

Thyroid Hormone Receptor Beta

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There is compelling evidence that the nuclear receptor TR β , a member of the thyroid hormone receptor (TR) family, is a tumor suppressor in thyroid, breast, and other solid tumors. Cell-based and animal studies reveal that the liganded TR β induces apoptosis, reduces an aggressive phenotype, decreases stem cell populations, and slows tumor growth through modulation of a complex interplay of transcriptional networks. TR β -driven tumor suppressive transcriptomic signatures include repression of known drivers of proliferation such as PI3K/Akt pathway, activation of novel signaling such as JAK1/STAT1, and metabolic reprogramming in both thyroid and breast cancers. The presence of TR β is also correlated with a positive prognosis and response to therapeutics in BRCA+ and triple-negative breast cancers, respectively. Ligand activation of TR β enhances sensitivity to chemotherapeutics. TR β co-regulators and bromodomain-containing chromatin remodeling proteins are emergent therapeutic targets.

TR β

tumor suppression

co-regulators

therapeutics

1. Introduction

Altered gene expression programming in cancer cells is often a consequence of a loss of function of cell-type specific transcriptional control mechanisms. Genetic mutations and epigenetic silencing of thyroid hormone receptor beta (TR β) is characteristic of a number of solid tumors and can be a marker for dedifferentiation [1][2][3][4][5]. TR β is a ligand-dependent transcription factor that responds primarily to triiodothyronine (T₃). TR β is recognized as a tumor suppressor and a positive prognostic indicator, however the mechanisms by which it regulates tumor growth remain unclear [6][7][8][9]. Recent studies indicate that TR β tumor suppressive effects are mediated in part through intracellular signaling pathways, including PI3K/Akt, Ras/MAPK, and JAK-STAT pathways, and induction of the mesenchymal-to-epithelial transition. Mutations in TR β that lead to thyroid hormone resistance have also been shown to be oncogenic [10]. Transcriptional regulation by TR β is critical for its function as a tumor suppressor because it acts as both a signal transducer and facilitator of long-term epigenetic programming for maintenance of cell identity.

2. TR β Satisfies the Criteria for a Tumor Suppressor

There is an abundance of evidence both in vivo and at the molecular level that highlight TR β tumor suppressor function. Loss of the transcription factor TR β , a member of the thyroid hormone receptor family, through mutation or epigenetic silencing is characteristic of thyroid and other endocrine-related cancers [1][2][6][7][8][9]. Restoration of TR β function in malignant cells decreases tumor growth in xenograft studies, supporting a tumor suppressor role for TR β [6][7][8]. In order to designate a particular factor as a tumor suppressor, there are criteria that need to be

met: (1) loss of the factor must result in cancer growth, and (2) restoration of the factor must reduce cancer growth [11][12]. Over the course of the last two decades, it has been demonstrated through multiple studies that TR β does indeed meet these criteria (Figure 1).

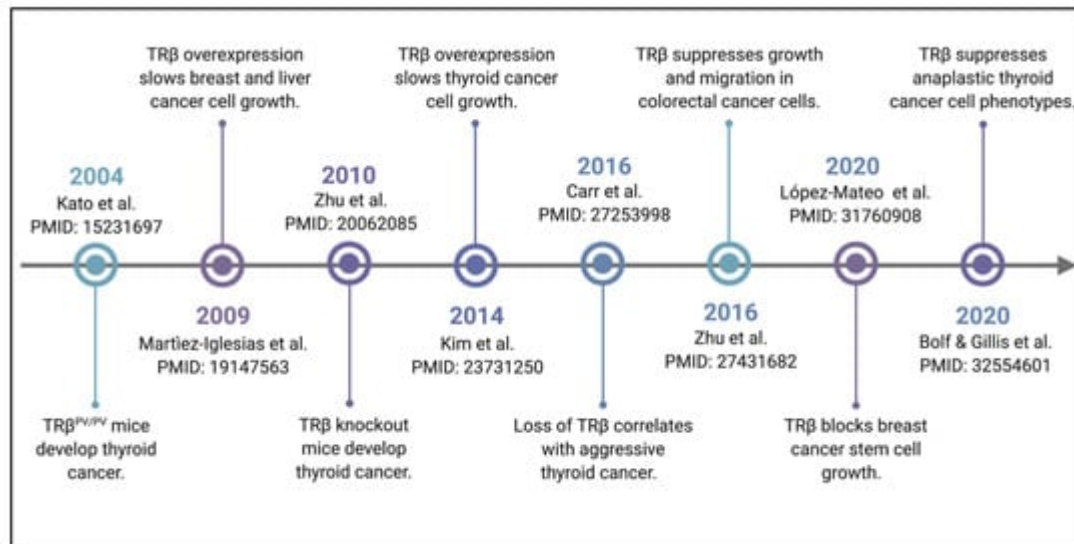


Figure 1. Timeline of seminal studies of TR β tumor suppression. TR β function was first linked to cancer growth when it was shown that an expression of ligand-binding domain mutant (TR β^{PV}) in mice led to spontaneous development of thyroid tumors. Increasing numbers of studies have demonstrated over the following two decades that TR β is a classically-defined tumor suppressor.

One of the first reports of potential TR β tumor suppressor activity was from a study of resistance to thyroid hormone [10]. Mice with a point mutation in the ligand-binding domain of TR β that renders it unable to bind ligand (denoted as TR β^{PV}) unexpectedly exhibited enlarged thyroid glands, in addition to the symptoms of resistance to thyroid hormone syndrome. Further examination of the enlarged thyroid glands in TR β^{PV} mutant mice by histology revealed that the mice had developed thyroid cancer. Further studies from the same group demonstrated that thyroid-specific knockout mice also spontaneously develop thyroid cancer [13]. Histological sections from tissues of TR β knockout mice showed evidence of anaplasia, capsular invasion, vascular invasion, and metastatic lesions in the lung. In human thyroid cancer tissues, loss of TR β expression is correlated with dedifferentiation [14]. Normal thyroid epithelial cells have the highest TR β expression, while TR β expression is lowest in anaplastic thyroid cancer cells, the most aggressive form of thyroid cancer. Combined, these results establish that loss of TR β results in cancer growth.

Restoration of TR β signaling in TR β -low or TR β -null cell lines has been shown to slow tumor growth in vivo. This was first shown in MDA-MB-468 triple negative breast cancer cells with TR β restored in a nude mouse xenograft model [6]. In the same study, SK-hep1 hepatocarcinoma cells with TR β restored showed reduced tumor growth [6]. Cells with restored TR β expression were also shown to have less metastatic potential than control cells. A separate study showed that FTC-133 follicular thyroid cancer cells with TR β restored show reduced growth in a xenograft study [9]. These TR β -expressing tumors showed evidence of reduced PI3K-Akt signaling and less blood vessel

formation compared to tumors without TR β expression. Most recently, TR β restoration has been shown to suppress growth and migration in colorectal cancer cells [15], and block cancer stem cell out growth in luminal A breast cancer cell lines [16]. Our group demonstrated that restoration of TR β in anaplastic thyroid cancer cells reprograms the transcriptome, promotes apoptosis, and suppresses many of their aggressive phenotypic traits [17]. Taken together, these results establish that restoration of TR β slows cancer growth.

3. Mechanisms of TR β -mediated Tumor Suppression

3.1. TR β Attenuates the PI3K-Akt Signaling Pathway via Genomic and Nongenomic Mechanisms

Phosphoinositide 3-kinase (PI3K) signaling is a potent tumor activating pathway that is implicated in many solid and hematologic tumors [18][19][20][21][22]. PI3K is recruited to ligand-bound, phosphorylated receptor tyrosine kinases (RTKs), and phosphorylates the membrane lipid phosphatidylinositol 4,5-bisphosphate (PIP2) to phosphatidylinositol (3,4,5)-trisphosphate (PIP3). PIP3 is a docking lipid that anchors protein kinase B (Akt) for phosphorylation and activation by phosphoinositide-dependent kinase-1 (PDK1) on thr308 and mammalian target of rapamycin complex 2 (mTORC2) on ser473. Akt is a multi-substrate kinase that phosphorylates targets involved in apoptosis regulation, cell cycle progression, angiogenesis, and metabolism. An important function of Akt is the indirect activation of mTORC1, which phosphorylates a myriad of targets such as p70S6K and eukaryotic translation initiation factor 4B (eIF4B) to increase cell metabolism and protein translation. PI3K-Akt pathway activation is frequently overactive due to gain-of-function mutations in PI3K, loss of expression of phosphatase and tensin homolog (PTEN), or amplifications in RTKs and Akt [19][21][23].

TR β has long been understood to directly alter the PI3K pathway through nongenomic mechanisms. Simoncini et al. first reported on the potential for hormone receptors to increase PIP3 content in endothelial cells [24]. Estrogen, dexamethasone, and thyroid hormone receptors all increased PIP3 levels following respective hormone treatment, suggesting a shared yet noncanonical role for hormone receptors in PI3K activation. In other normal cells such as human fibroblasts, treatment with 15 min of 10 nM T₃ induced Akt phosphorylation, and phosphorylation of mTORC2 and p70S6K was observed after 30 min T₃ exposure [25]. This effect was abrogated with PI3K inhibitors LY294002 and wortmannin. This rapid impact of T₃ was unlikely due to TR β -mediated transcription; indeed, TR β was shown to directly bind to the RTK localization subunit of PI3K, p85 α , independently of ligand (**Figure 2**) [25]. Interestingly, 100 nM of T₃ did result in reduced TR β -p85 α binding and increase in PI3K activity in fibroblasts [25]. These findings were confirmed in GH4C1 and CHO cells treated with 100 nM T₃ for only five minutes [26], suggesting a rapid and conserved nongenomic function of TR β across diverse mammalian cell types.



lines investigated which resulted in either an increase or decrease in Akt phosphorylation [29]. This may reflect the levels of endogenous TR β in cell lines as well as individual genetic backgrounds of the cells. Notably, the experiments were conducted at 24 and 48 h of T₃ exposure, indicating that gene expression could have been at play in conjunction with p85 α binding. In MDA-MB-468 and SK-Hep1 cells transduced with TR β , pAkt was blunted in the presence of Insulin-like growth factor 1 (IGF-1) compared to control cells, suggesting a protective effect of TR β on the PI3K-Akt pathway [6]. Indeed, qPCR revealed a reduction in the RTKs epidermal growth factor receptor 1 (*EGFR1*), HER3 (*ERBB3*), and *IGFR1* in both cell lines [6].

In vivo studies using the follicular thyroid cancer cell lines FTC-133 and FTC-236 transfected with TR β revealed a decrease in pAkt, mTORC1, p70S6K, and eIF4B [9]. There was also a decrease in vascular endothelial growth factor (VEGF) levels which stimulates endothelial cells to promote angiogenesis by way of the PI3K pathway, further implicating a broad-spectrum tumor suppressive role of TR β . Additionally, TR β transduction resulted in reduced autocrine signaling in an MCF-7 model [16]. TR β -T₃ decreased expression of vascular endothelial growth factor receptor 9 (FGFR9) and cognate ligands FGF3 and FGF4, while blunting estrogen-mediated induction of FGF9. While PI3K activity itself was not measured, this study confirmed an additional mechanism of TR β modulation of players in the PI3K-Akt pathway.

There were similar findings in colorectal cancer cells in which long-term T₃ exposure resulted in reduced ser473 Akt phosphorylation by an unknown mechanism [15]. However, as we have recently described, TR β may play a critical genomic role in PI3K regulation in anaplastic thyroid cancer (ATC) [30]. While short term (30 min) T₃ exposure failed to reduce pAkt levels, long term exposure (24 h) reduced pAkt and pmTORC1 levels concordantly with changes in gene expression. T₃-TR β in ATC cells increased phosphatase levels such as phosphatidylinositol 4,5-bisphosphate 5-phosphatase A (*INPP5J*), inositol polyphosphate 4-phosphatase type II (*INPP4B*), and PH domain and leucine rich repeat protein phosphatase 1 (*PHLPP1*). Importantly, INPP4B is a potent tumor suppressor of thyroid cancer in vivo [31]. Conversely, TR β -T₃ decreased levels of receptor tyrosine kinases *ERBB3* (HER3), *FGFR3*, and *FGFR4*. This impact on PI3K pathway attenuation resulted in increased sensitivity to the PI3K inhibitors LY294002 and buparlisib, providing a provocative implication on the relationship between TR β status in cancer patients and response to therapies.

A major consequence of PI3K-Akt signaling in cancer cells is the increase in cell metabolism. While the impact of TR β on normal metabolism is well studied [32][33], there is little known on the tumor suppressor's role in cancer cell metabolism. We were able to determine that TR β and T₃ potentially modulate key metabolic pathways in triple negative breast cancer and ATC cells. Stearic acid is known to exhibit tumor suppressor functions in breast cancer by inducing apoptosis [34]. In our MDA-MB-468 cells transduced with TR β , T₃ induced expression of enzymes in the stearic acid synthesis pathway, including Acetyl-CoA synthetase short chain family member 2 (ACSS2), glutaminase, and 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB1). In ATC cells, we noticed the potential for TR β and T₃ to regulate glycogen metabolism, an oncogenic metabolic pathway that has been observed in many cancer models such as breast, colorectal, and pancreatic cancer [35][36][37][38]. Glycogen is a storage form of glucose for cancer cells to advantageously breakdown via glycogen phosphorylase in times of low cellular energy or oxidative stress (**Figure 3**) [39]. TR β and T₃ decreased expression of the brain isoform of

glycogen phosphorylase (PYGB) and differentially regulated expression of key signaling proteins that activate PYGB such as cell migration inducing hyaluronidase (CEMIP), and the beta inhibitory subunit of phosphorylase kinase (PHK) [40]. Since these studies highlight two specific metabolic pathways regulated by TR β in cancer cells, further exploration will be required to ascertain the extent of how TR β induces global metabolic changes in cancer cells.

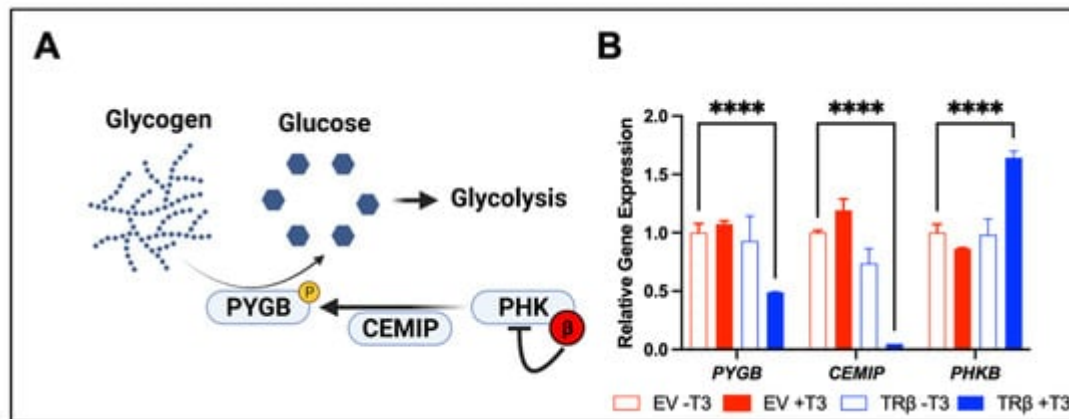


Figure 3. TR β may regulate glycogen metabolism (A) in anaplastic thyroid cancer cells. RNA-sequencing [17] revealed a novel function of liganded TR β on metabolism in a cancer cell model (B). TR β and T $_3$ induced significant changes in gene expression in the glycogen pathway to decrease levels of PYGB and the glycogen signaling protein CEMIP. TR β also enhanced the inhibitory beta subunit of PHK which phosphorylates and activates PYGB to enhance glycogen breakdown and potentially cell survival. Significance was determined using two-way ANOVA followed by Dunnett's multiple comparisons test (**** $p < 0.001$).

3.2. TR β Differentially Influences JAK-STAT Signaling

Another important signaling cascade in cancer is the JAK-STAT pathway. Immune modulators such as interferons and interleukins activate cognate receptors to recruit Janus kinases (JAKs) to the membrane to phosphorylate specific signal transducer and activator of transcription proteins (STATs) [41]. Although the JAK-STAT pathways are best studied in immune cells to promote cell growth and the immune response, cancer cells can take advantage of the signaling pathway to contribute to malignant phenotypes [42][43][44]. STAT3 and STAT5 typically demonstrate tumor promoting activity by inhibiting apoptosis through repression of *BAX* and *BAK* transcription, along with induction of *BCL2* transcription (Figure 2) [45][46][47]. Conversely, JAK1 and STAT1 have been shown to induce apoptosis in a variety of cell models, likely through *BCL2* repression and *CDKN1A* (p21) transcription [48][49][50][51]. TR β has been shown to specifically regulate activity of certain JAK-STAT pairs. For example, Guignon et al. showed that a ligand-binding domain mutant TR β resulted in enhanced prolactin expression and sustained phosphorylation of STAT5 in a mouse model of breast cancer [52]. STAT5 is known to inhibit apoptosis and encourage cell cycle progression by promoting *BCL2* and *CCND1* (cyclin D) transcription, respectively [47][53]. Introduction of wildtype TR β attenuated prolactin-induced p-STAT5 levels which were further reduced with addition of T $_3$. Park et al. showed that TR β decreased JAK2, STAT3, and STAT5 phosphorylation and activation in MCF-7-TR β cells [8]. This led to a decrease in tumor size and proliferation with an increase in apoptosis. In an ATC model

with stably-transduced TR β , we observed differential regulation in opposing JAK-STAT pathways [17]. STAT3 signaling was downregulated in the ATC cells while STAT1 signaling was induced compared to control cells. STAT1 activation led to induction of apoptosis as evident from Caspase 3 and poly (ADP-ribose) polymerase (PARP) cleavage. Importantly, we were able to activate STAT1 independently of TR β with 2-(1,8-Naphthyridin-2-yl)phenol. This study revealed a novel target in ATC, highlighting the importance of better understanding the tumor suppressor program of TR β .

3.3. TR β Regulation of Cell Cycle Progression

The cell cycle is a crucial target for aggressive cancers (**Figure 2**). Perez-Juste et al. first observed that overexpression of TR β with T₃ had profound effects on neuron development in murine neural crest-derived cells [54]: TR β activation led to a decrease in MYC and cyclin D1 expression with a concomitant increase in the cell cycle regulator p27. Since p27 can directly inhibit cyclin-dependent kinases (CDKs), the investigators unsurprisingly observed a decrease in phosphorylated retinoblastoma protein (Rb), resulting in cell cycle arrest. The authors later confirmed the direct relationship of TR β to the cell cycle promoter MYC by elucidating a negative thyroid response element (TRE) on the MYC promoter [55]. Porlan et al. expanded on these observations by showing that TR β in 3T3 cells inhibited proliferation and the cell cycle via decreasing pRb, cyclin D 1, 2, and 3, and cyclin E [56]. Yen et al. showed similar findings in HepG2 cells using 10 nM T₃ for multiple days; there was an increase in p21 and decrease in cyclin E and pRb [57]. In pancreatic adenocarcinoma cell lines, TR β decreased cyclins D1 and E but increased p21, which led to an increase in p27 [58]. This excitingly allowed for an enhanced response to the antiproliferative agents gemcitabine and cisplatin. The impact of TR β on cell cycle has also been observed in vivo; Martinez et al. observed a decrease in cyclin E in hypothyroid patients with hepatocellular carcinoma or breast cancer [59]. These authors also noted increased p27 expression in their SK-TR β mouse model.

Lin et al. expanded on the mechanism by showing that TR β with T₃ increases endoglin expression to stabilize p21 protein in hepatocellular carcinoma cells [60]. Cell cycle arrest was also measured in MCF-7-TR β cells with long term T₃ exposure; transcriptomic analysis revealed a decrease in cell cycle related gene transcripts, including MYC and members of the E2F family [16]. Finally, we recently performed RNA-sequencing to capture the full cell cycle signaling pathway with TR β and 24 h of T₃ [17]. We observed a decrease in CCND1 and MYC expression and an increase in CDKN1A, highlighting the importance of TR β on cell cycle regulation. Importantly, we showed that TR β enhanced the efficacy of palbociclib, a CDK4/6 inhibitor. Palbociclib is frequently used to treat ER⁺ and HER2⁺ breast cancers and is in clinical trials for several solid tumors [61][62][63][64]. However, resistance to CDK inhibition often develops, highlighting a potentially useful diagnostic and role for TR β in predicting response to CDK inhibitors.

3.4. Impact of TR β on TGF- β Signaling

Another important signaling pathway in cancer is the transforming growth factor beta (TGF- β) signaling cascade. TGF- β stimulates its cognate receptor to induce dimerization and autophosphorylation to phosphorylate mothers against decapentaplegic homolog (SMADs) [65][66][67]. The SMAD complex is translocated to the nucleus to regulate gene transcription (**Figure 2**). In normal cells, TGF- β signaling regulates the cell cycle and can promote

apoptosis. In cancer cells, however, mutations in TGF- β , SMADs, or SMAD binding partners can induce a tumor promoting gene expression program [65][66][67]. While TR α and T₃ positively regulated TGF- β signaling in liver cancer cells [57], TR β and T₃ appear to negatively regulate TGF- β . This was first observed in GH₄C₁ cells as well as an in vivo model [68]. TR β and T₃ downregulated TGF- β signaling induction, partly by directly competing for SMAD binding sites, resulting in decreased fibrosis. In transduced MCF-7 cells, López-Mateo et al. noted that TR β -T₃ could blunt TGF- β -induced SMAD2 and SMAD3 phosphorylation in MCF-7 cells, leading to a decrease in both SMAD2 and SMAD3 transcriptional activity [16]. TGF- β signaling attenuation is a notable and conserved feature of liganded TR β that further highlights its function as a broad-spectrum, potent tumor suppressor.

3.5. TR β Inhibits Epithelial–Mesenchymal Transition

Aggressive cancers display hallmarks of epithelial–mesenchymal transition (EMT) as the cell becomes more metastatic. TR β has been shown to reduce EMT in several cancer models (**Figure 2**). First, Martinez-Iglesias et al. demonstrated that TR β reduced expression of vimentin, beta catenin, and matrix metalloproteinase 1 and 9 (MMP1 and MMP9) in breast and liver cancer models, leading to a decrease in malignancy in vivo [6]. Dentice et al. further showed an increase in E cadherin with T₃ in colon cancer cells [69]. We also showed that there is a direct and positive relationship between TR β expression/activation and mesenchymal–epithelial transition (MET) in thyroid cancer [14]. TR β directly regulates the expression of the RUNX family transcription factor 2 (RUNX2), a master EMT transcription factor. There was an inverse relationship observed between TR β and RUNX2 expression in thyroid cancer from normal cells to the highly dedifferentiated anaplastic thyroid cancer. T₃ reduced RUNX2 expression in normal and ATC cells, and TR β knockdown increased RUNX2, increasing the expression of MMP2, MMP13, cyclin D1, osteopontin (OPN), and cadherin 6. Transfected TR β also repressed RUNX2 and EMT markers in MDA-MB-231 cells; conversely, TR β -knockdown in breast epithelial-like MCF10A cells caused an increase in RUNX2 and EMT markers [70]. López-Mateo et al. confirmed a decrease in EMT genes such as vimentin and snail family transcriptional repressor 2 (SLUG) in estrogen receptor alpha positive (ER α ⁺) breast cancer cells [16]. We recently observed more evidence of MET in a transduced ATC model in which TR β and T₃ increased transcript levels of E cadherin and decreased vimentin mRNA [17].

3.6. TR β Promotes Cancer Cell Re-Differentiation

EMT is closely correlated with dedifferentiation, a phenotype that does not resemble the original tissue of origin but more closely resembles a stem cell [71]. Dedifferentiation is a crucial process in the cancer cell to evade the immune system, enhance proliferation, promote angiogenesis, and develop drug resistance [72][73]. Modulation in expression of specific tissue markers is often correlated with dedifferentiation. For example, breast cancer cells increase expression of cytokeratins, proteins that are secreted into the extracellular matrix (ECM) or attached at the cell surface [74][75]. These keratins are advantageous modulators of the ECM that allow for enhanced cancer cell migration and invasion [76]. TR β decreased the expression of keratins 8 and 18 in MCF-7 cells [6][59]. These two keratins, amongst other keratin isoforms, were also reduced in stem cell models of ER α ⁺ breast cancer [16]. Furthermore, we observed a decrease in mRNA and protein levels of keratins 5 and 14 in a triple negative breast cancer model. It may be possible that TR β canonically regulates keratin expression, as this has been observed in organisms such as *Xenopus laevis* [77].

TR β appears to induce re-differentiation in cells and encourage expression of normal cell markers, agnostic of cell type. Perra et al. noted a striking difference in rats with preneoplastic liver lesions treated with the selective TR β agonist sobetirome (GC-1): TR β activation resulted in loss of dedifferentiation markers and reacquisition of differentiated liver proteins [78]. This phenomenon was also detected in colon cancer cells, in which T₃ induced robust expression of normal colon markers sucrase isomaltase and intestinal alkaline phosphatase and slowed the proliferation of the cancer cells [69].

In addition to breast and colon cancer models, TR β has shown to induce re-differentiation in thyroid cancer cells. We recently demonstrated that TR β and T₃ induced the re-expression of several key thyroid specific genes that are lost in dedifferentiated thyroid cancer [17]. These included iodothyronine deiodinase 2 (*DIO2*), dual oxidase 1 (*DUOX1*), thyroid peroxidase (*TPO*), and thyroglobulin (*TG*). Excitingly, we were also able to induce expression of these genes plus six other thyroid specific markers by using the potent TR β -specific analog GC-1 to activate the low level of TR β expressed in ATC [79]. The sodium iodide symporter (NIS) transcript and protein level were increased using GC-1, which allowed for a significantly higher intake of iodide in cell culture models. These studies not only demonstrate the role of TR β in re-differentiation programming but could have functional significance, as induction of NIS could be exploited for radioactive iodine treatment in thyroid and breast cancers.

Finally, in the course of dedifferentiation, aggressive cancers become more stemlike. This allows for unlimited replicative potential and evasion from the immune system [71]. TR β appears to reduce the stem cell population in both breast and thyroid cancers. López-Mateo et al. showed that TR β activation in MCF-7 cells reduced the mammosphere population [16]. This was associated with a decrease in the breast stem cell markers aldehyde dehydrogenase (ALDH1) and CD44, with an increase in the monolayer marker CD24. An increase in CD24 expression is not only notable for demonstrating a decrease in the stem cell population, but it can also be used as a drug target for promoting tumor cell clearing by macrophages in the tumor microenvironment [80][81]. They also observed a decrease in SRY-box transcription factor 2 (SOX2) and NANOG, which are downstream of CD44 and TGF- β signaling. We also observed a decline in the stem cell population in both ATC and MDA-MB-468 breast cancer cells by manipulating TR β levels [17]. We noted that ALDH, POU5F1 (encodes OCT3/4), CD44, FUT4 (encodes SSEA-1), and PROM1 expression were significantly downregulated in cancer cells transduced with TR β . We have also recently been able to see this change in ATC cells with GC-1 that resulted in stem cell death, increase in CD24 expression, and decrease in CD44 expression [79]. We also observed an enhanced efficacy to the inhibitors buparlisib (PI3K), sorafenib (MAPK), and palbociclib (cell cycle) in the stem cell population. The use of TR β screening and specific activation may help reduce the stem cell population and increase the efficacy of clinically relevant therapeutics in ATC patients.

3.7. TR β Interactions with Epigenetic Modulators Are Key to Tumor Suppression

In its capacity as a transcription factor, TR β is a hub for incoming molecular signals that include fluctuations in hormone levels, input from cellular signaling pathways, and post-translational modifications. It must integrate all of these signals to recruit the necessary coregulators and execute a transcriptional response. TR β has a diverse repertoire of potential binding partners in normal cells, as evidenced by immunoprecipitation to mass spectrometry

studies [82][83], and by our own proximity ligation assays [84]. By complexing with a variety of co-regulators TR β acts to coordinate complex gene regulatory events that have variety of implications in maintenance of cellular homeostasis and tumor suppression. Disruption of these crucial interactions in cancer cells may lead to either a loss of response to T₃ or to aberrant transcription.

Many coactivators have been implicated in T₃-dependent gene activation by TR β , including the steroid receptor coactivator (SRC), p300/CBP histone acetyl transferases, and the mediator-like TR associated proteins (TRAP)/DRIP [85]. SRC interacts directly with liganded TR β and serves as an adapter molecule to facilitate recruitment of p300/CBP to acetylate histones and interact with components of basal transcriptional machinery. The TRAP complex is a multisubunit coactivator complex that interacts with liganded TRs and recruits RNA polymerase II to promoters. Chromatin immunoprecipitation experiments have demonstrated that upon T₃ binding, TR β first recruits SRC proteins and p300, resulting in histone acetylation, followed by the TRAP complex [86]. Together, these coactivators facilitate transcriptional activation through a stepwise process of acetylation of histones to relax the local chromatin and subsequent recruitment of the basal transcriptional machinery. Compounds that target the specific interactions between nuclear hormone receptors and SRC have been developed and have shown early signs of therapeutic benefit in vivo [87].

TR β also complexes with a variety of nuclear co-repressors. Specifically, evidence suggests that TR β represses gene expression via the recruitment of either nuclear co-repressor 1 (NCoR1) or silencing mediator for retinoid or thyroid-hormone receptors (SMRT, NCoR2) [88][89][90]. NCoR1 and SMRT are highly homologous and contain three similar nuclear receptor interaction domains. Furthermore, both NCoR1 and SMRT bind to TR β , as well as other nuclear hormone receptors via similar mechanisms at specific residues [91]. The seminal article that first identified NCoR1 as a crucial regulatory protein found that it bound TR β at amino acid residues 203–230, but that amino acid residues 230–260 act to stabilize this interaction [92]. NCoR1 and SMRT directly recruit and interact with Class II histone deacetylases (HDAC), and recruit Class I HDAC's via linker proteins such as Sin3a or Sin3b [93][94][95][96]. NCoR1 itself has been demonstrated to be critical for suppression of breast cancer growth in coordination with TR β [97]. HDAC inhibitors may be useful in combination with hormone therapy, particularly in the context of anti-estrogen or anti-androgen [98][99] resistance. The future use of compounds that can promote interactions between TR β and its coregulators, or block interactions with negative regulators, may be an attractive way to enhance the beneficial effects of thyroid hormones or thyromimetics.

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