Molecular Pathways: The Metabolic Regulator Estrogen-Related Receptor α as a Therapeutic Target in Cancer

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Abstract

The estrogen-related receptor α (ERRα) is an orphan member of the nuclear receptor superfamily of transcription factors whose activity is regulated by the expression level and/or activity of its obligate coregulators, peroxisome proliferator-activated receptor γ coactivator-1 α and β (PGC-1α or PGC-1β). Under normal physiologic conditions, and in responding to different environmental stimuli, the ERRα/PGC-1 complex is involved in regulating metabolic homeostasis under conditions of high energy demand in brown adipocytes, proliferating T cells, and muscle. Interestingly, increased expression and activity of the ERRα/PGC-1 axis has also been shown to correlate with unfavorable clinical outcomes in both breast and ovarian tumors. The observation that ERRα activity is manifest in all breast tumor subtypes with particularly high activity being evident in ERRα-negative, HER2-positive, and triple-negative breast cancers has raised significant interest in targeting this receptor for the treatment of those breast cancers for which therapeutic options are limited. Clin Cancer Res; 18(22); 6089-95. ©2012 AACR.

Background

The nuclear receptor (NR) superfamily is composed of a group of structurally related transcription factors that regulate diverse physiologic functions. Although the transcriptional activity of many NRs is regulated by small-molecule lipophilic ligands—estrogens, glucocorticoids, or androgens—other members of this family have been classified as “orphans” for which a physiologically relevant ligand has not yet been identified. In general, however, upon binding their cognate ligands, these receptors undergo a conformational change that increases their DNA binding activity. The DNA bound receptor then nucleates the assembly of a large complex of transcriptional coregulators that results ultimately in an increase or a decrease in target gene transcription.

Dysregulation of NR function and/or the pathways under their control has been causally linked to processes of pathologic importance in the reproductive, immune, and cardiovascular systems as well as in a significant number of different cancers. Given this degree of involvement in a diverse range of processes, it is not surprising that 10% to 15% of the currently approved drugs in the United States target this family of transcription factors (1). One particularly useful target is the estrogen receptor (ER), the intracellular mediator of the actions of the female sex hormone 17β-estradiol, heightened activity of which has been associated with both the initiation and progression of breast cancer. Indeed, therapeutic targeting of this receptor, and pathways that regulate the production of 17β-estradiol and other estrogens, has proved to be extremely useful in both the treatment and prevention of ER-positive breast cancers.

Driven by the success of targeting ER in breast cancer and capitalizing on what has been learned about NR function in general, a high level of interest continues to be expressed in targeting other NRs in cancer. It was of significance, therefore, that an association between elevated expression of the orphan NR estrogen-related receptor α (ERRα) and a poor clinical outcome in both breast and ovarian tumors was observed in several independent studies (2–4). ERRα shares significant sequence homology and structural similarity to ER (5). It was initially considered, therefore, that ERRα might exhibit similar activities as ER and that it would play a role in breast cancer. However, a comprehensive evaluation of the impact of ERRα activation on ERα-dependent transcriptional regulation in MCF-7 breast cancer cells revealed surprisingly few genes that were coregulated by these receptors (6). This was in agreement with other studies, using ChIP-on-chip to evaluate ERα and ERRα binding sites in MCF7 cells, which concluded that only approximately 18% of ERα target genes also contain an ERRα one or more binding sites (7). Interestingly, Gene Ontology analysis of the genes implicated in these studies revealed that, whereas ERα is primarily involved in the regulation of genes involved in tissue development and cell proliferation, ERRα controls the expression of genes involved in the regulation of cellular energy metabolism, such as those encoding enzymes in the tricarboxylic acid (TCA) cycle and oxidative phosphorylation (8). It now appears, therefore, that despite the sequence homology, ERα and ERRα regulate distinct...
biologic processes and should be considered functionally distinct transcription factors.

A causal role for ERRα in breast cancer pathogenesis was first shown in studies which showed that shRNA-mediated knockdown of ERRα expression dramatically inhibited the growth of ERRα-negative MDA-MB-231 cells when propagated as xenografts in mice (6). Similar results were observed in other in vitro and in vivo models of breast cancer where ERRα inhibition was accomplished using small molecule antagonists (9–11). Together these definitive findings established a fundamental role for ERRα in tumor growth and confirmed the importance of ER-independent activities of this receptor in breast tumor biology. These findings also provided the rationale for the exploitation of ERRα as a therapeutic target in breast cancer. To further assess the clinical significance of ERRα, a genomic signature designed to evaluate the activity of this receptor was used to profile more than 800 breast tumors. This analysis revealed a shorter disease-free survival in patients with tumors exhibiting elevated ERRα activity (11). Importantly, this signature also revealed that the ERRα activity signature is elevated in tumors that are either HER2-positive or ER-negative, or in those that contain P53 mutations. Interestingly, the ability of ERRα antagonists to inhibit proliferation in cellular models of breast cancer correlates with the intrinsic transcriptional activity of this receptor manifest in these cells. On the basis of these findings it has been proposed that ERRα antagonists may have utility as treatments for breast tumors in which this receptor exhibits elevated transcriptional activity. Not surprisingly, considerable interest has been expressed of late in developing ERRα antagonists that are suitable for clinical use. Furthermore, the information that is emerging on the pathways that are upstream and downstream of this receptor has highlighted other targets the inhibition of which may afford useful therapeutic synergism with ERRα antagonists.

Coregulators Function as Protein Ligands of ERRα

Most NRs contain a complex ligand-binding pocket, which upon binding small-molecule hormones or lipophilic compounds undergoes a conformational change that allows it to interact with transcriptional coregulators and to regulate target gene transcription. However, despite having a defined ligand-binding domain (LBD), crystallographic analyses of ERRα have indicated that the ligand-binding pocket of ERRα is filled by bulky amino acid side chains, and it has been concluded that the receptor can only accommodate extremely small ligands (~3–4 carbons; refs. 12, 13). In addition, comparison of the structure of ERRα with that of other agonist-occupied NRs reveals that the LBD of this receptor is able to adopt an “active” conformation and is capable of binding coactivator proteins in the absence of a bound ligand. Consequently, it has been suggested that the transcriptional activity of ERRα may not be regulated by ligand binding per se but by the expression level and/or activity of its obligate coregulators (coactivators and corepressors; refs. 12, 14–17). Although many coactivators have been shown to interact with and regulate the activity of ERRα, 2 of its most robust coactivators are the peroxisome proliferator-activated receptor γ coactivator-1 α and β (PGC-1α or PGC-1β; refs. 18–20). Under normal physiologic conditions, the ERRα/PGC-1 complex is involved in regulating metabolic homeostasis in tissues, such as brown adipocytes and muscle, in which energy demand is high. PGC-1α expression and/or activity is acutely upregulated in response to cold, fasting, exercise, and hypoxia resulting in the induction of gene expression programs involved in thermogenesis, gluconeogenesis, fatty acid oxidation, mitochondrial biogenesis, and angiogenesis (14, 20–25). Most of these responses have been shown to be mediated by ERRα. PGC-1β expression, on the other hand, does not seem to be regulated by these acute stresses but rather it is induced by high-fat diets and in response to immune challenges. In this manner, it upregulates the expression of genes required for fatty acid synthesis and host immunity (26–28). It remains to be determined if other coregulators can couple with ERRα to regulate transcription. Regardless, however, it is clear that independent of whether or not a small-molecule physiologic regulator of ERRα exists that this receptor has evolved to respond to “protein ligands” (coregulators) as a means to regulate its transcriptional activity.

Signaling Pathways That Impinge Upon and Regulate ERRα/PGC-1 Activity in Breast Cancer

It is likely that some of the stimuli that regulate the ERRα and PGC-1α/β complexes in normal physiology are also involved in regulating ERRα activity in cancer. These pathways are summarized in Fig. 1. For instance, the expression of PGC-1α is induced by hypoxia in skeletal muscle, resulting in hypoxia-inducible factor (HIF)–independent but ERRα-dependent expression of VEGF and increased angiogenesis (29). The same mechanism may also be operative in hypoxic regions of tumors. Supporting this hypothesis, we and others have shown that activation of ERRα/PGC-1 induces the expression of VEGF in breast cancer cells in vitro and in a xenograft model of breast cancer (30, 31). Conversely, inhibiting ERRα activity using diethylstilbestrol, a nonspecific ERRα antagonist, has been shown to reduce angiogenesis in breast cancer xenografts (32). When taken together, these studies highlight a potential role for ERRα in tumor angiogenesis. Interestingly, ERRα and HIF-1 have been shown to physically interact and in doing so to coregulate the expression of several endogenous HIF-1 target genes. The impact of this cross-talk on the regulation of processes of pathologic importance in tumors remains to be determined.

The expression of PGC-1α, PGC-1β, ERRα, and those of their target genes involved in the TCA cycle, oxidative phosphorylation, and glycolysis, were shown to be upregulated in breast cancer cells that have metastasized to the brain (33). Although the signaling events that lead to the upregulation of the ERRα/PGC-1 axis in these cells have not
been defined, it has been shown that these changes in gene expression enable the adaptive metabolic events and changes in redox balance that allow the metastasized tumor cells to survive in the nutrient-deprived (low glucose) environment of the brain. This result suggests that the ability of ERRα to regulate metabolic function likely contributes to its pathogenic actions in cancer.

The activity of the ERRα/PGC-1 complex is also positively regulated by oncocogenic pathways that are highly relevant in breast cancer. HER2 activation, for example, has been shown to initiate a signaling cascade that leads ultimately to the phosphorylation of several serine residues located at the N-terminus of ERRα and these modifications have been shown to increase receptor transcriptional activity (34–36). Furthermore, HER2 activation also increases the expression of PGC-1β. Not surprisingly, it has been shown that (i) PGC-1β expression is elevated in HER2-expressing breast cancer cells and (ii) knockdown of HER2 reduces PGC-1β expression in HER2-amplified breast cancer models (37).

Recently, PGC-1β was shown to be a direct downstream target of c-MYC and that activation of phosphoinositide 3-kinase (PI3K)/AKT, by either heregulin or insulin-like growth factor (IGF)-I, resulted in increased expression of c-MYC and a subsequent increase in the expression of PGC-1β (11). Importantly, knockdown of PGC-1β reduced the growth of those breast cancer cells in which it was expressed (11, 37). The induction of PGC-1β by c-MYC is particularly significant given that this oncogene is frequently overexpressed in a wide variety of tumors. More specifically, it has been shown that 15% to 45% of breast cancers exhibit overexpression/amplification of MYC and that this overexpression is associated with a poor clinical outcome (38, 39). This likely relates in part to MYC-dependent induction of PGC-1β expression and the subsequent increased expression of those ERRα target genes involved in oxidative phosphorylation and the TCA cycle. Indeed, we have proposed that ERRα is a primary integrator of the MYC-induced anapleurotic processes required for biomass synthesis in cancer cells (Fig. 2). Although most of the pyruvate produced during glycolysis is converted to lactate, a significant amount is diverted into the TCA cycle to form citrate. In most normal cells the TCA cycle operates as a closed system. However, in rapidly proliferating cells, including cancer cells, citrate is shuttled out of the mitochondria, where it is converted to acetyl CoA and used for fatty acid biosynthesis (40, 41). Unless replenished, citrate removal...
interrupts flux through the TCA cycle, resulting in decreased synthesis of the biosynthetic intermediates required for protein and nucleotide synthesis. This situation is mitigated in most cancer cells by increased glutaminolysis; uptake of glutamine, and its subsequent oxidative deamination to form α-ketoglutarate; α-ketoglutarate then enters the TCA cycle and replenishes citrate and the other constituent organic acids (42–44). ERRα/PGC-1 regulates the transcription of all of the enzymes that constitute the TCA cycle and supports the biochemical reactions required for biomass synthesis. Given that most MYC-transformed cells are dependent on glutaminolysis for growth and survival, it is tempting to speculate that this protein may coordinate the refueling of biosynthetic intermediates in part through upregulation of the ERRα/PGC-1 axis. By extension, it is expected that targeting the ERRα/PGC-1 axis would be beneficial in treating tumors with MYC amplification/overexpression. Significantly, we have determined that a gene signature enriched for the TCA cycle and oxidative phosphorylation genes predicts poor survival in multiple cohorts of breast cancer patients. In addition, a potential role for ERRα in glycolysis has also been implicated by studies using ChIP-on-chip analyses (45). It has further been proposed that ERRα/PGC-1 is an essential component of the processes that enable cells to upregulate glycolysis under conditions in which mitochondrial oxidative phosphorylation is unable to meet bioenergetics demands.

Although PGC-1α is likely also to affect tumor cell metabolism through its actions on ERRα, the expression of this coactivator is not directly regulated by MYC. However, its expression has been shown to be upregulated by PI3K- and mTOR-dependent signaling activities. Specifically, mTOR, through its actions on YY1, induces PGC-1α expression in skeletal muscle cells (46). Whether this mechanism operates in the same way in cancer cells remains to be determined.
Recently, using a gene signature derived from ERRE1/PGC-1α/β regulated genes, we showed that ERRE1/PGC-1α/β activity is elevated in HER2-positive tumors and those tumors in that elevated MYC activity is apparent (11). The importance of this observation was highlighted by studies that found that (i) the latency of MMTV-Neu (HER2) breast tumors was significantly increased when propagated in an ERRα+/− background and (ii) overexpression of PGC-1α increased tumor growth in HER2/Neu-driven xenograft models of breast cancer (31, 47). These results confirm the importance of this signaling axis in breast cancer pathogenesis and suggest that targeting the ERRE1/PGC-1 axis should provide additional therapeutic options in these types of cancers.

Similar to other NRs, ERRE1 was also found to have significant cross-talk with the WNT signaling pathway. Specifically, it was shown that ERRα physically interacts with β-catenin (β-cat) and T-cell factor/lymphoid enhancer factor (TCF/LEF) in breast cancer cells (48). In this manner (i) ERRα influences the activity of TCF/LEF on several endogenous target genes and (ii) ERRα transcriptional activity is enhanced by activation of β-cat. Significantly, WNT11, one of the target genes coregulated by ERRα and β-cat, was shown to be involved in breast, prostate, and colon cancer cell migration, and it was also shown that this activity can be inhibited by knockdown of ERRα, β-cat, or WNT11, activities that are completely reversed by the addition of exogenous recombinant WNT11. Similar cross-talk between ERRα and WNT signaling has also been shown to be involved in osteoblastogenesis (49).

Finally, posttranslational modifications of ERRα by phosphorylation (protein kinase C), sumoylation, and acetylation at the N-terminus and within the DNA-binding domain have been shown to regulate the transcriptional activity of this receptor (34, 36, 50–52), although the biologic relevance of these modifications and their regulation has not been established.

Clinical–Translational Advances

Given the ascribed functions of ERRE1 and PGC-1 in energy metabolism, it is not surprising that the initial efforts to develop modulators of this receptor were focused on the identification of molecules with agonist activity for use in the treatment of metabolic diseases such as diabetes and obesity. However, compounds with significant ERRE1 agonist activity have yet to be identified (13). Interestingly, several antagonists/inverse agonists have been described that have been shown to inhibit ERRE1 activity both in vitro and in vivo. Although none of these compounds have or are likely to advance to the clinic, they have been extremely useful tools to probe ERRE1 biology. The first selective ERRE1 antagonist described in the literature, XCT790, [(2E)-3-(4-((2,4-bis(trifluoromethyl)benzyl)oxy)-3-methoxyphe

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