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The NF κ B pathway promotes tamoxifen tolerance and disease recurrence in estrogen receptor positive breast cancers

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Abstract

The purpose of this study was to identify critical pathways promoting survival of tamoxifen-tolerant, estrogen receptor α positive (ER+) breast cancer cells, which contribute to therapy resistance and disease recurrence. Gene expression profiling and pathway analysis was performed in ER+ breast tumors of patients before and after neo-adjuvant tamoxifen treatment and demonstrated activation of the NF κ B pathway and an enrichment of EMT/stemness features. Exposure of ER+ breast cancer cell lines to tamoxifen, *in vitro* and *in vivo*, gives rise to a tamoxifen-tolerant population with similar NF κ B activity and EMT/stemness characteristics. Small molecule inhibitors and CRISPR/Cas9 knock out were used to assess the role of the nuclear factor κ B (NF κ B) pathway and demonstrated that survival of tamoxifen-tolerant cells requires NF κ B activity. Moreover, this pathway was essential for tumor recurrence following tamoxifen withdrawal. These findings establish that elevated NF κ B activity is observed in breast cancer cell lines under selective pressure with tamoxifen *in vitro* and *in vivo*, as well as in patient tumors treated with neo-adjuvant tamoxifen therapy. This pathway is essential for survival and regrowth of tamoxifen-tolerant cells, and, as such, NF κ B inhibition offers a promising approach to prevent recurrence of ER+ tumors following tamoxifen exposure.

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Keywords

ER+ breast cancer; tamoxifen tolerance; tumor recurrence; NFκB pathway

Introduction

Over 70% of breast tumors express estrogen receptor α (ER) and are typically treated with endocrine therapies, such as tamoxifen or aromatase inhibitors. Despite the relative success of endocrine agents, resistance to treatment is common, resulting in metastatic relapse for which there is no cure. In fact, over 50% of recurrences and 2 out of every 3 deaths from ER + breast cancer will occur after completing 5 years of adjuvant endocrine therapy (1, 2). One hypothesis to explain these late recurrences in ER+ disease, is that a small population of tumor cells “persist” in the presence of tamoxifen, for years to even decades, and eventually grow out as a recurrent tumor. These recurrent tumors are frequently therapy resistant, metastatic and lethal. Thus, one way to prevent lethal recurrence is to eradicate the population of persister cells. However, little is known about the nature of these cells in ER+ breast cancers or how they eventually contribute to tamoxifen resistance and disease recurrence.

The notion of a drug-tolerant persister cell population was first introduced in lung cancers treated with EGFR inhibitors (3) and subsequently described in other cancers (Reviewed in (4)). A drug-tolerant phenotype was shown to be transiently acquired via an altered chromatin state to protect the population from eradication by targeted therapeutics. Tolerant cells can display considerable plasticity with the ability to revert back to drug sensitivity once the drug is removed or to develop complete drug resistance (Reviewed in (5)). However, in breast cancer and particularly in ER+ breast cancer, the concept of drug tolerance is less well developed. For ER-negative breast cancers, some examples of treatment-induced drug tolerance have been reported. These include HER2-amplified breast cancer cells treated with lapatinib, which acquire dependency on the lipid hydroperoxidase GPX4 (6). In triple negative breast cancer, residual tumor cells remaining after treatment with doxorubicin and cyclophosphamide chemotherapies adopt a reversible drug-tolerant state that does not involve clonal selection, and pharmacologic inhibition of oxidative phosphorylation delayed residual tumor regrowth (7).

In ER+ breast cancers, traditional approaches to model therapy failure have largely focused on prolonged exposure of ER+ breast cancer cells to tamoxifen or estrogen deprivation. This approach is necessary to reach a stable resistant phenotype but may fail to elucidate early cellular adaptations that occur under therapeutic selection and that can contribute to the eventual development of resistance. While it is known that diverse mechanisms that give rise to endocrine therapy resistance, including perturbations to ER signaling complex (8, 9), crosstalk between ER and growth factor receptor signaling (10), and/or mutations in ESR1 gene (11, 12), it is not clear how these various mechanisms arise. Importantly, it was shown in lung cancer that multiple clones, each with different resistance mechanisms, can arise from a drug-tolerant/persister population, suggesting that drug-tolerant tumor cells are not limited in their evolution; rather, they may serve as a latent reservoir of cells capable of

giving rise to multiple resistance mechanisms (13). Whether this occurs in ER+ breast cancer is unknown. Thus, the purpose of this study was to examine early changes in ER+ breast cancer cells and tumors under the selection pressure of tamoxifen and identify mechanisms that may contribute to their therapy tolerance. Clearly, eradication of a tamoxifen-tolerant tumor cell population would represent a highly promising new therapeutic strategy in the treatment of ER+ breast cancer.

In this report, we demonstrate that tamoxifen-tolerant persister cells can be identified in ER+ breast cancer cell lines, xenograft tumors, and samples from breast cancer patients. In each of the studied settings, activation of the pro-inflammatory NF κ B pathway and a gain of epithelial-to mesenchymal (EMT)/stem-like features are observed. The NF κ B pathway is required for survival and regrowth of tamoxifen-tolerant cells, as well as tumor recurrence. Our findings provide compelling evidence that pharmacological targeting of the NF κ B pathway can be exploited to eradicate tamoxifen-tolerant cells to prevent disease recurrence.

Materials and Methods

Reagents

4-hydroxy-tamoxifen (4OHT) and dimethyl fumarate (DMF) were purchased from Sigma. IKK7 was purchased from Selleck Chemicals. TNF α was purchased from R&D Systems. The antibodies for ER α (8644), p52 (37359), c-Rel (4727), RelB (4922), and TBP (8515) were purchased from Cell Signaling. The antibodies for p65 (sc-372) and p50 (sc-8414) were purchased from Santa Cruz. The antibody for β -actin (A5441) was purchased from Sigma.

Gene Expression Analysis in Patient Tumor Samples

Tumor gene expression data was obtained from breast cancer patients (details in Supplementary Table 1) enrolled in a pre-operative window trial ([ClinicalTrials.gov](https://clinicaltrials.gov/ct2/show/study/NCT00738777) Identifier: [NCT00738777](https://clinicaltrials.gov/ct2/show/study/NCT00738777)), in which patients received an oral loading dose of 40 mg of tamoxifen twice daily for the first seven days, followed by a daily dose of 20 mg until surgery. The clinical trial protocol was approved by the local medical ethical authorities, in accordance with appropriate international ethical guidelines, and written informed consent was obtained from all patients. A core needle biopsy of the tumor was taken prior to treatment (n=62) and post-treatment tumor material (n=40) was obtained during surgery 20.7 ($\pm$ 9.6) days later. Paired material was available for 27/74 patients. RNA was isolated and hybridized to a custom full genome array by Agendia as previously described (14). Feature Extraction software v11.5.1.1 was used to quantify fluorescent intensities and those were normalized using DataPrint software v1.15. Missing values were imputed with knn=10, data was batch corrected for date of RNA extraction using ComBat from the R package sva, and the median value was used in case multiple probes mapped to a single gene. Expression data are available through Gene Expression Omnibus (GEO accession number GSE147271). Differential analysis between pre- and post-tamoxifen samples was performed with Limma v.3.37.3. Expression changes were considered significant if $FC < -1$ or $FC > 1$ and $adj.P.Val < 0.005$ (Supplementary Table 2). Results were interpreted with GSEA software with MsigDBv7.0 Hallmark gene sets on default settings (15) (Supplementary Table 3). GSEA

enrichment plots were generated with a custom R script by Dr. Thomas Kuilman (<https://github.com/PeeperLab/Rtoolbox/blob/master/R/ReplotGSEA.R>).

Cell Lines, Culture Conditions and Drug Treatments

The human ER+ breast cancer cell lines MCF-7, T47D, ZR75-1, and BT474, were obtained from Dr. Debra Tonetti (University of Illinois at Chicago). HCC1428 cells were purchased from ATCC. These cells were routinely maintained in RPMI 1640 media (Invitrogen Life Technologies) with phenol red supplemented with 10% FBS, 1% non-essential amino acids, 2 mmol/L L-glutamine, 1% antibiotics penicillin-streptomycin, and 6 ng/mL insulin. NF κ B-RE-GFP cells were obtained from Dr. Elaine T. Alarid (University of Wisconsin-Madison). These cells were generated from MCF-7 cells stably transfected with 3X- κ B reporter, which has three enhancer elements (Ig κ , I κ B α and the palindromic consensus sequence) upstream of the thymidine kinase promoter driving green fluorescent protein (GFP) expression, as described in (16). All cell lines are routinely authenticated by short tandem repeat analysis and tested for mycoplasma using LookOut Mycoplasma PCR Detection Kit (Sigma).

Clonogenic Assay

Cells were seeded at clonogenic density of 1,000 cells per well in 6-well plates in phenol red-proficient media with 10% complete FBS. After overnight attachment, cells were treated as indicated. Media was changed and fresh treatment added every 3–4 days for 2 weeks. After 2 weeks, colonies were stained with 1% crystal violet in methanol and water (1:4) and imaged using ImageJ software. Colony area was quantified automatically using the ColonyArea ImageJ plugin (17). Alternatively, plates were scanned with Celigo Imaging Cytometer (Nexcelom Bioscience). Confluence ratio is calculated in brightfield using the confluence application. For GFP+ cell, GFP expression is measured in green fluorescence using the confluence application.

RT-Quantitative PCR (QPCR)

Total RNA was isolated using Trizol and RT-QPCR performed as previously described (18). Fold change was calculated using the $\Delta\Delta$ Ct method with 36B4 serving as the internal control. All QPCR primers used were validated and previously reported (18).

FACS Analysis

Clonogenic cells were trypsinized, washed and re-suspended in Hank's Balanced Salt Solution buffer + 2% FBS. Flow cytometry of live cells was performed to quantify GFP+ cells using a Fortessa instrument (BD Biosciences). Sorting of live cells to isolate the GFP+ population was run using a MoFlo cell sorter (Beckman Coulter).

Western Blot

Whole cell extracts were prepared using the M-PER reagent (Thermo Scientific). Nuclear lysates were collected using NE-PER kit (Thermo Scientific). Proteins were separated by SDS-PAGE (Bio-Rad Laboratories), transferred to nitrocellulose membranes (Thermo Scientific), blocked for 1 hour in buffer containing 5% nonfat dry milk (Lab Scientific) or 5% bovine serum albumin, and incubated with the appropriate primary antibody overnight.

The next day, secondary antibody was applied and the signal visualized on a Molecular Imager ChemidocXRS (Bio-Rad Laboratories) using the Pierce Supersignal West Pico chemiluminescent substrate (Thermo Scientific). Images were obtained using Quantity One software (Bio-Rad Laboratories).

Aldefluor Assay

ALDH1 activity assay (Stem Cell Technologies) and FACS analysis were conducted according to manufacturer's instructions.

Mammosphere (MS) assay

Breast cancer cells were seeded at single cell density on low attachment plates in media described by Dontu et al. (19), supplemented with 1% methyl cellulose to prevent cellular aggregation. After 7 days, the number of MS 75µm in diameter was determined using a Celigo imaging cytometer, and MS forming efficiency (MFE) was calculated.

Immunofluorescence and Microscopy

Cells were seeded on non-coated glass coverslips and treated according to the clonogenic assay protocol. After treatment, cells were fixed with 4% paraformaldehyde for 15 minutes and permeabilized using 0.2% Triton X-100 for 20 minutes. Cells were then blocked with 1x casein for 1 hour and incubated with the primary antibodies for 1 hour. After washing with TBS, coverslips were incubated with the secondary antibodies for 1 hour: Alexa Fluor 594 (Thermo Scientific #A21207) and Alexa Fluor 488 (Thermo Scientific #A-11001). Cells were then washed with TBS and mounted with ProLong Gold anti-fade reagent (Life Technologies). Images were acquired at ×63 magnification using a Leica DMi8 microscope (Leica).

In vivo Studies

All mouse experiments were carried out at the University of Illinois at Chicago animal facility, and conducted in accordance with institutional procedures and guidelines, and after prior approval from the Institutional Animal Care and Use Committee. Female athymic nude mice (nu/nu), aged 5 week-old, were purchased from Harlan. Five million MCF-7 cells were injected orthotopically into the thoracic mammary glands and supplemented with estrogen pellets. Tumor formation was monitored by palpitation and once tumors were detected (~0.1 cm² in size), mice were randomized into either vehicle control or treatment groups. To study NFκB pathway activation, mice were treated with either vehicle control or tamoxifen (500 µg/animal s.c., in peanut oil) for 5 days/week for 2 weeks (n=3 tumors per group). To study tumor recurrence, mice were treated with vehicle, DMF (30mg/kg, oral gavage suspended, in 0.8% methyl cellulose), tamoxifen (500 µg/animal s.c., in peanut oil), or the combination of DMF with tamoxifen daily 5 days/week for 4 weeks (n=10 tumors per group). Tumor sizes were measured daily with an electronic caliper and tumor area was calculated as $\text{length}/2 \times \text{width} \times \pi$.

Statistical Analysis

Data are presented as mean $\pm$ SEM from at least three independent determinations. Statistical analysis consisted of 1- or 2-way ANOVA followed by Tukey posttest, or t-test, as appropriate.

Results

Early changes in pathway activation status in ER+ tumors from patients treated with neo-adjuvant tamoxifen therapy

Data from a neo-adjuvant window trial allowed us to investigate early tamoxifen-induced effects in ER+ breast tumors (Fig. 1A). Patients underwent a core needle biopsy of the tumor prior to treatment and subsequently received tamoxifen until the date of routine surgery at an average of 21 days later. Patient characteristics are described in Supplementary Table 1. Gene expression was generated using tumor tissues isolated before and after treatment. GSEA analysis identified a number of pathways regulated by tamoxifen treatment including tumor necrosis factor (TNF) signaling via the pro-inflammatory NF κ B pathway (Fig. 1B–D, Supplementary Table 3, Supplementary Fig. 1). Although the NF κ B pathway has previously been implicated in endocrine resistance (20–22), these findings in patient tumors suggest that even short-term tamoxifen treatment may enhance NF κ B signaling in ER+ tumors. We examined whether this change may be the result of an increase in immune cell infiltration into the tumors following TAM treatment. However, no significant difference in the percentage of tumor infiltrating lymphocytes or specific immune cell subset (CD4, CD8, and CD68) was observed after TAM treatment (Supplementary Fig. 2), suggesting altered NF κ B signaling in the tumor cells.

Tamoxifen exposure results in NF κ B activation in cell lines

To determine if changes observed in tumors from patients treated with tamoxifen can be modeled *in vitro*, clonogenic assays were performed using ER+ breast cancer cell lines cultured in growth media (phenol-red proficient + 10% FBS) in the presence or absence of 4-hydroxytamoxifen (4OHT). As shown in Fig. 2A and Fig. 2B, 4OHT caused an overall suppression of clonogenic growth, as expected. However, in each cell line tested, a number of tamoxifen-tolerant clones were able to grow under the selective pressure of 4OHT. Multiple rounds of clonogenic assays were performed and demonstrated that cells become increasingly more refractory to 4OHT exposure (Fig. 2C), suggesting that the tamoxifen-tolerant population may be a precursor to the development of resistance.

The unsupervised discovery of NF κ B as the top-enriched pathway in tumors from patients treated with neo-adjuvant tamoxifen therapy (Fig. 1) motivated us to probe this pathway in tamoxifen-tolerant cells. Indeed, several approaches revealed that the NF κ B pathway is activated in tamoxifen-tolerant cells *in vitro*, similar to the activation observed in patient samples. RT-QPCR analysis showed elevated NF κ B-target gene (23–25) expression in both MCF-7 (Fig. 2D) and T47D cells (Supplementary Fig. 3A). In addition, a cell line stably expressing an NF κ B-RE driven GFP reporter demonstrated an increase in the percentage of GFP+ cells in response to 4OHT, implying enrichment of NF κ B-active cells upon continuous 4OHT exposure (Fig. 2E). Finally, MCF-7 xenograft tumors in mice exposed to

tamoxifen also demonstrated an increase in NF κ B-target gene expression (Fig. 2F). Together, these findings suggest that tamoxifen exposure gives rise to a tamoxifen-tolerant population, and that increased NF κ B signaling is an early event occurring in these cells both *in vitro* and *in vivo*, as was observed in human tumors.

Tamoxifen-tolerant cells require NF κ B signaling for their survival and regrowth

To understand the role of NF κ B activation in tamoxifen-tolerant cells, we utilized two NF κ B pathway inhibitors – IKK7 (an IKK α / β kinase inhibitor (26)) and DMF (an inhibitor of p65 nuclear translocation and DNA binding (27)). Both inhibitors significantly reduced the outgrowth of colonies, and in particular of tamoxifen-tolerant colonies (Fig. 3A). Similar results were observed in T47D cells (Supplementary Fig. 3B). Given that NF κ B inhibitors block colony outgrowth, we hypothesized that this inhibition would be most-relevant in preventing cell and tumor regrowth following cessation of tamoxifen treatment. To test this, tamoxifen withdrawal studies were conducted both *in vitro* and *in vivo*. The *in vitro* approach demonstrated that regrowth of cells following withdrawal of tamoxifen was substantially attenuated by IKK7 and DMF (Fig. 3B). Similarly, MCF-7 xenograft tumor growth *in vivo* following tamoxifen withdrawal was examined. Seven out of 10 xenograft tumors displayed regrowth within 30 days, whereas 0 out of 10 tumors recurred if DMF and tamoxifen were administered together (Fig. 3C). Importantly, DMF monotherapy had no effect on tumor growth, suggesting that i) there is no indication of NF κ B-dependence in growing tumors in the absence of tamoxifen, and ii) the presence of tamoxifen is necessary for the induction of NF κ B activity and dependence, thereby allowing for the growth inhibition by DMF. These findings strongly suggest that the activation of NF κ B following tamoxifen exposure is required for the survival of a cell population that is capable of giving rise to a recurrent tumor.

NF κ B family members p65 and p50 are required for tamoxifen-tolerant cell survival

We next investigated which NF κ B transcription factor family members may be involved in the survival of tamoxifen-tolerant cells. Western blot analysis revealed that nuclear p65 and p50 levels are increased after 2 weeks of exposure to 4OHT, whereas total levels were unchanged (Fig. 4A–4C). Similar results were observed in T47D cells (Supplementary Fig. 3C). This elevation in nuclear p65 and p50 is accompanied by reduced protein expression of the NF κ B signaling inhibitor I κ B α (Fig. 4B), which acts to sequester inactive p65 and p50 in the cytoplasm, suggesting a mechanism by which this pathway is activated. To investigate possible causal involvement of p65 and p50, these genes were knocked out individually in MCF-7 cells using CRISPR-Cas9 (Supplementary Fig. 4). A significant reduction in the ability of tamoxifen-tolerant clones to survive was observed (Fig. 4D). These findings suggest that p65 and p50 are critical drivers of tamoxifen-tolerance in ER+ breast cancer cells.

NF κ B-positive cell retain ER but are insensitive to tamoxifen

To understand how the NF κ B pathway is activated upon tamoxifen exposure, we first asked whether 4OHT could directly affect the pathway. Short-term exposure of MCF-7 cells to 4OHT suppressed ER-target genes, as expected, but did not directly stimulate endogenous NF κ B-target genes or exogenous NF κ B-RE-GFP reporter activity (Supplementary Fig. 5),

suggesting that the effect is not direct. Rather it appears that NF κ B-positive cells, based on elevated NF κ B-RE-driven GFP expression, grow at a similar rate in the presence or absence of 4OHT, whereas NF κ B-negative cells are growth suppressed by 4OHT (Fig. 5A). As a result, the NF κ B-positive cell population expands over time with 4OHT treatment (Fig. 5B). Are the tamoxifen-insensitive NF κ B-positive cells still ER+? To address this, we examined ER expression by QPCR (Fig. 5C), and found comparable ER mRNA levels between the NF κ B-positive and NF κ B-negative cell populations. These results were confirmed on the protein level using immunofluorescence (IF) for ER and GFP, showing that NF κ B-positive cells readily express ER protein (Fig. 5D). Furthermore, although NF κ B-positive cells failed to respond to 4OHT, they do proliferate upon estrogen (E2) treatment, suggesting they retain functional ER signaling while being insensitive to tamoxifen (Fig. 5E).

Tamoxifen-tolerant cells display EMT/stem-like features

To examine whether all NF κ B-positive cells give rise to tamoxifen tolerance, we sorted GFP-positive and -negative populations after two weeks of 4OHT treatment. We found that both populations give rise to a similar number of tamoxifen-tolerant colonies (Fig. 6A), suggesting that each population reverts back to the naive population's response to 4OHT. Moreover, a similar level of NF κ B activity was observed in the secondary clones, indicating that GFP-negative cells give rise to GFP-positive cells, and vice versa, following a second round of selection (Supplementary Fig. 6). This data suggests that cell plasticity may be an underlying feature of tamoxifen-tolerance. Both EMT and stemness have overlapping de-differentiation features and display significant plasticity (28–31). Given that EMT and stemness-associated genes were also elevated in samples from patients treated with tamoxifen (Fig. 1B, 6B), we decided to investigate the EMT and stem-like properties of tamoxifen-tolerant cells. We confirmed that expression of multiple factors associated with EMT and stemness were increased following 4OHT exposure (Fig. 6C). This observation was confirmed in tamoxifen-tolerant T47D cells (Supplementary Fig. 3D). Moreover, ALDH1 activity, a marker of stemness in breast cancer (32), was elevated in tamoxifen-tolerant tumor cells in an NF κ B-dependent manner (Fig. 6D). In addition, NF κ B-positive cells were more capable of forming mammospheres than NF κ B-negative cells (Fig. 6E). Together, these findings suggest that a distinct EMT/stem-like cell population expands in an NF κ B-dependent manner in response to tamoxifen exposure, and that the plasticity of this population may contribute the development of tamoxifen resistance through various mechanisms.

Discussion

This study provides novel mechanistic insights into tamoxifen-tolerance in ER+ breast cancer. We identified a tolerant cell population, driven by the NF κ B pathway, in all biological systems studied (ER+ breast cancer cells, xenograft tumors, and patient samples). We also identified a mechanism underlying the observed tolerance to tamoxifen – the expansion of an NF κ B-active, EMT/stem-like population of cells that express functional ER but are insensitive to tamoxifen. Rather, these cells are reliant on NF κ B transcription factors (p65 and p50) for survival and growth. The expansion of a tamoxifen-tolerant population under the selective pressure of tamoxifen is highly clinically relevant, as we have

demonstrated that these cells become increasingly more refractory to growth suppression by tamoxifen, and retain their regrowth capability *in vitro* and *in vivo* to support tumor recurrence.

In other fields of oncology, drug-tolerant persister cells have been reported previously. Some of the reported strategies that these cells utilize for survival include (as reviewed in (4)): negligible growth and low cell cycling, altered metabolism, epigenetic reprogramming, stem-like properties, low immunogenicity, and modulation of their microenvironment. Here, we reveal a novel feature of drug-tolerant persister cells in a breast cancer-specific context: the expansion of an NF κ B+ ER+ population with short-term selective pressure from tamoxifen treatment. The elevated NF κ B activity in these cells does not appear to be directly stimulated by tamoxifen, since short term treatment with 4OHT does not up-regulate NF κ B target genes. Rather, it appears that tamoxifen allows a subpopulation of the tumor cells with NF κ B activity to expand. The reliance on canonical NF κ B signaling as an initial survival strategy employed by ER+ tamoxifen-tolerant cells is in line with prior studies reporting that primary ER+ tumors with higher levels of constitutive NF κ B activation are more likely to acquire treatment resistance and metastasize, and are associated with poor outcome (20–22). Also of interest is our finding that NF κ B+, tamoxifen-tolerant cells retain functional ER, which is stabilized in the nucleus upon tamoxifen treatment (in line with previous reports (33)), but is insensitive to tamoxifen antagonism. Several potential mechanisms could explain the lack of ER response to tamoxifen. For example, post-translational modifications of ER, such as S305 phosphorylation or K303 acetylation, could explain the loss of tamoxifen antagonism (34–36). Alternatively, these cells may gain a reliance on NF κ B signaling, thereby masking the growth inhibitory effect of tamoxifen.

Current thinking in the field of endocrine therapy resistance suggests that resistance may occur *de novo* (i.e. prior to exposure) or can be acquired over the course of therapy, which typically lasts for 5–10 years. In acquired resistance, it is thought that tamoxifen initially acts as an ER-antagonist in breast cancer to switch off growth, but during the years of exposure, residual cancer cells can mutate and adapt to grow in a tamoxifen environment (37). We propose two possible scenarios by which can NF κ B-driven, stem-like/plastic, tamoxifen-tolerant cell population could contribute to resistance. First, there may an intrinsic subpopulation of cells in some ER+ tumors that have active NF κ B, expand rapidly in response to tamoxifen treatment, and contribute to *de novo* resistance. A similar selection mechanism was recently proposed for aromatase inhibitor tolerance/resistance, where an enrichment of cells bearing ESR1 mutations could rapidly be detected in tumors of women treated with aromatase inhibitors (38). Alternatively, tolerance may be an early step in the development of acquired endocrine therapy resistance. The long-term survival of an NF κ B-driven, tamoxifen-tolerant cell population that no longer relies on ER for growth and survival could allow for adaptation, the development of other resistance mechanisms, and tumor recurrence.

Similar to other reports of a transient and reversible drug-tolerant state in other tumor types (3), and consistent with its stem-like features, the tamoxifen-tolerant phenotype in breast cancer displays significant cellular plasticity. Importantly, NF κ B is driving this plastic stemness state as indicated by ALDH1 activity and mammosphere forming capacity. This is

consistent with other reports of NF κ B promoting stem-like phenotypes in breast cancer (39, 40), and cancer stem cells' reliance on inflammatory cytokines and networks (41, 42). It is becoming clearer that cancer stem cells display remarkable genetic and phenotypic heterogeneity, and a metastable EMT program bestows this plasticity (43). In tamoxifen-tolerance, we identified an ER⁺ EMT/stem-like population driven by the NF κ B pathway that gives rise to tumor recurrence. It should be noted that our findings appear to indicate a partial EMT since E-cadherin levels were not altered in tamoxifen-tolerant cells (data not shown). This phenomenon has been referred to as 'partial EMT' where cells are characterized by a hybrid epithelial/mesenchymal state, where they maintain cell-cell adhesion and expression of proteins such as E-cadherin, but also express several EMT associated genes (44, 45). Additionally, recent clinical studies demonstrated partial EMT in carcinoma cells allows for a rapid and transient adaptation to cytotoxic or molecularly targeted therapy (46).

One important implication of our findings is that targeting NF κ B in addition to standard ER-blocking endocrine drugs could be a beneficial therapeutic strategy to prevent the development of resistance and eventual recurrence. Unfortunately, targeting NF κ B in the clinic has proved challenging. While multiple NF κ B inhibitors have been investigated, most have failed in the clinic due to the innate immune system's reliance on NF κ B, as well as considerable toxic side effects (47). This raises the issue of how to safely and effectively inhibit the NF κ B pathway. One option is to use DMF (Tecfidera®), an orally bioavailable drug approved by the FDA in 2013 to treat multiple sclerosis. DMF is safe in humans and shows none of the immune-suppressive side effects (48). Alternatively, a water soluble parthenolide analog has gained some attention as a safe and effective NF κ B inhibitor in other types of cancer, such as prostate, bladder and lung (49, 50) and may be potentially useful in targeting tamoxifen-tolerant cells.

In summary, the findings reported here describe a novel tamoxifen-tolerant, ER⁺, NF κ B-dependent cell population with EMT/stem-like features that emerges in ER⁺ breast cancer cell lines, xenograft tumors and patient tumors upon tamoxifen treatment. Targeting these cells using NF κ B inhibitors may address the urgent unmet need of how to prevent the development of endocrine resistance and metastatic relapse in tamoxifen-treated breast cancer patients.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Implications

Understanding initial changes that enable survival of tamoxifen-tolerant cells, as mediated by NF κ B pathway, may translate into therapeutic interventions to prevent resistance and relapse, which remain major causes of breast cancer lethality.

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Figure 1.

NF κ B pathway is active in patients treated with neo-adjuvant tamoxifen therapy. **A**, Setup of a neo-adjuvant trial in which patients with small ER+ breast tumors received tamoxifen for several weeks. Pre-treatment biopsies were compared to surgical specimens taken several weeks later. **B**, Top five enriched gene sets (FDR q-value < 0.05) following tamoxifen treatment when comparing surgical specimens to pre-treatment biopsies. **C**, GSEA enrichment plot of the 'TNF α signaling via NF κ B' geneset. **D**, Heatmap of genes in the 'TNF α signaling via NF κ B' geneset that were found to be significantly differentially expressed when comparing surgical specimens to pre-treatment biopsies.

Figure 2.

Tamoxifen-tolerant cell populations display elevated NFκB activity *in vitro* and *in vivo*. **A**–**B**, Clonogenic growth was conducted in ER+ breast cancer cell lines cultured in growth media (GM) in the presence or absence of 1μM 4-hydroxytamoxifen (4OHT). Dissociated single cells were seeded at clonogenic density and re-treated twice weekly for 2 weeks. Colonies were then fixed and stained with crystal violet. Representative pictures of MCF-7 cells are shown (**A**). Colony confluence (area covered by colonies) was quantified with Celigo imager (**B**). Data for each cell line is normalized to the GM control, which was set to 100%. **C**, Clonogenic growth following multiple rounds of 2-week treatments with 4OHT as described in (**A**) were quantified in MCF-7 cells. Data is normalized to GM control.

* $P < 0.05$. **D**, MCF-7 cells were seeded and treated as in (**A**) for 2 weeks. NFκB-target genes are measured by RT-QPCR. **E**, MCF-7 cells stably transfected with 3x κB-RE-GFP reporter are treated as in (**A**) with GM $-/+$ 1μM 4OHT for 2 weeks. The percentage of GFP+ cells was determined by FACS. **F**, NFκB-target genes were measured in MCF-7 xenograft tumors. Mice were randomized into treatment groups of either vehicle control or tamoxifen (500 μg/animal s.c. in peanut oil) and treated for 2 weeks. After treatments, tumors were excised and RNA isolated. pS2 was used as a control ER-target gene. * $P < 0.01$, ** $P < 0.005$, *** $P < 0.001$.

Figure 3.

NFκB pathway is required for the survival and regrowth of tamoxifen-tolerant cells *in vitro* and *in vivo*. **A**, NFκB pathway inhibitors (IKK7 and DMF) alone or in combination with 4OHT were added to MCF-7 cells treated as described in Fig. 1A. Data was normalized to own controls, each set to 100%. **B**, MCF-7 cells were treated with 4OHT, IKK7 (1μM), or DMF (20μM) alone or in combination for 2 weeks. After 2 weeks, all drugs were withdrawn and regrowth (% confluence) was monitored by Celigo cell imager. **C**, MCF-7 xenograft tumor growth curves are shown for mice treated with: vehicle (Veh), DMF, tamoxifen (Tam), and Tam+DMF for 4 weeks, and then monitored for an additional 6 weeks after all therapies were withdrawn. Tumor recurrence between Tam vs Tam+DMF is significantly different, $p=0.0015$ using a Fisher's exact test analysis. End point comparison of mean tumor area ($\text{length}/2 \times \text{width} \times \pi$) for Tam vs Tam+DMF is indicated. *** $P<0.001$.

Figure 4.

Nuclear p65 and p50 are required for the survival of tamoxifen-tolerant cells. **A-C**, Western blot analysis of nuclear (**A**) or whole cell lysates (**B**) of MCF-7 cells treated as in Fig. 1A are shown. TBP or β-actin served as loading controls. Densitometry quantitation is shown (**C**). N-Nuclear, T-total. **D**, Clonogenic assay was conducted in MCF-7 parental wild type (WT) or in p65 or p50 CRISPR/Cas9 knock out clones. * $P < 0.01$, ** $P < 0.005$.

Figure 5.

Uninhibited outgrowth of NF κ B+ cells underlies tamoxifen tolerance. **A-B**, MCF-7- κ B-RE-GFP reporter cells were treated in GM $\pm$ 1 μ M 4OHT for 2 weeks. The outgrowth (confluence) of GFP+ cells (left panel) and GFP- (right panel) was monitored and quantified using a Celigo imager. **B**, The ratio of GFP+/total cells was calculated over the treatment period. **C**, ER expression was measured by RT-QPCR in sorted MCF-7- κ B-RE-GFP reporter cells treated with 1 μ M 4OHT for 2 weeks. **D**, Expression of ER (red) and GFP (green) was examined by immunofluorescence. DAPI staining of nuclei is shown in blue. **E**, The GFP+ cell population of MCF-7- κ B-RE-GFP reporter cell line was quantified in response to treatments with 1 μ M 4OHT and 10nM E2 for 2 weeks. NS, not significant, * P <0.01, ** P <0.005, *** P <0.001.

Figure 6.

Tamoxifen-tolerant cells have EMT/stemness features controlled by the NF κ B pathway. **A**, Sorted NF κ B⁺ vs NF κ B⁻ tamoxifen-tolerant cells based on GFP expression were reseeded for another round of clonogenic assay and quantified. NS, not significant. **B**, EMT pathway was enriched in patients treated with neo-adjuvant tamoxifen therapy. **C**, Expression of EMT and stemness factors were measured by RT-QPCR in MCF-7 clonogenic cells treated with GM $-/+$ 1 μ M 4OHT for 2 weeks. **D**, ALDH⁺ population measured by FACS in MCF-7 cells clonogenic cells treated with 1 μ M 4OHT for 2 weeks. Representative histograms for GM vs 4OHT are shown (right panel). Inhibitors, IKK7, 1 μ M, or DMF, 20 μ M, were added for the last week in culture. **E**, Mammosphere (MS) formation was quantified in sorted NF κ B⁺ vs NF κ B⁻ tamoxifen-tolerant cells. MS > 75 μ m in diameter were quantified and MS forming efficiency (MFE) was calculated. * P <0.01, ** P <0.005, *** P <0.001.