p53: Protection against Tumor Growth beyond Effects on Cell Cycle and Apoptosis

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The tumor suppressor p53 has established functions in cancer. Specifically, it has been shown to cause cell-cycle arrest and apoptosis in response to DNA damage. It is also one of the most commonly mutated or silenced genes in cancer and for this reason has been extensively studied. Recently, the role of p53 has been shown to go beyond its effects on cell cycle and apoptosis, with effects on metabolism emerging as a key contributor to cancer growth in situations where p53 is lost. Beyond this, the role of p53 in the tumor microenvironment is poorly understood. The publication by Wang and colleagues demonstrates for the first time that p53 is a key negative regulator of aromatase and, hence, estrogen production in the breast tumor microenvironment. It goes further by demonstrating that an important regulator of aromatase, the obesity-associated and tumor-derived factor prostaglandin E2, inhibits p53 in the breast adipose stroma. This review presents these findings in the context of established and emerging roles of p53 and discusses possible implications for the treatment of breast cancer. Cancer Res; 75(23); 5001–7. ©2015 AACR.

Background

Traditional tumor suppressor functions of p53

The tumor suppressor p53, encoded by the TP53 gene, is the most commonly silenced or mutated gene in cancer, with 50% to 55% of human cancers having experienced the loss of wild-type p53 activity (reviewed in ref. 1). Under normal conditions, p53 levels are low and, in some cases, undetectable. However, stress signals such as DNA damage, oncogene activation, and hypoxia stabilize p53 protein and induce increased cellular p53 levels by posttranslational modifications such as phosphorylation and acetylation. Activated p53 causes a variety of responses including cell-cycle arrest or apoptosis, thereby providing a critical barrier against tumor development (reviewed in refs. 1, 2). As a transcription factor, activated p53 binds to a number of genes that contain p53-binding sites within their regulatory regions. Bioinformatic studies have found more than 4,000 putative p53-binding sites in the existing human genome. Somatic mutations in TP53 are common in cancers and are associated with poor prognosis and low response to chemotherapy (3).

Numerous p53 target genes have been identified as downstream effectors of p53 with changes in cell function being dependent on the regulation of several genes (2). For example, p53 mediates cell apoptosis by activating mitochondrial and death receptor–induced apoptotic pathways, both pathways resulting in the induction of caspase signaling, which then induces apoptosis. The mitochondrial pathway is mainly regulated by p53 effector Bcl-2 proteins such as Bax (4) and PUMA (5). In tumors with wild-type p53, p53 responses can be inhibited by downregulating p53 activity or its effectors’ activity. For instance, in estrogen receptor–positive (ER+) breast cancers, ER prevents the p53-mediated apoptotic response by directly interacting with p53 (6).

Although most p53 mutations result in inactivation or dysfunction of p53, some mutations in p53 lead to the selective loss of apoptotic functions while retaining the ability to induce cell-cycle arrest. Certain p53 mutations lead to p53 becoming oncogenic through gain-of-function mechanisms (7). Cell-cycle arrest driven by p53 requires the transcription of p21, which is a cyclin-dependent kinase inhibitor, or other p53 target genes such as 14–3–3σ and GADD45 (8). In general, DNA damage or stress will increase levels of p53 protein, which in turn induces p21 transcription and leads to cell-cycle arrest at G1, allowing cells to survive until the damage has been repaired or the stress removed (9, 10). The G1 arrest is primarily regulated by p21, whereas G2 arrest is stimulated by GADD45, p21, and 14–3–3σ (11). The role of p53 to suppress tumor growth and promote apoptosis via these pathways is well-characterized. However, novel roles for p53 are emerging and these are proving important contributors to the tumor suppressor functions of p53.

p53 as a metabolic checkpoint

Emerging evidence suggests that p53 is also involved in the regulation of metabolism and cell homeostasis without causing cell-cycle arrest or apoptosis (12). For example, nutrient deficiency leads to the activation of p53 through direct phosphorylation at Ser15 by AMP-activated protein kinase (AMPK), a key regulator of cell metabolism (13). p53 also regulates metabolism and cell homeostasis in normal cells and tissues. Lipin1 is a recently identified p53 target gene that regulates the expression of genes involved in fatty acid oxidation through PPARα (14). Under nutrient/glucose deprivation conditions, p53 is upregulated by AMPK and stimulates Lipin1 and malonyl-CoA decarboxylase expression, leading to an increase in fatty acid oxidation (14, 15).
This allows cells to use fatty acids as an alternative energy source. Reciprocally, p53 also promotes the expression of AMPK, leading to the negative regulation of mTOR (16). The PI3K/Akt/mTOR pathway can suppress apoptosis and stimulate proinflammatory gene expression, which in turn promotes cancer growth and progression (17). Negative regulation of mTOR is also observed in autophagy, which can be induced by starvation and metabolic stresses.

Oncogenic transformation is often associated with enhanced aerobic glycolysis and reduced oxidative phosphorylation, which is known as the Warburg effect. Aerobic glycolysis allows cancer cells to generate ATP as well as stimulate anaerobic metabolism of intermediates such as α-ketoglutarate to support cancer cell proliferation and survival (18). Recently, p53 has been shown to inhibit the Warburg effect by reducing glycolysis and enhancing oxidative phosphorylation via upregulation of genes including TIGAR and SCO2 (synthesis of cytochrome oxidase 2), as well as inhibiting the expression of glucose transporters GLUT1, GLUT3, and GLUT4 (19, 20). SCO2 increases mitochondrial respiration and TIGAR inhibits glycolysis and promotes NADPH production and glutathione recycling, whereas repression of glucose transporters blocks the uptake of glucose (19).

In summary, a number of genes are regulated by p53 to maintain metabolism and energy homeostasis in cells/tissues under normal and stressed physiologic conditions. Changes in tumor cell metabolism are now recognized as a hallmark of cancer (21) and p53 is integral to this process.

**Dysregulated metabolism as a driver of estrogen production in the breast adipose**

Adipose tissue is responsible for energy storage and acts as an endocrine organ that regulates metabolism via endocrine, autocrine, and paracrine processes. Dysregulated adipose tissue plays a crucial role in cancers (22). In postmenopausal women, breast adipose tissue becomes the main site for estrogen production; obesity can lead to an increase in estrogen levels by increasing the expression of aromatase, the enzyme that catalyzes the final step in estrogen biosynthesis, and this has been shown in mouse models of obesity and in women (23–25). Adipocytes and adipose stromal cells (ASCs) are major components of adipose tissue and ASCs have been shown to contribute to the production of estrogens. Leptin produced from adipocytes can promote ER⁺ breast cancer growth (26, 27).

However, ASCs appear to be the main site of aromatase, and stimulates the expression of aromatase. Unpublished data from Sasano and colleagues showed enhanced aromatase expression and staining in tightly packed undifferentiated ASCs around tumor cells in patients with breast cancer. This process of undifferentiation and increased stromal cell proliferation is known as desmoplasia, which leads to the formation of a dense fibroblast layer surrounding malignant epithelial cells; it is essential for structural and biochemical support of tumor growth (31, 32).

**Li–Fraumeni syndrome**

Li–Fraumeni syndrome (LFS) is a rare autosomal dominant hereditary syndrome with the majority of affected individuals carrying germ line mutations in the *TP53* gene (33). LFS is characterized by a high susceptibility of developing a number of malignancies, predominantly in childhood and early adult life. Half of individuals with LFS develop at least one LFS-associated cancer by age 30 and 15% to 35% of cancer survivors with LFS will develop multiple primary tumors over their lifetimes (34). It has also been proposed that patients with LFS have deregulated metabolism, including increased oxidative stress and hypoxia, to provide a microenvironment conducive to tumor formation, which can be one complication of dysfunctional p53 for these patients (35). Breast cancer is the most common type of cancer in women with LFS and the majority of tumors are ER⁺ (36).

Moll and colleagues previously found that wild-type p53 can accumulate in the cytoplasm of tumor cells in inflammatory breast cancers, leading to functional inactivation of p53 (37). Interestingly, Molinari and colleagues demonstrated that estradiol caused the cytoplasmic accumulation of wild-type p53 in MCF7 breast cancer cells, leading to the G₁/S transition (38). A number of posttranslational modifications have been described to explain this change in subcellular localization, including phosphorylation (Ser15, Thr14, Ser20, Thr81), acetylation, and monoubiquitination (39). Of interest, AMPK has been shown to phosphorylate p53 at Ser15 (40). Coupled to findings demonstrating that p53 inactivation results in increased estrogen production in mouse mammary epithelial cells (41), we hypothesized that tumor suppressor p53, a downstream target of the LKB1/AMPK pathway, has a role in the regulation of aromatase in human breast ASCs.

**Key Findings**

**PGE₂ as a regulator of p53**

Prostaglandins regulate cell migration and invasion in cancer, and high prostaglandin levels are associated with many cancers including those of the breast. PGE₂ is a key inflammatory mediator produced in adipose tissue in the context of obesity and breast cancer. Obesity-associated inflammatory foci in the human breast are associated with elevated levels of COX2 and PGE₂ (25). Meanwhile, stabilized p53 binds to its target genes in the nucleus, whereas inactivated and dysfunctional wild-type p53 are accumulated in the cytoplasm. Abnormal subcellular localization of p53 can be an indication of tumorigenic processes in tissues (13, 42, 43). We therefore examined the effect of PGE₂ on p53 in ASCs. Our results show decreased p53 transcript expression, nuclear protein...
Figure 1. Established and emerging roles of p53 in preventing tumor growth. A, signaling pathways involved in regulating aromatase in response to PGE2 in ASCs. B, interplay between PGE2-p53-aromatase in the breast microenvironment. C, role and regulation of p53 in breast carcinogenesis.
expression, and phosphorylation at Ser15 in ASCs (44). The mechanism for transcriptional regulation of p53 remains to be determined, but AMPK is known to activate p53 through phosphorylation at Ser15, and our earlier studies have demonstrated an inhibitory effect of PGE₂ on AMPK, providing a potential mechanism for the decreased protein expression and activity of p53 in the presence of PGE₂ (13, 30). As a result of decreased phosphorylation, p53 nuclear localization is also decreased. This is consistent with findings in clinical samples of breast cancer, where we demonstrate by immunofluorescence that tumor-associated ASCs have lower nuclear p53 intensity and increased perinuclear intensity compared with normal ASCs (44). Perinuclear p53 represents inactive p53 (45). Our findings also demonstrate that PGE₂ causes an increase in ASC proliferation. Considering the important role of p53 in regulating cell-cycle arrest and apoptosis, it is possible that this PGE₂-mediated increase in cell proliferation is mediated by the downregulation of p53.

p53 as a novel regulator of aromatase
Aromatase has tissue-specific promoters and promoters I3/II are activated by PGE₂, leading to an increase in aromatase expression and estrogen production in tumor-associated ASCs of postmenopausal women (46). To study the effects of p53 on aromatase expression, we used the small-molecule RITA to stabilize p53 and induce its activity in ASCs. Our study reveals that RITA-stabilized p53 inhibits the PGE₂-mediated expression of PII and induces its activity in ASCs (44). Perinuclear p53 represents inactive p53 (45). Our findings also demonstrate that PGE₂ causes an increase in ASC proliferation. Considering the important role of p53 in regulating cell-cycle arrest and apoptosis, it is possible that this PGE₂-mediated increase in cell proliferation is mediated by the downregulation of p53.

Implications
Implications for interactions among p53, estrogen, and ER in breast cancers
In contrast to ER⁻ breast cancers, which frequently harbor mutations in the p53 tumor suppressor, ER⁺ breast cancers are predominantly wild-type for p53. In ER⁺ breast cancers, the interaction between p53 and ER demonstrated the repressive effect of ER on the p53-mediated apoptotic response induced by DNA damage (6). Overexpressed aromatase results in increased estrogen biosynthesis and breast tumor growth in ER⁺ postmenopausal breast cancers. Estrogen and ERα are negative regulators of p53 and are able to inactivate p53 in tumor epithelial cells. In addition, estrogen increases p53–ERα interactions (52). This mechanism may also be relevant to observations in Li–Fraumeni–associated breast cancers, as the majority of germ line TP53-mutated breast cancers are hormone receptor–positive (36). Interestingly, Duong and colleagues found that Mdm2 directly interacts with ERα in a ternary complex with p53 and is involved in the regulation of ERα turnover. RITA treatment caused dissociation of the p53/Mdm2/ERα complex, which leads to a co-stabilization of p53 and ERα proteins in breast cancer cells (53). However, it is disputable that ERα is expressed in adipose stromal cells (54, 55). The lack of ERα expression was observed by Knowler and colleagues, whereas Booth and colleagues detected ERα transcript and protein expression in ASCs (55, 56). Therefore, the mechanism of p53, estrogen, and ERα in ASCs needs to be determined.

Implications for the treatment of estrogen-dependent breast cancer
Because of its established role as a tumor suppressor, an enormous effort has been made to target p53 for the treatment of breast cancer. Current approaches for p53 targeting include wild-type p53 activation and restoration and mutant p53 reactivation. There are several strategies to target p53, including...
inhibition of p53 degradation through disrupting the p53–HDM2 interaction, gene therapy that introduces wild-type p53 into cancers, restoration of mutant p53 to wild-type p53, elimination of mutant p53, and p53-based vaccines (reviewed in ref. 57). The conventional strategies for restoration of p53 function in tumors are aimed at protecting wild-type p53 from proteasomal degradation. Most inhibitors of p53–HDM2 interactions have extremely high binding affinities to HDM2. Non-HDM2-targeting p53 modulators have also been considered as potential therapeutics for cancers (58). For instance, p28 (NSC745104) is the first non–HDM2-mediated peptide inhibitor of p53 ubiquitination, and a clinical phase I trial has showed that p28 was tolerated with no significant adverse events, demonstrating a proof-of-concept for this new class of cancer treatment (58).

Nutlin and RITA are both considered as potential therapeutics for wild-type p53 cancers. Nutlin-3 is a potent and selective inhibitor of HDM2–p53 interactions by binding to HDM2. In contrast, RITA is a p53 activator that binds to p53 thereby preventing HDM2–p53 interactions and proteasomal degradation (45). A mechanistic study revealed that RITA-stabilized p53 abrogates key oncogenic pathways such as Akt and c-Myc in cancer cells (59). Interestingly, human fibroblasts and lymphocytes were shown to be less sensitive to the proapoptotic effects of RITA than tumor cells, whereas our studies demonstrate that RITA, at these concentrations, inhibits estrogen production in breast ASCs. This suggests that p53 could be targeted to inhibit aromatase and breast cancer cell growth. These HDM2 inhibitors or p53 activators have been suggested to be only effective in wild-type p53 containing cancers. However, our results demonstrate that in breast ASCs, where p53 mutations are rare, stimulation of p53 would inhibit estrogen production and hence provide a novel strategy for the treatment of estrogen-dependent breast cancer. Reports have also demonstrated p53-independent effects of RITA, and although effects on cell viability were not observed in our studies, others have previously found that 1 μmol/L RITA can cause cell death in p53-null cells (60).

Our results also demonstrate that PGE$_2$ suppresses p53 expression in ASCs. Whether this also occurs in breast cancer cells remains to be determined; however, previous studies have demonstrated that overexpression of COX2, the rate-limiting step in prostaglandin synthesis, is associated with the repression of p53 target genes in normal human mammary epithelial cells (61). Inhibition of COX2 using nonsteroidal anti-inflammatory drugs is associated with a decreased breast cancer risk and has been proposed as a means of breast-specific aromatase inhibition. Therefore, COX2 inhibitors may be useful for the treatment of estrogen-dependent breast cancers by restoring p53 expression and inhibiting estrogen production and cancer cell growth.

**Implications for p53 status and ER$^+$ breast cancer therapies**

Aromatase inhibitors and antiestrogens are most common therapies for estrogen-dependent breast cancers. Aromatase inhibitors have been reported to be more effective than the antiestrogen tamoxifen in treating breast cancer. Studies have reported the effect of these therapies on p53 expression and activity. For instance, Ichikawa and colleagues found that the levels of wild-type p53 in tamoxifen-treated breast cancer cells increased in a time-dependent and a dose-dependent manner (62). Another report also demonstrated that aromatase inhibitors letrozole, anastrozole, and 4-hydroxyandrostenedione and antiestrogens tamoxifen and faslodex induced growth suppression and cell-cycle arrest that was associated with upregulation of wild-type p53 protein and mRNA levels (63).

Nearly one third of breast tumors carry mutations in the p53 gene, which are correlated with high histologic grade and rapid progression (64). Recently, studies in whole-genome analysis indicated that p53 mutations were significantly correlated with aromatase inhibitor resistance (65). p53 protein accumulation is found to be associated with aromatase inhibitors resistance, and nuclear accumulation is suggestive of mutations in the TP53 gene. p53 has been considered as a prognostic biomarker in oncology, with p53 overexpression being associated with a shorter disease-free interval, and both early and late recurrence in ER-positive postmenopausal breast cancer patients treated with aromatase inhibitors (66, 67). Taken together, p53 status has potential prognostic value for estrogen-dependent postmenopausal breast cancer.

**Conclusions**

The tumor suppressor function of p53 in breast cancer is multifaceted; it has established roles in stimulating cell-cycle arrest and apoptosis and emerging roles in the control of metabolic function. We now show that p53 is a key regulator of aromatase and estrogen production in the breast adipose tissue. Targeting p53 may therefore be a novel strategy for the treatment of estrogen-dependent breast cancer.

**Disclosure of Potential Conflicts of Interest**

No potential conflicts of interest were disclosed.

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**References**


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Correction: p53: Protection against Tumor Growth beyond Effects on Cell Cycle and Apoptosis

In this article (Cancer Res 2015;75:5001–7), which appeared in the December 1, 2015 issue of Cancer Research (1), there were errors in Fig. 1A: the arrow between PKA and LKB1 should have been an inhibitory line, and the arrows between LKB1 and AMPK were missing. The corrected figure appears below. The online journal has been updated and no longer matches the print.

Reference

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