Conditional, Genetically Encoded, Small Molecule–Regulated Inhibition of NFkB Signaling in RPE Cells

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PURPOSE. Nuclear factor κB (NFkB) is a ubiquitously expressed, proinflammatory transcription factor that controls the expression of genes involved in cell survival, angiogenesis, complement activation, and inflammation. Studies have implicated NFkB-dependent cytokines or complement-related factors as being detrimentally involved in retinal diseases, thus making inhibition of NFkB signaling a potential therapeutic target. We sought to develop a conditional and reversible method that could regulate pathogenic NFkB signaling by the addition of a small molecule.

METHODS. We developed a genetically based, trimethoprim (TMP)-regulated approach that conditionally inhibits NFkB signaling by fusing a destabilized dihydrofolate reductase (DHFR) domain to an inhibitor of NFkB, IκBz, in ARPE-19 cells. We then challenged ARPE-19 cells with a number of stimuli that have been demonstrated to trigger NFkB signaling, including LPS, TNFα, IL-1β, and A2E. Western blotting, electrophoretic mobility shift assay, quantitative PCR, ELISA, and NFkB reporter assays were used to evaluate the effectiveness of this DHFR-IκBz approach.

RESULTS. This destabilized domain approach, coupled with doxycycline-inducibility, allowed for accurate control over the abundance of DHFR-IκBz. Stabilization of DHFR-IκBz with TMP prevented IL-1β, A2E-, LPS-, and TNFα-induced NFkB-mediated upregulation and release of the proinflammatory cytokines IL-1β and IL-6 from ARPE-19 cells (by as much as 93%). This strategy is dosable, completely reversible, and can be cycled “on” or “off” within the same cell population repeatedly to confer protection at desired time points.

CONCLUSIONS. These studies lay the groundwork for the use of destabilized domains in retinal pigment epithelium (RPE) cells in vivo and in this context, demonstrate their utility for preventing inflammatory signaling.

Keywords: NFkB, IκBz, destabilized domain, retinal pigment epithelium, inflammation

Nuclear factor κB (NFkB), a proinflammatory transcription factor, is fundamental to cellular innate immunity, and plays a central role in orchestrating an effective inflammatory response in the face of pathogenic and host-derived insults. At the ocular surface, it is clear that NFkB is required to neutralize bacterial and viral pathogens from subsequently compromising the eye and vision. However, mounting evidence suggests that aberrant, uncontrolled activation of NFkB in the retina may impact many forms of retinal degeneration. Yet methods to conditionally and specifically target NFkB signaling within certain cell layers in the retina are lacking. In this study, we sought to identify a genetically based, regulatable approach to limit NFkB signaling and validate its use in retinal pigment epithelium (RPE) cells.

NFkB activation is initiated by exposure to diverse stimuli such as interleukins (e.g., IL-1α, IL-1β), tumor necrosis factors (e.g., TNFα), or bacteria-derived cell wall components (e.g., lipopolysaccharide [LPS]). In turn, activated NFkB increases the synthesis of complement-related genes (e.g., complement component 3) as well as cytokines, such as IL-1β and IL-6. Additionally, NFkB activation provides the “priming step” for subsequent inflammasome assembly and release of mature forms of these cytokines. Classical initiation of NFkB activation originates by engagement of the aforementioned diverse stimuli with cell surface receptors, such as the IL-1 receptor (IL-1R), TNF receptor 1, or the toll-like receptor (TLR) 2/1. Activation of these receptors leads to phosphorylation, ubiquitination, and degradation of the inhibitor of NFkB, IκBz. Without IκBz, NFkB translocates to the nucleus wherein it induces transcriptional upregulation of inflammatory cytokines. Interestingly, IκBz is transcriptionally regulated by NFkB, thus providing a negative feedback loop for subsequently repressing NFkB activity by removing it from the nucleus.

Transient activation of NFkB under conditions of microbial or viral invasion is necessary to produce a cytoprotective inflammatory response that, due to feedback mechanisms, eventually resolves upon eradication of the insult. However, chronic, unregulated activation of NFkB has been linked to several inflammatory states, such as atherosclerosis, inflammatory bowel disease, arthritis, and cancer. Similarly, constitutive inflammasome activity is also correlated with a pathologic inflammatory state in diseases such as Alzheimer’s disease, gout, and age-related macular degeneration (AMD). Therefore, inhibition of either NFkB “priming” or inflammasome assembly has the potential to ameliorate phenotypes linked to many forms of chronic inflammation or even complement activation.
Increasing evidence links retinal degeneration and age-related retinal decline with classic markers of inflammasome activation. For example, the RPE from AMD patients with geographic atrophy or neovascularization exhibits increased nucleotide-binding oligomerization domain-like receptor family pyrin domain-containing 3 (NLRP3) staining at diseased sites. Moreover, components of drusen, such as oxidized low-density lipoprotein, double-stranded RNA, and amyloid β, are known activators of either NFκB priming or inflammasome assembly. Furthermore, N-retinylidene-N-retinyl-ethanolamine (A2E), the major phototoxic fluorescent component of lipofuscin, has been found to prime and activate the NLRP3 inflammasome in RPE cells, resulting in significant amounts of IL-1β production in isolated retinal cells and in Stargardt disease mice that lack ATP binding cassette subfamily A member 4 (ABCA4). We have chosen to focus on developing an approach for inhibiting the proinflammatory “priming” activity of NFκB in cultured human RPE cells as a proof of principle, while envisioning that this approach may ultimately serve as a potential therapeutic strategy for treating retinal diseases characterized by chronic inflammation.

To circumvent these potential issues, we reasoned that we could use a destabilized domain-based approach to control the steady-state protein levels (and therefore the inhibitory activity) of IκBα in a small molecule (trimethoprim [TMP])-dependent manner, as previously accomplished with multiple other transcription factors and signaling proteins. We developed a genetically encoded, small molecule–dependent, reversible strategy for inhibition of NFκB signaling that uses a destabilized domain of *Escherichia coli* dihydrofolate reductase (DHFR) fused to IκBα. In the absence of a small molecule stabilizer, TMP, the fusion protein is ubiquitinated and degraded by the proteasome. However, in the presence of TMP, the DHFR-IκBα fusion protein is stabilized and can prevent NFκB signaling (Fig. 1). This strategy prevented IL-1α, IL-1β, IL-6, and TNFα-induced, NFκB-mediated upregulation and release of the proinflammatory cytokines IL-1β and IL-6 from human immortalized RPE cells (ARPE-19) in a small molecule–dependent fashion. This approach is doseable, completely reversible, and can be cycled “on” or “off” repeatedly. We envision that conditional inhibition of NFκB using this method could eventually be used as a novel way to prevent inflammatory processes associated with retinal degeneration, while minimizing the potential pleiotropic effects associated with direct small-molecule inhibitors of NFκB or constitutive NFκB inhibition.

### MATERIALS AND METHODS

#### Plasmids

A human cDNA clone of wild-type IκBα was purchased from Clontech (Tucson, AZ, USA) followed by puromycin selection (GFP) along with a pLKO puro shSCRAM vector (Sigma-Aldrich Corp., St. Louis, MO, USA). Stable NFκB ARPE-19 reporter cells were generated by cotransfecting cells with a plasmid encoding for 5xNFκB responsive elements driving the expression of a secreted luciferase, *Gaussia* luciferase (GLuc), plasmid called “5NF-GLuc” here onward, described previously and a constitutively expressed green fluorescent protein (GFP) along with a pLKO puro shSCRAM vector (Sigma-Aldrich Corp., St. Louis, MO, USA) followed by puromycin selection and flow cytometry–assisted cell sorting based on GFP signal. Human IL-1α and human TNFα were purchased from PeproTech (Rocky Hill, NJ, USA). LPS was purchased from Sigma-Aldrich Corp., 4-HNE was purchased from Enzo (Farmingdale, NY, USA), and A2E was purchased from Gene and Cell Technologies (Vallejo, CA, USA).

#### Cell Culture

Vesicular stomatitis virus glycoprotein G (VSV-G)-pseudotyped lentivirus was made by co-transfecting HEK-293T cells with the pLenti CMV/TO destination vector by an LR Clonase II reaction (Life Technologies, Carlsbad, CA, USA). Stable NFκB ARPE-19 reporter cells were generated by cotransfecting cells with a plasmid encoding for 5xNFκB responsive elements driving the expression of a secreted luciferase, *Gaussia* luciferase (GLuc), plasmid called “5NF-GLuc” here onward, described previously and a constitutively expressed green fluorescent protein (GFP) along with a pLKO puro shSCRAM vector (Sigma-Aldrich Corp., St. Louis, MO, USA) followed by puromycin selection and flow cytometry–assisted cell sorting based on GFP signal. Human IL-1α and human TNFα were purchased from PeproTech (Rocky Hill, NJ, USA). LPS was purchased from Sigma-Aldrich Corp., 4-HNE was purchased from Enzo (Farmingdale, NY, USA), and A2E was purchased from Gene and Cell Technologies (Vallejo, CA, USA).

#### Western Blotting

For typical Western blotting experiments, (e.g., Fig. 2J–L), cells were plated at 200,000 cells per well of a 12-well plate in complete Dulbecco’s modified Eagle’s medium (DMEM)/F12
media containing 10% serum. The next day, cells were treated as indicated. For Western blotting involving production of cytokines, ARPE-19 cells were plated as described above followed by gradual serum removal over the course of a week until the serum was removed completely followed by indicated treatments. At appropriate time points, ARPE-19 cells were lysed in plate with either radioimmunoprecipitation assay (RIPA) buffer (50 mM Tris, pH 7.4, 150 mM NaCl, 1% Triton X-100 [vol/vol], 0.1% SDS [wt/vol], 0.5% sodium deoxycholate [wt/vol]) supplemented with Halt Protease and Phosphatase inhibitors (Pierce, Rockford, IL, USA) and benzonase (Sigma-Aldrich Corp.) or a buffer containing 50 mM HEPES pH 8, 10 mM KCl, 2 mM MgCl₂, and 1.0% SDS also supplemented with benzonase. Cells were lysed at RT for approximately 1 to 2 minutes, followed by freezing at −80°C. Lysates were thawed on ice and spun at 21,000 rpm for 5 to 10 minutes at 4°C. The supernatant was collected and subjected to a bicinchoninic acid assay (BCA; Pierce). Where indicated, nuclear extracts were obtained by using the NE-PER kit (Pierce). Samples were denatured in Laemmli buffer with reductant, followed by loading on a 4% to 20% Tris-Gly SDS-PAGE gel. Proteins were transferred to a nitrocellulose membrane using a G2 Fast Blotter (Pierce) or iBlot2 (Life Technologies). Blots were typically dried for 1 hour at RT before staining with Ponceau S (Sigma-Aldrich Corp.) and blocking (LI-COR, Lincoln, NE, USA). An appropriate LI-COR anti-mouse or anti-rabbit IR-conjugated secondary was used. All blots were imaged and quantified on a LI-COR Odyssey CLx.

NfκB Electrophoretic Mobility Shift Assay (EMSA)

Cells were plated at a density of 500,000 cells per well of a six-well plate and treated with media containing DMSO or dox/TMP for 48 hours before stimulation with IL-1α (25 ng/mL) for an additional 24 hours (in the presence of DMSO or dox/TMP). Nuclear fractionation and lysis were accomplished as described previously. Nuclear lysates (5 μg) were incubated with 0.5 to 1.0 μL IRDye 700 NFκB probe (LI-COR) in binding buffer (10 mM Tris pH 7.5, 50 mM KCl, 3.5 mM DTT, 0.25% Tween 20, poly[dI*dC]) for 30 minutes at RT. Samples were then run on a non-denaturing 4% polyacrylamide gel in 0.5x Tris/Borate/EDTA buffer until resolved. The resulting gel was visualized on a LI-COR Odyssey CLx.

Quantitative PCR (qPCR)

Cells were harvested by trypsinization, washed, and frozen at −80°C for at least 1 hour before use. mRNA was then extracted from cell pellets using an Aurum Total RNA kit (BioRad, Hercules, CA, USA). Although we did not assess the quality of every RNA preparation, with this method of isolation we routinely obtain RNA integrity numbers of >8.9 (TapeStation 2200; Agilent Technologies, Santa Clara, CA, USA). A total of 100 ng RNA was reverse transcribed with qscript cDNA SuperMix (Quanta Bioscience, Beverly, MA, USA). cDNA was diluted 2× with water, and analyzed using TaqMan probes and TaqMan Advanced Fast Master Mix (Life Technologies). The probes used were as follows: human β-actin (HS03023880), human 1xBz (HS00155671), human IL-1β (HS00174097), human IL-6 (HS00985639), and human IL-18 (HS01038788), all from Life Technologies.

For array-based work, diluted cDNA was applied to a fast 96-well Human NfκB pathway TaqMan array plate (Life Technologies) and run under fast conditions using the master mix described above. All Ct values within each plate were normalized to the 18S ribosomal RNA endogenous control, and then plates were compared to each other (IL-1α + dox/TMP versus IL-1α + DMSO) using QuantiStudio Real Time PCR Software (Thermo Fisher Scientific, Waltham, MA, USA). ΔΔCt values were calculated and expressed as relative quantities (also known as fold-change). Wells with no Ct determination after 40 cycles were considered as “not amplified.”

Enzyme-Linked Immunosorbent Assay (ELISA)

Cells were plated at a density of 200,000 cells per well of a 12-well plate in complete DMEM/F12 media containing 10% serum. Over the course of a week, the serum was gradually removed, and after 1 week, serum was removed completely. Cells were then treated with either DMSO or dox/TMP for 48 hours before stimulation with IL-1α, A2E, or a combination thereof for an additional 24 hours in serum-free media. Conditioned media was collected, spun, and frozen at −80°C until further use in an IL-1β Ultrasensitive ELISA (0.31–20 pg/mL; Life Technologies) or IL-6 ELISA (15–1540 pg/mL; Life Technologies). Significant dilutions (up to 1:1000) of some IL-1α-treated samples were required when assaying for IL-6 to fall within the standard curve.

NfκB-Responsive Gaussia Luciferase (GLuc) Assay

To indirectly measure NfκB activity, we used a system developed by Badr et al. that relies on 5xFκB responsive elements to drive expression of a secreted luciferase, GLuc. The luciferase assay was performed as described previously using conditioned culture media.

Statistical Analysis

To determine significance for Western blotting (NfκB degradation), qPCR, ELISA (IL-1β), IL-6) or GLuc assays, an unpaired one- or two-tailed t-test was used assuming equal variance. For TaqMan gene array values, a one-sample t-test was used comparing the values to a hypothetical mean of 1 (i.e., unchanged). Values were determined to be significant when P values were less than 0.05.

Supplemental Methods

Viability Assays. Cells were plated in a 96-well plate at a density of 15,000 cells per well in full media. Over the course of 1 week, the serum was gradually lowered and completely removed after 1 week. Cells were then treated with either DMSO or dox/TMP for 72 hours. Cells were then analyzed by three different assays: (1) a resazurin mitochondrial reduction potential assay, (2) a lactate dehydrogenase (LDH) release assay (G-Bioscience, St. Louis, MO, USA), and (3) an ATP assay (Cell Titer Glo 2.0; Promega, Madison, WI, USA).

Transepithelial Electrical Resistance (TEER). Cells were plated at a density of 50,000 cells per well on an uncoated, 0.4-μm polyester transwell insert (12-well plate; Corning, Corning, NY, USA). Cells were allowed to polarize and
Figure 2. Generation of an inducible system to regulate IkBα abundance in ARPE-19 TR cells. Bright-field (A–D) and green fluorescence (E–H) images of DHFR-YFP and DHFR-IkBα stable cells treated with either DMSO, dox (100 ng/mL), or dox combined with TMP (1 μM) for 48 hours. (I) Dox/TMP has no effect on endogenous IkBα expression, and DHFR-IkBα transcript levels are inducible and do not change with TMP addition. (J) Protein levels of DHFR-YFP and DHFR-IkBα are tightly regulated, inducible, and dose-dependent. ND, not detected. (K) The DHFR-based strategy can be completely turned off after simple removal of dox/TMP within 48 hours (DHFR-YFP) or 72 hours (DHFR-IkBα). (L) DHFR-YFP and DHFR-IkBα can be repeatedly cycled on and off. Representative data shown of n ≥ 3 independent experiments for all panels.
form tight junctions over the course of a week. TEERs (after blank subtraction) were measured using an EVOM2 meter (World Precision Instruments, Sarasota, FL, USA) and then DMSO or dox/TMP was added to both sides of the transwell. TEERs were re-assessed after 48 hours and the difference between the two readings was calculated.

**RESULTS**

**Validation of the DHFR-Based Destabilized Domain Approach in ARPE-19 Cells**

We generated constructs encoding for DHFR-YFP (as a control) and DHFR-IkBz. To confer an additional level of control over our genes of interest, we generated them as doxycycline (dox)-inducible (also known as “Tet-On”) constructs. After lentiviral infection of ARPE-19 TR cells and subsequent stable selection, heterogeneous populations of cells expressing DHFR-YFP (control cells) demonstrated tight regulation of DHFR-YFP expression and stability (Figs. 2A–C, 2J). In the presence of dox alone, neither fluorescence nor fusion protein (Fig. 2J) was detected. However, upon addition of dox and TMP, which stabilizes newly synthesized DHFR fusion proteins, YFP fluorescence is detectable (Fig. 2G), as is the protein (Fig. 2J). DHFR-IkBz cells were used as an absolute negative fluorescence control (Figs. 2D, 2H). Under untreated, basal levels, there was a small, approximately 2-fold increase in hBz transcript in DHFR-IkBz cells, indicating slight leakiness of the dox-regulated system (Fig. 2I). However, in the absence of dox, no DHFR-IkBz protein was detectable, and endogenous levels of IkBz were identical to control cells (Fig. 2I). After addition of dox, a large, approximately 10-fold increase in IkBz transcript levels was observed (Fig. 2I), and a small amount of DHFR-IkBz was detectable under +dox steady-state levels (Fig. 2J). Although addition of TMP had no effect on DHFR-IkBz transcript levels (Fig. 2I), since TMP stabilization occurs at the protein level, it dose-dependently increased DHFR-IkBz protein levels with the addition of increasing TMP (Fig. 2J). Concomitantly, as DHFR-IkBz was stabilized, endogenous IkBz was reduced in an apparent compensatory autoregulatory mechanism.39 TMP addition (1 nM) to cells expressing DHFR-YFP stabilized the fusion protein such that it was detectable by Western blotting and dose-dependently stabilized DHFR-YFP to a plateau of 1 μM (Fig. 2J).

Next, we assessed whether the stabilization of the DHFR fusion proteins was reversible. DHFR-YFP and DHFR-IkBz cells were induced with dox/TMP for 48 hours followed by washing with Hanks’ balanced salt solution and replacement with fresh media lacking dox/TMP for 16 to 72 hours. Sixteen to 24 hours after removal of dox/TMP, DHFR-YFP levels decreased by 99% and were completely undetectable by 48 hours after removal of dox/TMP (Fig. 2K). The DHFR-IkBz fusion protein, however, required a longer period of “washout” to become undetectable. Within 24 hours of dox/TMP removal, only 60% of the fusion protein was degraded (Fig. 2K). This value increased to 95% degradation by 48 hours, and complete degradation by 72 hours of washout (Fig. 2K). Again, endogenous IkBz protein levels were inversely proportional to the levels of stabilized DHFR-IkBz (Fig. 2K). Subsequently, we determined whether our system could be cycled between an “on” (i.e., stabilization of the fusion protein) or “off” (degradation of the fusion protein) state repeatedly. Stabilization of the DHFR fusion proteins was accomplished by 48 hours of dox/TMP followed by a 72-hour washout period, restabilization for 48 hours, and a final 72-hour washout period. Using these parameters, we were able to effectively cycle both DHFR-YFP and DHFR-IkBz in an “on/off/on/off” manner over the course of a 10-day experiment (Fig. 2L). It is important to note that a 72-hour treatment of the ARPE-19 cells with dox/TMP itself had no effect on cell viability as measured by mitochondrial reduction potential (Supplemental Fig. S1A) or lactate dehydrogenase (LDH) release (Supplemental Fig. S1B). Furthermore, the ATP content of the cells remained unchanged after treatment (Supplemental Fig. S1C) and both the DHFR-YFP and DHFR-IkBz cells did not differ in their ability to form tight junctions and maintain a reasonable TEER (Supplemental Fig. S1D).

**DHFR-IkBz Is Regulated Similarly to Endogenous IkBz After IL-1α Administration**

We tested whether DHFR-IkBz was properly phosphorylated and turned-over after stimulation with the prototypical inflammatory cytokine, IL-1α (shown previously to activate NFκB signaling40 through the IL-1R41 and has been used previously in ARPE-19 cells).22 At the protein level, DHFR-IkBz behaved much like endogenous IkBz, albeit at higher overall steady-state levels. Thirty minutes after addition of IL-1α, a portion of DHFR-IkBz was robustly phosphorylated and degraded (Fig. 3A). This degradation was maximal at 1 hour post IL-1α treatment, similar to that of endogenous IkBz in IL-1α-treated DHFR-YFP-expressing cells (Figs. 3A, 3B). The extent of DHFR-IkBz phosphorylation and subsequent degradation paralleled phosphorylation (activation) of the IkB kinase complex (IKK) subunits α/β (Fig. 3A), strongly suggesting that DHFR-IkBz, like endogenous IkBz, is phosphorylated by IKK, which in turn promotes its ubiquitination and degradation.42 After 1 hour of treatment, DHFR-IkBz and endogenous IkBz levels began to rebound and reach approximately 1.2-fold over untreated IkBz values by 6 to 24 hours (Figs. 3A, 3B).

**Stabilization of DHFR-IkBz Prevents NFκB Nuclear Translocation and Downstream Gene Expression**

We tested whether stabilization of DHFR-IkBz prevented IL-1α-induced NFκB nuclear translocation. ARPE-19 cells were pretreated with dox/TMP for 48 hours, followed by treatment with IL-1α for 24 hours, and then subjected to nuclear protein extraction. As we predicted, ARPE-19 cells expressing stabilized DHFR-IkBz demonstrated virtually no nuclear NFκB signal even after IL-1α stimulation (Fig. 4A), demonstrating that it can sequester NFκB in the cytosol in an inactive conformation. Next, we wished to confirm whether stabilized DHFR-IkBz could in fact dampen or prevent NFκB transcriptional signaling. Cells were treated as described above, then harvested and processed for an EMSA using a fluorescently labeled NFκB consensus oligonucleotide. Only in cells treated with IL-1α did we observe a detectable shift in the migration of the NFκB oligonucleotide, an indication of NFκB nuclear translocation and DNA binding (Fig. 4B). Importantly, there was a substantial reduction in the intensity of this band only in cells with stabilized DHFR-IkBz, demonstrating that our strategy can indeed repress IL-1α-induced NFκB nuclear translocation and activity (Figs. 4A, 4B). Furthermore, transcriptional analysis of identically treated cells revealed that stabilization of DHFR-IkBz significantly reduced IL-1α-induced, NFκB-dependent IL-1β39 and IL-6 transcripts by 90% and 82%, respectively (Figs. 4C, 4D; P < 0.01), while having no appreciable effect on IL-18 levels (Fig. 4E), a gene that is constitutively produced and regulated independently of NFκB.44
Subsequently, we sought to identify additional NFκB-target genes that were differentially regulated by DHFR-IκBα stabilization by using TaqMan transcriptional arrays. Only one gene of the 93 assayed was identified to be consistently upregulated (≥2-fold in two independent replicates, \( P < 0.05 \)) in IL-1α-stimulated dox/TMP-treated versus IL-1α-stimulated DMSO-treated DHFR-IκBα cells. This gene was the B-cell lymphoma 2 gene (BCL2, Fig. 4F). This hit was unexpected; BCL2 has been demonstrated to be upregulated after NFκB activation.45,46 Our data suggest that this gene may be differentially regulated in ARPE-19 cells or under these specific conditions. The vast majority of hits (16) were found to be reduced (≤2-fold decrease, \( P > 0.05 \)) in IL-1α-stimulated dox/TMP versus IL-1α-stimulated DMSO cells (Fig. 4F). These results confirmed our previous observations of downstream NFκB signaling at the transcriptional level after IL-1α stimulation were also paralleled at the translational level, as indicated by Western blotting (Fig. 5A). In these experiments, we again used IL-1α as a NFκB “priming” stimulus, but also treated cells with N-retinylidene-N-retinylethanolamine (A2E), the main fluorescent component of lipofuscin47 and lysosomotropic agent,48 which induces the assembly of the NLRP3 inflammasome22 responsible for ultimately cleaving certain pro-cytokines, such as pro-IL-1β and pro–IL-18. IL-1α treatment resulted in phosphorylation of NFκB at Ser536 (pS536), a highly conserved residue that is potently phosphorylated in response to inflammatory stimuli49 (Fig. 5A). However, NFκB pS536 is independent of IκBα regulation50 and is not necessarily an indication of NFκB activity or translocation.51 Thus, levels of pS536 NFκB did not differ substantively between DHFR-YFP or DHFR-IκBα under any condition used (Fig. 5A). In contrast, levels of intracellular pro–IL-1β as well as IL-6 after IL-1α or IL-1α/A2E treatment were decreased by a minimum of 90% in ARPE-19 cells with DHFR-IκBα stabilized

\[ \text{Stabilization of DHFR-IκBα Prevents the Production and Release of NFκB-Dependent Cytokines} \]

Our observations of downstream NFκB signaling at the transcriptional level after IL-1α stimulation were also paralleled at the translational level, as indicated by Western blotting (Fig. 5A). In these experiments, we again used IL-1α as a NFκB “priming” stimulus, but also treated cells with N-retinylidene-N-retinylethanolamine (A2E), the main fluorescent component of lipofuscin47 and lysosomotropic agent,48 which induces the assembly of the NLRP3 inflammasome22 responsible for ultimately cleaving certain pro-cytokines, such as pro-IL-1β and pro–IL-18. IL-1α treatment resulted in phosphorylation of NFκB at Ser536 (pS536), a highly conserved residue that is potently phosphorylated in response to inflammatory stimuli49 (Fig. 5A). However, NFκB pS536 is independent of IκBα regulation50 and is not necessarily an indication of NFκB activity or translocation.51 Thus, levels of pS536 NFκB did not differ substantively between DHFR-YFP or DHFR-IκBα under any condition used (Fig. 5A). In contrast, levels of intracellular pro–IL-1β as well as IL-6 after IL-1α or IL-1α/A2E treatment were decreased by a minimum of 90% in ARPE-19 cells with DHFR-IκBα stabilized

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by dox/TMP (Fig. 5A). In fact, levels of IL-6 post stabilization of DHFR-IκBα were not detectable even after IL-1α or IL-1α/A2E treatment (Fig. 5A). A2E alone caused no detectable effects using Western blotting techniques. As expected, levels of intracellular pro–IL-18 were not changed with any condition tested, regardless of cell line (Fig. 5A).

ELISA was used to monitor changes in secreted canonical NFκB-dependent cytokines. IL-1α increased IL-1β secretion in...
DMSO-treated DHFR-YFP and DHFR-IκBa cells from “not detected” (values at or below the blank) to 6.4 ± 2.5 and 7.7 ± 2.9 pg/mL, respectively (Fig. 5B). In contrast, A2E minimally, but consistently, increased IL-1β secretion from “not detected” to 0.8 ± 0.2 and 0.9 ± 0.2 pg/mL in DMSO-treated DHFR-YFP and DHFR-IκBa cells, respectively (Fig. 5B). As expected, the combination of NFκB priming (achieved by IL-1α treatment) and inflammasome assembly (achieved by A2E treatment) substantially increased IL-1α-mediated IL-1β secretion in DMSO-treated DHFR-YFP and DHFR-IκBa cells to 32.1 ± 4.1 and 32.5 ± 6.6 pg/mL, respectively (Fig. 5B). After addition of dox/TMP, there were no significant changes in IL-1β secretion levels in DHFR-YFP cells treated with IL-1α, A2E, or the combination thereof when compared with DMSO-treated cells (Fig. 5B). In contrast, stabilization of DHFR-IκBa significantly reduced IL-1β secretion in IL-1α-treated cells by 88% (7.7 ± 1.8 vs. 0.9 ± 0.3 pg/mL, *P < 0.01) and similarly decreased IL-1β levels by 83% (34.3 ± 1.4 vs. 5.96 ± 0.6 pg/mL, *P < 0.01) in IL-1α/A2E-treated cells (Fig. 5B) when compared with the corresponding DHFR-YFP control cells. A2E-mediated slight increases in IL-1β were not affected by DHFR-IκBa stabilization (Fig. 5B).
Secretion levels of IL-6 after IL-1α treatment were substantially increased compared with DMSO-only treated cells to 182 ± 42.7 ng/mL (4666-fold) in DHFR-YFP cells and 224 ± 43.9 ng/mL (6500-fold) in DHFR-IxBz cells (Fig. 5C). For simplicity, a zoomed-in view of low, but detectable, basal secretion of IL-6 is shown in Supplemental Figure S2A. Surprisingly, treatment with A2E resulted in a consistent decrease in IL-6 secretion, irrespective of co-treatment with IL-1α or dox/TMP (Fig. 5C, Supplemental Fig. S2A), in agreement with previous observations.22 It is also important to note that treatment with dox/TMP appeared to consistently increase secretion of IL-6 in DHFR-YFP-expressing cells (Fig. 5C), in agreement with previous studies.22 Stabilization of DHFR-IxBz significantly prevented the secretion of IL-6 after IL-1α stimulation (292.5 ± 42.7 vs. 54.4 ± 16.2 ng/mL, −81%, P < 0.01, Fig. 5C). A2E treatment (69.3 ± 25.5 pg/mL vs. 5.5 ± 9.5 pg/mL, −93%, P < 0.05, Supplemental Fig. S2A), or the combination thereof (200.5 ± 41.2 vs. 16.4 ± 7.2 ng/mL, −92%, P < 0.01, Fig. 5C) when compared with the corresponding DHFR-YFP control cells.

The IkBz Destabilized Domain Strategy Can Be Used to Dampen NFkB Signaling From Multiple Initiating Stimuli

In addition to IL-1α, a number of other pathogen-associated molecular patterns or other stimuli can trigger activation of NFkB signaling, albeit through different cell surface receptors and mechanisms. These molecules include bacterial-derived LPS, TNFx and A2E,22 among others. We tested the ability of these stimuli to activate NFkB signaling using an ARPE-19 GLuc reporter cell line. We did not observe NFkB activation when using 4-hydroxynonenal (4-HNE), in agreement with previous observations51 (Supplemental Fig. S2B). In contrast to previous findings,22 we did not detect NFkB activation using A2E (Supplemental Fig. S2B). However, both LPS (0.1–10 μg/mL, Fig. 6A, P < 0.05, P < 0.01) and TNFx (0.25–25 ng/mL, Fig. 6B, P < 0.05, P < 0.01) caused significant increases in the secretion of GLuc, indicating activation of NFkB. Next, we assessed whether our DHFR-IxBz strategy was broadly applicable for dampening NFkB signaling triggered by these stimuli. ARPE-19 cells treated with LPS (10 μg/mL, 24 hours) demonstrated an approximately 9– to 12-fold increase in Il1β transcript levels, which were significantly reduced by 75% in dox/TMP-treated DHFR-IxBz cells (Fig. 6C, P < 0.01). IL-6 transcript levels were minimally increased after LPS administration by approximately 2.5-fold in both DHFR-YFP and DHFR-IxBz cells (DMSO-treated cells, Supplemental Fig. S2C). IL-6 levels were further increased by 93% in DMSO-treated cells treated with LPS/dox/TMP. However, stabilization of DHFR-IxBz reduced IL-6 transcript levels by 43% compared with DMSO/LPS-treated cells (Supplemental Fig. S2C). Cells treated with TNFx (2.5 ng/mL, 24 hours) showed a robust 26– to 35-fold increase in Il1β transcript levels (Fig. 6D), without any discernible effect on IL-6 transcript levels (Supplemental Fig. S2D). Stabilization of DHFR-IxBz significantly reduced TNFx-associated Il1β induction by 72% (Fig. 6D, P < 0.05). Our data highlight the general applicability of this DHFR-IxBz system for conditionally dampening NFkB signaling in response to a variety of stimulating stimuli.

DISCUSSION

We have presented a novel, small molecule–regulated strategy to conditionally prevent NFkB-mediated proinflammatory signaling using a DHFR-based destabilized domain fused to IkBz. To the best of our knowledge, this is the first demonstration of destabilized domain technology in RPE cells, and the first destabilized domain approach to specifically target NFkB signaling. Upon expression and stabilization of the DHFR-IkBz fusion protein with dox/TMP cells are protected from the proinflammatory effects of IL-1α, TNFx and LPS, reducing NFkB-dependent gene expression and cytokine production by approximately 80% to 90%. Suppression of NFkB signaling to this extent has been achieved previously using various small-molecule NFkB inhibitors (there are more than 700 of them identified so far55) or by using a constitutively expressed “super repressor” version of IkBz that cannot be phosphorylated or degraded after exposure to stimulus.56 However, our approach is unique in that although it is genetically encoded, it is conditional and can be cycled “on” or “off” repeatedly at will, simply by addition or omission of an orally available small molecule or molecules. We speculate that such a regulatable strategy (which could be targeted to particular retinal cells using cell-specific promoters) will be beneficial for manipulating cellular pathways within the retina (such as stress-responses) that are otherwise difficult to accurately regulate, or have the potential for significant off-target/damaging effects if constitutively activated or repressed. We feel compelled to mention, however, that patients given TMP and sulfamethoxazole may have an increased risk of developing a drug-induced thrombocytopenia or megaloblastic anemia, especially in the immunocompromised.54 Recently, a few cases of TMP/sulfamethoxazole-associated aseptic meningitis, as seen in some patients taking nonsteroidal anti-inflammatory drugs, have been reported, and is potentially linked to increased IL-6 release in certain contexts.57 To evaluate the safety of a long-term regimen of TMP, future in vivo studies are warranted. Nonetheless, we are cautiously optimistic that this DHFR-based approach can safely and effectively be used in vivo54,55 in the eye to regulate protein abundance.

Given that NFkB regulates more than 500 genes involved in inflammation, cell growth, apoptosis, and carcinogenesis, it is difficult to predict the effects of long-term NFkB inhibition in the eye or within the RPE. Mice lacking NFkB subunit RelA/p65 (the subunit we focused on in this article) die in utero,56 whereas NFkB/p105 null mice appear to have normally developed eyes and RPE cells, and are resistant to Adl RNA-mediated gene deletion.57 To complicate the situation further, a previous study found that inhibition of NFkB signaling may not affect RPE cells in a similar fashion to other commonly used cells.58

Although we validated our DHFR-IkBz approach by focusing primarily on IL-1β and IL-6, both of which have been implicated in AMD,59–61 we also identified reductions in a number of separate genes that have previously been linked to retinal degeneration. For example, VCAM1, TLR2, and IL-8 transcripts were all found to be substantially reduced in IL-1α-treated cells with stabilized DHFR-IkBz. VCAM1 has been shown to play an important role in oxidative-stress-mediated angiogenesis in the retina62 and has been known to contribute to TNFx-mediated angiogenesis.63 TLR2 has been demonstrated to potentiate inflammation originating from AMD-related carboxyethylpyrrole-adducted proteins64 and activation of TLR2 causes experimental choroidal neovascularization (CNV).65 IL-8 polymorphisms have been associated with wet AMD.65–67 However, inhibition of NFkB also reduced transcript levels of chemokine (C-C motif) ligand 2 (CCL2, also known as MCP-1). Mice deficient in Ccl2 develop drusen-like deposits consisting of autofluorescent subretinal macrophages, but were less susceptible to laser-induced CNV.68 Ultimately, to further clarify the potential benefits or deterrents of long-term NFkB inhibition in the retina and its eventual relevance to...
retinal degeneration, we must test the DHFR-I\(B\) strategy directly in mice.

NF\(\kappa\)B-dependent genes, such as IL-8 and TNF\(\alpha\), are clearly linked to the development of CNV; however, we also believe that DHFR-I\(B\)–mediated NF\(\kappa\)B inhibition could protect against inflammasome-mediated ‘‘dry’’ AMD–related symptoms, such as geographic atrophy. Because NF\(\kappa\)B-dependent ‘‘priming’’ not only produces inflammatory pro-cytokines, but also transcriptionally upregulates NLRP3, a necessary component required for the NLRP3 inflammasome complex, DHFR-I\(B\)–mediated inhibition of NF\(\kappa\)B priming, in theory, could also indirectly modulate inflammasome assembly. NLRP3 is unique when compared with other NLRPs, such as NLRP1 or NLRP6, in that its basal level of expression is generally not sufficient for inflammasome activation in resting cells. Surprisingly, NLRP3 expression in ARPE-19 cells is postulated to be constitutive, not necessarily inducible, and thus possibly NF\(\kappa\)B-independent in these immortalized cells. Nonetheless, we indeed found that our DHFR-I\(B\) method significantly prevented IL-1\(\beta\)-primed, A2E-exacerbated secretion of IL-1\(\beta\). It is yet to be determined whether this inhibition is due solely to prevention of inflammasome priming, inflammasome assembly, or both, which is a topic for future studies.

In summary, our current study demonstrates a proof-of-principle use of DHFR-I\(B\) to prevent NF\(\kappa\)B-mediated inflammatory signaling in cultured RPE cells. Ultimately, we envision that a DHFR or alternative destabilized domain-based strategy could effectively be used to temporally and conditionally control a number of different signaling pathways (including inflammation) in different tissues in the eye, and is therefore an exciting tool for potentially treating retinal diseases caused by diverse genetic or environmental insults.

**FIGURE 6.** Stabilized DHFR-I\(B\) also prevents LPS and TNF\(\alpha\)-mediated NF\(\kappa\)B priming. (A, B) LPS and TNF\(\alpha\) induce NF\(\kappa\)B activity in a dose-dependent manner. 5NF-GLuc ARPE-19 cells were treated with the indicated concentrations of LPS or TNF\(\alpha\) for 24 hours followed by assessment of GLuc activity in the media. \(n = 3\), *\(P < 0.05\), **\(P < 0.01\), unpaired, one-tailed \(t\)-test assuming equal variance. (C, D) qPCR of IL-1\(\beta\) transcripts ± LPS (10 \(\mu\)g/mL, 24 hours) or TNF\(\alpha\) (2.5 ng/mL, 24 hours) ± dox/TMP. \(n = 3\), *\(P < 0.05\), **\(P < 0.01\), unpaired, two-tailed \(t\)-test assuming equal variance. Mean ± SD for all bar graphs in this figure.
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References


