its coactivators is enhanced by ligand activation (98). Some coactivators, however, activate PPARγ constitutively. Among these are ARA70 and SHP (119, 120). Additionally, interaction with certain coactivators may be enhanced by only a subset of the PPARγ ligands. For example, binding to PGC-1α is reportedly enhanced by the addition of 15d-PGJ2 and troglitazone (121), but not rosiglitazone (117). This contrast, however, may not be valid because the effects of 15d-PGJ2 and troglitazone were determined through an endogenous immunoprecipitation of PGC-1α, whereas the absence of this activity for rosiglitazone was determined through an exogenous immunoprecipitation of GST-tagged PGC-1α. Importantly, many of PPARγ's co-activators are promiscuous, a fact exemplified by PGC-1α's binding to NF-κB (121), nuclear respiratory factor-1 (NRF-1) (118), estrogen receptor α (ERα), the retinoic acid (RA) receptor, and thyroid receptor β (117). Clearly the availability of these coactivators is an important determinant of PPARγ's activity in tumors. Madjalaweh and Ro provide a much more extensive review of PPARγ's coactivators, as well as its corepressors (122).

5.4. Corepressors

Any PPARγ that is not part of an active complex normally exists in an inactive form, bound to a corepressor, such as SMRT or NCoR (98). Under most circumstances, interaction with a ligand causes PPARγ to dissociate from the corepressor and bind to a coactivator (98). The corepressor, in turn, may be freed to bind to other transcription factors, thereby transrepressing their target genes, an effect which, as previously mentioned, was observed during treatment of a multiple myeloma cell line with troglitazone (109). Ligand activation also enhances SUMOylation of PPARγ, a change which initiates the recruitment of PPARγ to NCoR-HDAC3 complexes associated with specific genes, thereby repressing their transcription by blocking the ubiquitylation-mediated destruction of the complexes (123). An extensive list of PPARγ corepressors is included in a review by Madjalaweh and Ro (122).

6. PPARγ TARGET PATHWAYS

6.1. Overview

Microarray studies have hinted at numerous pathways that may be modulated by PPARγ ligands. The first of these papers characterized the effect on known markers of differentiation, such as RegIA and keratin20, in Moser and COS7 cells, finding that these differentiation markers were mostly up-regulated (124). A more recent

paper profiled the influence of three different PPARγ agonists on several pathways in HCT116 colon cancer cells, based on changes in the levels of mRNA transcripts of representative genes (125). Some of the processes characterized and the accompanying genes used as markers are as follows: the cell cycle (MDM2 decreased, CHEK2 and RBX1 somehow altered), cytokine-cytokine receptor interaction (IL18 and VEGFB somehow altered), ubiquitin-mediated proteolysis (UBE2E1 and RBX1 somehow altered), phosphatidylinositol signaling (INPP5D decreased), Wnt signaling (RBX1 somehow altered), the “colorectal cancer pathway” (APPL decreased), and calcium signaling (SLC25A4 somehow altered). Several genes involved in apoptosis, such as BCL-X (L), MCL-1, BAX (126), XIAP (127), and Survivin (128), are also reportedly modulated by PPARγ so as to favor this process. In contrast, PPARγ has been shown to up-regulate Hsp70 in Caco2 colon cancer cells and MCF7 breast cancer cells (71, 129), an effect which *prevents* radiation-induced apoptosis (71). Although these observations provide promising directions for future research, their reliability is unknown. Numerous mechanisms of PPARγ activity are already known to be context-dependent and may, therefore, vary widely between individual tumors. Accordingly, the development of clinical treatments exploiting this receptor will depend upon understanding the precise mechanisms by which these pathways are influenced. The pathways that follow are more thoroughly researched and include discussions of their mechanisms.

6.2. Well studied non-genomic targets

6.2.1. Beta-catenin

PPARγ is believed to inhibit signaling by the beta-Catenin pathway, whose contribution to tumor biology is well established. The activity of beta-Catenin is important in promoting epithelial-mesenchymal transition (130), an important process in tumor progression. The protumorigenic activity of Wnt/beta-Catenin signaling arises from the nuclear localization of beta-Catenin, which activates the TCF/LEF families of transcription factors by displacing them from the corepressor Groucho/TLE (131). This results in an up-regulation of cyclin D and c-myc, both of which exert pro-tumorigenic effects (132). In non-malignant cells this event is prevented by a destruction complex containing Axin, APC, and the kinase GSK-3β, which phosphorylates beta-Catenin, thereby targeting it for proteasomal degradation (133). Canonical Wnt signaling, however, leads to the formation of a membrane-bound complex containing Fz, LRP6, Dvl, and Axin (134), effectively removing Axin from the destruction complex and deactivating it (135).

Speculation regarding PPARγ's influence on the Wnt/beta-Catenin pathway began when early APC (+/-) mice models failed to demonstrate a chemopreventive effect for PPARγ ligands against colorectal carcinogenesis, whereas a protective effect was observed during treatment of wild-type mice with mutagenic agents (46). Importantly, APC is an established tumor suppressor that is necessary for the proper function of the beta-catenin destruction complex (136); a loss-of-function mutation of

this gene increases the nuclear localization of beta-Catenin within a subset of cells in the tumor (137). In one study seeking to resolve this issue, tumors were induced in both wild-type and PPARγ (+/-) mice through treatment with azoxymethane (46). Tumor formation was enhanced in the PPARγ (+/-) mice, relative to the wild-type mice, while beta-Catenin was up-regulated in their colon epithelial tissue prior to the onset of these tumors. The next year, PPARγ activation by both troglitazone and GW7845 was found to increase the proteasomal degradation of beta-Catenin in NIH 3T3-L1 cells (138). Interaction between beta-catenin and PPARγ was also soon demonstrated through immunoprecipitation in two other laboratories (112, 113). Another group of researchers failed to repeat the PPARγ-mediated degradation of beta-Catenin; however, they found that the PPARγ ligands troglitazone, rosiglitazone, and GW1929 all repressed the activity of a beta-Catenin transcription complex during co-expression of PPARγ and RXR (114). Repression of the Wnt signaling pathway, therefore, would appear to require sufficient expression of both PPARγ and RXR. Importantly, the nuclear localization of beta-Catenin is strongly modulated by both intrinsic and paracrine signals, even in the presence of an APC mutation (139); therefore, PPARγ's influence on such signals may partially mediate PPARγ's impact on beta-Catenin activity. On the other hand, such signals may completely abrogate PPARγ's influence on this pathway. It should be mentioned that in clinical colorectal cancer samples, nuclear-localized beta-Catenin immunohistochemistry staining reportedly shows no significant correlation with overall PPARγ staining intensity (37).

The process of sorting through the mechanisms of PPARγ activity on this pathway is further complicated by its effect on E-Cadherin. E-Cadherin is a membrane protein whose expression is inversely correlated with malignancy, while restored expression of this receptor reduces malignant characteristics (140). Importantly, E-Cadherin sequesters beta-Catenin at the cell membrane, thereby preventing its localization to the nucleus (140). A recent paper has found that ciglitazone and linoleic acid treatments in several prostate cancer cell lines lead to an up-regulation of E-Cadherin, along with an even more reliable down-regulation of N-Cadherin (141). The effects of these ligands, moreover, are PPARγ dependent, since they are reversed by the PPARγ antagonist GW9662 (141). They also lead to a repression of both beta-Catenin and c-myc expression, indicating that the full pathway is, in fact, influenced by these treatments. The clinical relevance of this mechanism is supported by the fact that the overall PPARγ immunoreactivity in clinical breast tumor samples is positively correlated with the localization of beta-Catenin to the membrane as well as the cytoplasm (36). One group has attributed this effect to a repression of Snail observed in non-small cell lung carcinoma cell lines (142). Snail otherwise directly represses the transcription of E-Cadherin (142). This repression is believed to have been somehow mediated by an inhibition of ERK through an unknown phosphatase, although the mechanism connecting these events is unknown.

6.2.2. STAT3/NF-kappaB

PPARgamma's ability to inhibit IL-6/STAT3/NF-kappaB signaling has been reported by numerous laboratories in a wide variety of cell types. The prospect of targeting this pathway is particularly exciting because it is part of an important epigenetic positive feedback loop (IL6→STAT3→NF-kappaB→Lin28→Let-7→IL6) that has been found to be active in half of all cancer cell lines screened (143). Among PPARgamma's effects on this pathway is an inhibition of STAT3's promotion of its target genes (109). These treatments, however, do not appear to impact STAT3's ability to activate NF-kappaB (109). STAT3-mediated processing of NF-kappaB requires the acetylation of STAT3 (144), an event which PPARgamma has not been shown to disrupt. Importantly, PPARgamma ligands appear to influence the binding of proteins to STAT3, rather than STAT3 phosphorylation (109).

Treatments with PPARgamma agonists have also been observed to reduce the ability of NF-kappaB to promote its target genes, an effect which has been established both *in vitro* in cell lines from multiple tissue sources (47, 121, 145, 146), and *in vivo* in an experimentally induced colitis model in mice (147). Among these agonists, 15d-PGJ2 is unique in that it has been observed to block NF-kappaB-mediated transcription in the absence of PPARgamma (although repression is enhanced through exogenous expression of PPARgamma), supposedly through direct inhibition of IKK (145). Importantly, this mechanism reduces the nuclear localization of NF-kappaB in the cell (145). In contrast, activation of PPARgamma by all ligands tested appears to block the interaction between NF-kappaB and its target genes (145). One mechanism that may explain this activity is a ligand-induced SUMOylation of PPARgamma that causes it to bind corepressor complexes associated with NF-kappaB target genes, an event which inhibits the transcription of these genes by blocking the degradation of the complexes (123). Alternatively, ligand activation of PPARgamma has been reported to promote its association with PGC-1, thus, reducing the availability of this coactivator for binding with NF-kappaB (121). While it has been reported that PPARgamma ligands can block the induction of IL-6 by stromal cells in a multiple myeloma cell line (supposedly through inhibition of NF-kappaB) (121), such treatments have not been reported to disrupt autocrine loops involving IL-6 in carcinoma cell lines. This effect would lead to a much more pronounced inhibition of their proliferation. PPARgamma may repress only a subset of NF-kappaB target genes that does not include Lin28. Importantly, the inhibition effects of PPARgamma agonists on both STAT3 and NF-kappaB are context-dependent, since repression of STAT3 through troglitazone depends upon the level of SMRT (109), while the trans-repression of NF-kappaB target genes is attenuated by knockdown of NCoR (123). Interference with STAT3/NF-kappaB signaling through these mechanisms, therefore, may be highly variable and unreliable in a clinical setting if not somehow guided by molecular profiling.

Alternatively, PPARgamma agonists can also block Tyk2-mediated phosphorylation of STAT3 through an unknown mechanism (34, 148). This mechanism is believed to mediate the growth inhibition effects that PPARgamma agonists have on the CD133+ subpopulation of glioblastoma cell lines during treatment with specific growth factors *in vitro* (34). Some other studies have established that Tyk2 expression contributes to metastasis (149, 150). Tyk2 is also reportedly expressed in an appreciable fraction of clinical prostate tumors, although thorough clinicopathological correlations have not been constructed (149). More recently, a head and neck cancer cell line has been reported to dependent upon the combination of pSrc and Tyk2 for STAT3 activation; therefore, it is likely that manipulation of this mechanism by PPARgamma agonists would depend upon combinations with other treatments for its effectiveness (151). Importantly, the inhibition of Tyk2 activity by PPARgamma agonists has not been reported in carcinoma cell lines.

6.2.3. Androgen receptor

For prostate cancer, the most attractive effect of PPARgamma ligands is their interference with androgen receptor signaling. Upon stimulation by androgen, this membrane-bound nuclear receptor internalizes and acts as a transcription factor for genes whose promoters contain androgen responsive elements (152). Among these is PSA (152), an important marker for detecting prostate cancer (153). Suppression of this activity was first noted when treatment of the androgen-dependent LNCaP cells with troglitazone caused a marked reduction of their PSA level (21). Likewise, an early clinical trial found that patients with androgen-dependent prostate cancer, as well as a subset of patients with androgen-refractory prostate cancer, encountered a drop in their PSA levels during troglitazone treatment (26). In yet another study, treatment of LNCaP cells with the PPARgamma agonists troglitazone, pioglitazone, and 15-d-PGJ2 reduced both the PSA level and the activity of an ARE reporter without altering the androgen receptor protein level (154). It has also been demonstrated through chromatin immunoprecipitation experiments that both troglitazone and ciglitazone block the recruitment of the androgen receptor to androgen responsive elements on the promoters of its target genes (155). The authors who performed the latter study have argued that this activity is independent of PPARgamma because the same effect was achieved by structurally similar analogues that failed to "activate" PPARgamma. In a previously mentioned study examining immunohistochemistry staining of PPARgamma in clinical tumor samples, however, it was argued that the tight inverse correlation observed between PPARgamma immunoreactivity and PSA level suggests that the effects of PPARgamma ligands on PSA are dependent upon binding of these ligands to PPARgamma (39).

6.3. Verified genomic targets

6.3.1. P53

Rosiglitazone reportedly promotes p53 expression at the transcriptional level in MCF7 breast cancer cells through recruitment of PPARgamma to an NF-

kappaB site on its promoter (156). A well described tumor suppressor gene, p53 is important for the induction of apoptosis, cell cycle arrest, and autophagy during various types of stress (157). This activity is likely mediated by its transrepression activity on Bcl-2, survivin, IGFR, Mcl-1, and PIK3CA and its transactivation of such targets such as p21, PTFG, Gadd45, and 14-3-3σ (157). This mechanism, however, is unlikely to account for many of the effects previously observed, seeing as loss-of-function p53 mutations are ubiquitous in most types of cancer. Certain types of tumors usually lack this mutation, and may, therefore, be more susceptible to this mechanism.

6.3.2. PTEN

Among the most attractive antitumor mechanisms arising from PPARγ's genomic activity is a direct activation of the PTEN promoter by the PPARγ-RXR heterodimer, an event which should exert pleiotropic effects through a suppression of Akt (158). As with p53, mutations of PTEN are highly frequent in most types of cancer. For pancreatic cancer, however, it has been reported that activation of PPARγ in the cell line PANC-1 through treatment with rosiglitazone increases the protein level of PTEN, while the reverse is true for the addition of PPARγ antagonist GW9662 (159). The growth suppression effects elicited by rosiglitazone in this cell line are especially pronounced, with almost no measurable growth in xenografts after the initiation of treatment (160). Although the immunoreactivity of PTEN has been found to be significantly reduced in clinical samples of pancreatic cancer (161), the cancer genome project has found that loss-of-function mutations of this gene are a rare event, occurring in only 1 out of 66 clinical samples in the COSMIC_pancreas data set of the Cancer Genome Workbench. It is, therefore, conceivable that the repression of PTEN may be overcome through activation of PPARγ in these tumors. If population mutation rates prove to be a reliable predictor of PTEN induction through PPARγ activity, then data from the Cancer Genome Workbench Datadump indicate that carcinomas of the oesophagus, head and neck, ovary, and lung may also be potential candidates for this mechanism, with PTEN mutation rates ≤ 2%. The directions for accessing this site are detailed in the Acknowledgements section.

7. PERSPECTIVE

Aside from its role as a specific target for anticancer treatments, PPARγ is now emerging as a potential biomarker for predicting patient prognosis. PPARγ staining may also become a useful tool for selecting treatments. Activation of PPARγ, for example, should lead to the up-regulation of ABCG2, which antagonizes several prominent chemotherapy drugs (67). PPARγ might also regulate additional multidrug resistance (MDR) proteins. A role for the PPARs in regulating MDR proteins has been reviewed by others (161). Considering the fact that other drugs are synergized by PPARγ activity (60, 62, 64, 66), if additional multidrug resistance proteins are not influenced by PPARγ, then PPARγ staining is most likely an independent predictor of drug resistance when combined

with these other markers. No correlation, however, has been constructed at present. PPARγ may also be useful for predicting resistance to radiotherapy, since it reportedly activates Hsp70 (71). Additionally, as the drive to develop inhibitors for targets downstream of COX-1/COX-2 progresses, an understanding of both the effect of such inhibitors on the expression of the lipoxygenases and the clinical significance of the various prostaglandins as PPARγ ligands will be important for optimizing such treatments. Biomarkers should also be established to predict which PPARγ target pathways are responsive to PPARγ activation within a given tumor, since nearly all of these pathways are context-dependent. Establishing the exact mechanisms of PPARγ activity in each target pathway, therefore, will likely be necessary.

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