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Atypical Activation of the Unfolded Protein Response in Cystic Fibrosis Airway Cells Contributes to p38 MAPK-Mediated Innate Immune Responses

Christoph J. Blohmke,* Matthew L. Mayer,† Anthony C. Tang,* Aaron F. Hirschfeld,* Christopher D. Fjell,‡ Marc A. Sze,‡ Reza Falsafi,‡ Shirley Wang,* Karolynn Hsu,* Mark A. Chilvers,* James C. Hogg,‡ Robert E. W. Hancock,† and Stuart E. Turvey*

Inflammatory lung disease is the major cause of morbidity and mortality in cystic fibrosis (CF); understanding what produces dysregulated innate immune responses in CF cells will be pivotal in guiding the development of novel anti-inflammatory therapies. To elucidate the molecular mechanisms that mediate exaggerated inflammation in CF following TLR signaling, we profiled global gene expression in immortalized human CF and non-CF airway cells at baseline and after microbial stimulation. Using complementary analysis methods, we observed a signature of increased stress levels in CF cells, specifically characterized by endoplasmic reticulum (ER) stress, the unfolded protein response (UPR), and MAPK signaling. Analysis of ER stress responses revealed an atypical induction of the UPR, characterized by the lack of induction of the PERK–eIF2α pathway in three complementary model systems: immortalized CF airway cells, fresh CF blood cells, and CF lung tissue. This atypical pattern of UPR activation was associated with the hyperinflammatory phenotype in CF cells, as deliberate induction of the PERK–eIF2α pathway with salubrinal attenuated the inflammatory response to both flagellin and *Pseudomonas aeruginosa*. IL-6 production triggered by ER stress and microbial stimulation were both dependent on p38 MAPK activity, suggesting a molecular link between both signaling events. These data indicate that atypical UPR activation fails to resolve the ER stress in CF and sensitizes the innate immune system to respond more vigorously to microbial challenge. Strategies to restore ER homeostasis and normalize the UPR activation profile may represent a novel therapeutic approach to minimize lung-damaging inflammation in CF. *The Journal of Immunology*, 2012, 189: 5467–5475.
IRE-1α (mitostil-requiring enzyme 1α), PERK (eukaryotic translation initiation factor 2-α kinase 3), and the transcription factor (TF) ATF6 (activating TF 6) (20). Together these three arms of the UPR mitigate ER stress by attenuating protein synthesis, facilitating protein folding, and increasing protein degradation.

A number of studies have identified cross-talk mechanisms between the UPR and proinflammatory pathways, including NF-κB signaling (20–22). Consequently, the goal of this study was to investigate how the UPR and ER stress might contribute to the damaging hyper-inflammatory phenotype in CF. By combining computational with biochemical approaches, we identify dysregulation of the homeostatic UPR system in CF, which appears to potentiate TLR5 signaling. Thus strategies to correct dysregulated stress response pathways may represent a novel therapeutic approach to alleviate lung-damaging inflammation in CF.

Materials and Methods

Human biological samples

The well-characterized, immortalized airway epithelial cell lines IB3-1 (compound heterozygote for CF mutations ΔF508 and W1282X) and C38 (IB3-1 transfected with CFTR by adenso-associated viral vector) were cultured as described (23). PBMCs were isolated from whole blood obtained from healthy control and CF donors (sweat test and CF mutation positive) using published techniques (24). All CF patients were clinically stable at the time of blood donation, and subjects receiving systemic corticosteroid medications were excluded.

Lung tissue from end-stage CF patients was obtained following transplantation. Control lung tissue was obtained from normal portions of the lung from patients undergoing surgery for lung cancer. All tissues were cryopreserved in tissue blocks. Studies were approved by the University of British Columbia Clinical Research Ethics Board (H09-01192), and informed consent was obtained from participants.

Cell stimulation assays

Cells were seeded into 96-well plates 16 h prior to stimulation and stimulated with optimized concentrations of flagellin (100 ng/ml; Invivogen), tunicamycin (20 μg/ml; Calbiochem), and/or P. aeruginosa PAO1 [multiplicity of infection (MOI) = 50:1]. For inhibitor studies, cells were incubated with a p38 MAPK inhibitor (SB203580, 1 μM; Cell Signaling) 1 h prior to exposure to tunicamycin (20 μg/ml) or flagellin (100 ng/ml). A specific inhibitor of the eIF2α phosphatase GADD34, salubrinal (100 μM; EMD), was applied 48 h prior to stimulation with flagellin or P. aeruginosa PAO1.

IL-6 concentration was determined by ELISA (eBioscience). Cells were stimulated in six-well plates (BD Biosciences) with 1 μg/ml flagellin for 2 h. Cells were lysed, and total RNA was harvested. RNA quality was determined using Bioanalyzer 2100 (Agilent Technologies). cDNA was synthesized using an RNA amplification kit (Kreatech), hybridized to human HT-12 expression bead chips and raw data processed with BeadStudio v3.4.0 (Illumina). Microarray data were deposited to the publically viewable National Center for Biotechnology Information Gene Expression Omnibus (accession number GSE35391, http://www.ncbi.nlm.nih.gov/geo/).

Global gene expression profiling

Cells were stimulated in six-well plates (BD Biosciences) with 1 μg/ml flagellin for 2 h. Cells were lysed, and total RNA was harvested. RNA quality was determined using Bioanalyzer 2100 (Agilent Technologies). cDNA was synthesized using an RNA amplification kit (Kreatech), hybridized to human HT-12 expression bead chips and raw data processed with BeadStudio v3.4.0 (Illumina). Microarray data were deposited to the publically viewable National Center for Biotechnology Information Gene Expression Omnibus (accession number GSE35391, http://www.ncbi.nlm.nih.gov/geo/).

Differential gene expression and network analysis

Further processing was performed using Bioconductor (http://www.bioconductor.org/) for quantile normalization. Differential expression of gene probes was calculated using the limma package with empirical Bayes methods (26). Adjusted p values were calculated using the Benjamini-Hochberg method (27). Gene ontology (GO; http://geneontology.org) overrepresentation analysis (ORA) was calculated using GOSTats (28), whereas ORA of TFs based on differentially expressed (DE) targets was calculated using CORNA (29), with data from TRANSFAC PRO (29), processed using the InnateDB Project (30). Network analysis was carried out as previously described (30, 31). Briefly, a list of protein-level interactions between DE genes (FC > ±1.4; p < 0.05) was obtained using InnateDB (32). Network analysis was carried out by visualizing these interactions into a single integrated network using Cytoscape (2.8.0 for Windows) and the software plugin Cerebral to appreciate cellular directionality, as previously described (33). Hub degree (or the number of protein-level interactions with other members of the network) was determined for each gene “node” in the network using cytoHubba (34). Further enrichment of the network was performed through the manual addition of interactions based on primary literature (35), focusing on genes curated in the KEGG pathway Protein processing in endoplasmic reticulum [KEGG:hsa04141] (36).

Results

Immortalized CF airway cells display evidence of ER stress, UPR activation, and enhanced inflammatory responsiveness

It remains unclear which molecular events in CF lead to excessive immune responses to flagellated pathogens such as P. aeruginosa. To generate testable hypotheses concerning the mechanisms underlying this increased immune response, gene expression profiling was performed on IB3-1 and C38 cells at baseline and 2 h after flagellin stimulation. The data were subjected to computational analysis using complementary approaches of GO and TF ORA methods (Tables II–IV). In addition, a comprehensive network of protein-level interactions between DE genes in IB3-1 compared to C38 cells was constructed (Fig. 1). The goal of this analysis was to facilitate unbiased identification of the transcriptional processes contributing to the increased responsiveness of immortalized CF airway cells to flagellin.

Table 1. Quantitative PCR primer sequences

<table>
<thead>
<tr>
<th>Gene</th>
<th>NCBI Accession</th>
<th>Forward (5’ → 3’)</th>
<th>Reverse (5’ → 3’)</th>
<th>CDS Region</th>
<th>Size (bp)</th>
<th>Tm (°C)</th>
</tr>
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<tbody>
<tr>
<td>ATF4</td>
<td>NM_001675.2</td>
<td>AAAGACAGAAGAAGATGCC</td>
<td>TGGTGTACAGTTCTGCGG</td>
<td>c. 214–421</td>
<td>208</td>
<td>55, 58</td>
</tr>
<tr>
<td>DDIT3</td>
<td>NM_001195053.1</td>
<td>GAATAGGAGAAGAATGCA</td>
<td>TGGCTCTCTTACGCTCCT</td>
<td>c. 197–437</td>
<td>241</td>
<td>46, 47</td>
</tr>
<tr>
<td>GADD34</td>
<td>NM_014330.3</td>
<td>CCTCTCTGGGCTCTCCYGG</td>
<td>TCCGGCAGACGATGCTCCA</td>
<td>c. 1570–1763</td>
<td>194</td>
<td>60, 60</td>
</tr>
<tr>
<td>GRP78</td>
<td>NM_005347.3</td>
<td>TGTTCCTTCCAGGTGGAAGAA</td>
<td>AGCTCACTGGGATGCTCA</td>
<td>c. 344–506</td>
<td>163</td>
<td>55, 57</td>
</tr>
<tr>
<td>IL-6</td>
<td>NM_0006000</td>
<td>GTGAAAGCAGAAAAAGGCTG</td>
<td>TGCAGAAGGATTCTGCTGAGGA</td>
<td>c. 232–338</td>
<td>107</td>
<td>58, 56</td>
</tr>
<tr>
<td>NRT2</td>
<td>NM_006164.3</td>
<td>GAATCTTGGAGAATTGGGAGGAG</td>
<td>TGGTGTACAGTTCTGCGG</td>
<td>c. 477–711</td>
<td>235</td>
<td>60, 59</td>
</tr>
<tr>
<td>PPA</td>
<td>NM_021130</td>
<td>TAAGGACATCAGGCTCTGGCCTTCTT</td>
<td>ATCCAAACACTAGCTGGCTGAG</td>
<td>c. 269–369</td>
<td>101</td>
<td>58, 58</td>
</tr>
<tr>
<td>XBP-1s</td>
<td>NM_001079539.1</td>
<td>ATGGATGGCCCTTCTGTTGGAAGA</td>
<td>TGGATGTGCAGCGACCT</td>
<td>c. 415–506</td>
<td>90</td>
<td>58, 59</td>
</tr>
<tr>
<td>XBP-1u</td>
<td>NM_005080.3</td>
<td>AGGCAGCTACGTCAGCTCCCTT</td>
<td>TGGATGTGCAGCGACCT</td>
<td>c. 495–624</td>
<td>130</td>
<td>59, 55</td>
</tr>
</tbody>
</table>

CDS Region, Coding sequence region; NCBI, National Center for Biotechnology Information; Tm, temperature.
We investigated GO terms to identify global molecular themes dysregulated in IB3-1 compared with C38 cells. Multiple GO terms (categorized as Biological Process) related to both ER stress and the innate immune response were significantly different between the cell lines (Tables II, III). These findings were further reinforced by the TF ORA, which returned a signature of TFs associated with the UPR (XBP-1, ATF6, DDIT3) as well as TFs activated downstream of the p38 MAPK signaling pathway related to inflammatory cytokine production (NF-κB, CREB1, AP-1) (Table IV).

When DE genes between cell lines were visualized graphically, DE genes related to ER stress and UPR were present in the network (Fig. 1). NF-κB (NFKB1) was not significantly different between IB3-1 and C38 under unstimulated conditions but, after flagellin treatment, was upregulated in IB3-1 and centered as one of the largest and most prominent hubs in the network, orchestrating the downstream upregulation of immune genes. Most strikingly, multiple gene nodes related to ER stress and UPR were found to be interacting with NF-κB, either directly through NFKB1 (such as HSP90AA1 and HSPA1A) or indirectly through NFKBIA (such as VCP and XBP1-ATF4). Taken together, this analysis revealed a pattern of enhanced inflammatory signaling in conjunction with ER stress, the UPR, and general stress response pathways in

Table II. GO terms categorized as “biological process” associated with ER stress and the UPR, overrepresented by DE genes in CF (IB3-1) compared with non-CF (C38) cells at baseline

<table>
<thead>
<tr>
<th>GO Term ID</th>
<th>p Value</th>
<th>Term</th>
</tr>
</thead>
<tbody>
<tr>
<td>GO:0032874</td>
<td>0.022</td>
<td>Positive regulation of stress-activated MAPK cascade</td>
</tr>
<tr>
<td>GO:0017148</td>
<td>0.035</td>
<td>Negative regulation of translation</td>
</tr>
<tr>
<td>GO:0050727</td>
<td>0.035</td>
<td>Regulation of inflammatory response</td>
</tr>
<tr>
<td>GO:00080134</td>
<td>0.016</td>
<td>Regulation of response to stress</td>
</tr>
<tr>
<td>GO:0070374</td>
<td>0.016</td>
<td>Positive regulation of ERK1 and ERK2 cascade</td>
</tr>
<tr>
<td>GO:0000165</td>
<td>0.033</td>
<td>MAPKKK cascade</td>
</tr>
</tbody>
</table>

ID, identification.
flagellin-stimulated immortalized CF cell lines. On this basis, we hypothesized that the integration of these pathways in CF cells was contributing to their heightened proinflammatory responses.

**Atypical activation of the UPR is a feature of CF cells**

To validate the computational predictions, we established the reliability of a panel of commonly accepted ER stress/UPR markers by treating IB3-1 and C38 cells with the ER stress inducer tunicamycin and measuring the expression of genes influenced by the three arms of the UPR:IRE-1 (XBP-1u, XBP-1s), ATF6 (GRP78), and PERK (GADD34, ATF4, NFR2, DDIT3) (37, 38). Tunicamycin induces ER stress by inhibiting N-linked glycosylation. Consistent with current understanding of the UPR, all gene expression increased in a time-dependent fashion except XBP-1u, which decreased as expected because under conditions of ER stress, XBP-1u is processed by IRE-1 to generate XBP-1s. NFR2 changes were modest, and this marker was not included in subsequent UPR analysis (Fig. 2A–D).

To ensure the validity and generalizability of our findings, we next profiled UPR activation in three complementary human model systems: immortalized CF and control airway epithelial cells, primary PBMCs from CF patients and healthy controls, and CF and control primary lung tissue (Fig. 3A, 3C, 3D, respectively). The primary PBMCs from CF patients and healthy controls, and CF and model systems: immortalized CF and control airway epithelial cells, next profiled UPR activation in three complementary human samples. In contrast, ATF4, GADD34, DDIT3, and GRP78 expression was not induced in parallel with XBP-1s, suggesting the PERK–eIF2α arm of the UPR is not activated in CF cells in all three model systems. A significant lack of activation of the PERK–eIF2α arm of the UPR in immortalized CF airway epithelial cells was confirmed at the protein level, as phosphorylation of eIF2α was lower in CF than in control cells (Fig. 3B). This unanticipated finding provides evidence of both ER stress in CF cells and an atypical activation of the UPR in immortalized CF airway cells.

**Pharmacological activation of the PERK–eIF2α pathway attenuates proinflammatory immune responses in CF airway cells**

Having identified an atypical pattern of UPR activation in CF cells in which the IRE-1 pathway was activated, in contrast to the absence of PERK–eIF2α pathway induction, we examined whether deliberate activation of the PERK–eIF2α pathway would beneficially modulate the inflammatory response pattern of CF airway cells. Upon activation of PERK, eIF2α is phosphorylated, which leads to ATF4-dependent transcription of DDIT3. This pathway is negatively regulated by the phosphatase GADD34, which dephosphorylates eIF2α. Salubrinal, a specific pharmacological inhibitor of GADD34, upregulates this pathway, as demonstrated by increased phosphorylation of eIF2α and induction of DDIT3.
expression (Fig. 4A, 4B). Pharmacological activation of the PERK–
eIF2α pathway through preincubation of IB3-1 cells with salubrinal (30 h) attenuated the inflammatory response to flagellin ($p < 0.001$) and 
P. aeruginosa (PAO1, MOI = 50:1; $p < 0.001$) (Fig. 4C, 4D).

Importantly, salubrinal treatment did not significantly affect cell
viability, as measured by MTS assay (data not shown).

ER stress, the UPR, and proinflammatory innate immune
responses are mechanistically linked through p38 MAPK
signaling

With the goal of increasing our mechanistic understanding of in-
flammation in CF and ascertaining potential anti-inflammatory
targets, we sought to identify the molecular pathways integrat-
ing ER stress, the UPR, and innate immune signaling. Informed by
the results of our gene expression profiling (Tables II–IV) and
literature reports implicating p38 MAPK signaling in CF inflam-
mation (11, 39), the activity of p38 MAPK was evaluated in re-
sponse to flagellin stimulation. Flagellin triggered an increased
and prolonged phosphorylation of p38 MAPK in IB3-1 cells
compared with control cells (Fig. 5). This differential signaling
was biologically relevant, as treatment of CF cells with the spe-
cific p38 MAPK inhibitor SB203580 reduced the exaggerated
proinflammatory immune response to baseline (Fig. 6A). These
data validate the results from the gene expression array analysis,
suggesting that p38 MAPK activity plays a significant role in the
proinflammatory immune response of IB3-1 cells to flagellin.

FIGURE 2. Tunicamycin induces expression of UPR markers. IB3-1 (A, C) and C38 (B, D) cells were treated with tunicamycin (20 μg/ml)
for 24 h ($n = 3$), and XBP-1u, XBP-1s, GRP78, GADD34, ATF4, NRF2, and DDIT3 expression
was measured. Expression values were nor-
malized to the housekeeping gene PPIA and are relative to baseline. Data are expressed as a log2
ratio and represent mean ± SEM.

FIGURE 3. Pattern of UPR activation in immortalized CF airway cells, blood cells, and lung tissue. Expression of UPR markers
XBP-1u, XBP-1s, GRP78, GADD34, ATF4, and DDIT3 at unstimulated conditions in (A)
IB3-1/C38 cells ($n = 3$), (C) CF PBMCs
($n = 8$), and (D) tissue from lung explants
($n = 4$) compared with their non-CF con-
trols. Expression values were normalized to
the housekeeping gene PPIA and are relative
to baseline. Data are expressed as a log2; ratio and represent mean ± 95% confidence inter-
val. *$p < 0.05$. (B) Phospho(p)-eIF2α protein
levels in CF (IB3-1) and non-CF (C38) airway
cells were determined by Western blot and
quantified by densitometry ($n = 3$). Statistical
comparison was performed by t test. **$p <
0.01$. 

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To investigate a potential link between ER stress and inflammation, we next sought to determine if ER stress–augmented inflammatory responses were also mediated by p38 MAPK. The level of ER stress was artificially enhanced by preincubation with tunicamycin. Subsequent stimulation with flagellin resulted in an augmented IL-6 response in both cell lines (Fig. 6A, 6B), suggesting that existing and increasing perturbation of the ER can potentiate the inflammatory immune response of immortalized airway epithelial cells. Similar to flagellin responses, the differences in tunicamycin-induced IL-6 were greater in IB3-1 than in C38 \( (p < 0.05) \). This ER stress–induced IL-6 production was dependent upon p38 MAPK activity, as pretreatment with SB203580 abrogated the IL-6 response to tunicamycin (Fig. 6A, 6B). Finally, to confirm that ER stress contributes to flagellin-induced p38 MAPK-dependent inflammatory gene expression, we demonstrated that SB203580 abolished IL-6 production from cells treated with both tunicamycin and flagellin (Fig. 6A, 6B). Together these data suggest that in IB3-1 cells, signaling and transcriptional pathways activated by ER stress and flagellin are mechanistically linked through p38 MAPK signaling, and that this pathway convergence in turn contributes to augmented inflammatory responses of immortalized CF airway cells.

**Discussion**

Inflammatory lung disease is the major cause of morbidity and mortality in CF. Although nonspecific anti-inflammatory medi-
cations (i.e., corticosteroids, ibuprofen) have been beneficial in clinical trials in slowing the decline in lung function in CF, clinical uptake is low owing to unacceptable side effects, such as growth impairment, weight gain, and risk of gastrointestinal bleeding. However, this “proof-of-concept” evidence has been the rationale in many studies for understanding the specific pathways mediating the increased inflammatory response to bacterial infection in CF, all with the goal of guiding the development of safe and effective anti-inflammatory therapies. Our group and others have generated evidence highlighting the importance of innate immune receptors, particularly TLR5, in mediating inflammatory responses to *P. aeruginosa* in CF (7, 9, 40). The mechanism or mechanisms underlying the increased immune response in CF, however, remain unknown.

This study aimed to identify pathways involved in the increased proinflammatory cytokine production occurring in CF in response to microbial stimuli. Our global gene expression profiling reflected a general theme of activated stress response mechanisms in immortalized CF airway cells that was already present at baseline, suggesting disturbance of cellular homeostasis. In particular, ER stress response mechanisms and the UPR were indicated in the GO functionality of ER stress relief mechanisms, such as autophagy (43). It is important to appreciate that in addition to misfolding of mutated CFTR protein, many factors are likely to have an impact on proteostasis to trigger ER stress in CF, including oxidative stress (11, 16, 17, 44–46), chronic infection (47), and decreased functionality of ER stress relief mechanisms, such as autophagy (21). Nevertheless, the literature contains conflicting results concerning the presence of ER stress in CF and the potential contribution of ER stress to CF inflammatory disease. Several studies report that ΔF508, the mutation found in 70% of all CF patients, is retained within the ER, leading to upregulation of protein degradation machinery (ER-associated degradation, autophagy) (43).

**FIGURE 6.** The flagellin- and tunicamycin-induced IL-6 responses are dependent on p38 MAPK activity. (A) Induction of ER stress with tunicamycin (6 h, 20 μg/ml) prior to flagellin stimulation significantly potentiates the proinflammatory immune response in immortalized CF cells. Pretreatment of IB3-1 cells with SB203580 (1 h, 1 μM) prior to flagellin (14 h, 100 ng/ml) or tunicamycin stimulation significantly decreases IL-6 production in (A) CF and (B) non-CF cell lines. Statistical analysis was performed by ANOVA using the Bonferroni posttest. Data are derived from at least three independent experiments. *p < 0.05, **p < 0.01, ***p < 0.001.

Our study expands the literature concerning ER stress and the UPR in CF. Although we confirmed an increased activity of the IRE-1 pathway in CF (evident by overexpression of *XBP-1s*), we also observed a lack of induction of the PERK–eIF2α pathway (evident by the lack of *DDIT3* induction and low levels of phospho-eIF2α at baseline conditions) (Fig. 3). However, we were able to induce the PERK–eIF2α pathway in the immortalized CF airway cells with ER stress inducer tunicamycin, indicating that in this model system this pathway is not defective but, rather, inactivated. A potential weakness of our study design was the use of immortalized airway cells. Indeed, C38 cells, although “corrected,” express not only wild-type CFTR but also mutant CFTR that still has the potential to induce ER stress. To specifically address this weakness, we validated this atypical pattern of UPR activation in both fresh blood cells and lung tissue from patients with CF (Fig. 3C, 3D). We also acknowledge that inflammation is a potential cause for ER stress (52–54), and with respect to the CF lung tissues (Fig. 3D), a clear interpretation of whether the increased UPR evident in these samples is due to inflammation or protein misfolding cannot be made. It has been suggested that this atypical pattern of UPR activation may be a fundamental cellular adaptation to chronic ER stress (55–57). PERK–eIF2α signaling is rapidly downregulated as a consequence of negative feedback loops within the UPR, which might indicate that long-term activation of this signaling axis is deleterious perhaps because of upregulation of CHOP and its targets (58, 59).

We hypothesized that this incomplete activation of the UPR was associated with the increased proinflammatory phenotype in CF by dysregulating inflammatory signaling events. We used two complementary approaches to test this hypothesis. First, we artificially increased ER stress in IB3-1 cells and subsequently stimulated with flagellin. Increased levels of ER stress exacerbated the IL-6 response to TLR5 signaling (Fig. 6A), supporting the hypothesis that imbalanced ER homeostasis augments proinflammatory TLR5 signaling. Second, on the basis of the evolutionary assumption that activation of the UPR network is beneficial in restoring cellular homeostasis, we elected to activate the PERK–eIF2α arm of the UPR rather than inhibiting the overactivated IRE-1–XBP-1 arm [as was performed by Martino et al. (52)]. Salubrinal inhibits GADD34 (60) and thus constitutively activates this pathway, as evidenced by the phosphorylation of eIF2α and the induction of *DDIT3* expression (Fig. 4). Intriguingly, preconditioning of immortalized CF airway cells with salubrinal significantly reduced the proinflammatory IL-6 response following exposure to both flagellin and live *P. aeruginosa* (Fig. 4C, 4D). Although reports

Nanua et al. (18) found that neither *XBP-1* splicing nor eIF2α phosphorylation was increased in CF cells compared with controls, suggesting that classical UPR activation is absent in CF cells.

...
have shown that inflammation is a potential cause for ER stress (52–54) and the data in Fig. 3D do not rule out that the increased inflammatory state leads to activation of the UPR, our results strongly suggest that this atypical activation of the ER stress response is associated with the proinflammatory phenotype of IB3-1 cells in response to infectious stimuli.

Our study was not designed to examine all consequences of atypical UPR activation in CF, but it is likely that incomplete activation of stress response mechanisms, such as the UPR, sensitizes the cell to innate immune signaling. Recently, two important stress response mechanisms have been reported to be dysfunctional in CF. The antioxidant response mediated by the TF NRF2 has been shown to be defective in CF cells, leading to increased oxidative stress and inflammatory responses (17). Autophagy, a catabolic process by which cells degrade dysfunctional content and organelles during periods of stress, is known to be activated by ER stress (61, 62); in turn, autophagy has been reported to decrease ER stress (63). Recently, Luciani et al. (21) reported that CF cells failed to induce autophagy in response to nutrient starvation, indicating that this important relief mechanism is dysfunctional in CF cells. Intriguingly, some reports have suggested that both the NRF2-mediated antioxidant response and autophagy are under the control of the PERK–eIF2α pathway (64–66). Thus, in the case of decreased induction of this pathway upon ER stress, homeostasis is not restored, possibly leading to sensitization of proinflammatory signaling events.

Our finding of atypical UPR activation in CF led us to investigate the link between imbalanced ER homeostasis and proinflammatory innate immune signaling. Numerous studies have shown that the proinflammatory response to infection is dysregulated in the CF airway. The mere absence of CFTR can induce increased NF-κB signaling (67, 68), supporting the concept that CF cells are at least more responsive to inflammatory stimuli, if not already proinflammatory, in the absence of infection. The results returned by our gene expression profiling prompted our investigation of the inflammatory response to infection in human airway epithelial cells ex vivo. Our data suggest that the activation profile of the UPR in CF cells and observed that the PERK–eIF2α arm of the UPR is not induced in CF cells. We report, to our knowledge, for the first time that this atypical activation of the UPR is associated with the hyperinflammatory phenotype of immortalized CF airway cells, as deliberate, therapeutic activation of the PERK–eIF2α pathway in IB3-1 cells attenuates proinflammatory immune responses to microbial stimuli. Furthermore, we provide evidence that unopposed ER stress induces inflammatory responses dependent on p38 MAPK activity, suggesting that ER stress provides an additional signal leading to increased and prolonged p38 MAPK activation, culminating in an exaggerated proinflammatory innate immune response. Strategies to restore ER homeostasis, normalize the UPR, and alleviate ER stress may prove useful in controlling the damaging proinflammatory immune response occurring in the airways of people with CF.

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Disclosures
The authors have no financial conflicts of interest.

References


