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The Yin and Yang of Cystic Fibrosis Transmembrane Conductance Regulator Function

Implications for Chronic Lung Disease

The cystic fibrosis (CF) transmembrane conductance regulator (CFTR) is a cAMP-activated anion channel, primarily expressed in ciliated epithelial cells that have an endoluminal lining of mucus. Genetic mutations in CFTR are known to induce its peripheral and/or endoplasmic reticulum-associated degradation affecting its cell surface expression and/or stability, resulting in the pathological manifestations of CF lung disease, including hypohydration and increased viscosity of mucus, predisposing affected individuals to recurrent infections. Recent studies have identified low levels of CFTR expression in inflammatory cells such as T cells, neutrophils, and macrophages (1–3), suggesting an additional role for CFTR in the pathogenesis of chronic inflammatory CF lung disease. CFTR has also been suggested to mediate internalization and phagocytosis (4, 5) of *Pseudomonas aeruginosa* (*Pa*), a common CF pathogen. A recent study suggests that a bacterial toxin, Cif (PA2934) secreted in outer membrane vesicles by

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Pa, reduces CFTR-mediated chloride secretion by human airway epithelial cells (6). In this issue of the *Journal*, Le Gars and colleagues (pp. 170–179) describe a novel mechanism for proteolytic cleavage of CFTR that disables the channel function (7).

Several recent studies demonstrate that membrane-CFTR expression/activity is modulated by cigarette smoke (CS) exposure (3, 8–10). The CFTR-dependent nasal potential difference is also suppressed in cigarette smokers (9, 11). These studies provide experimental evidence supporting the concept of acquired CFTR dysfunction induced by CS and its role in pathogenesis of chronic obstructive pulmonary disease (COPD). The CS-induced CFTR dysfunction has been suggested to modulate lipid-raft platforms initiating inflammatory-apoptotic responses and aberrant autophagy (3, 12). The mechanisms by which CS modulates membrane-CFTR levels and activity may include the induction of unfolded protein response, as the *Cfr* gene is a target of the unfolded protein response protein ATF6 (13, 14). In addition, CS may induce accumulation of

CFTR as an immature B-form in the endoplasmic reticulum (3) by inducing its misfolding. Oxidants and CS may also interfere directly with CFTR protein function by altering key cysteine residues in CFTR to affect its potentiation or open channel probability (15).

The current study by Le Gars and colleagues describes an important and novel observation that neutrophil elastase promotes CFTR degradation (7), raising the intriguing possibility that this mechanism contributes to the pathogenesis of chronic obstructive lung disease. Recent studies demonstrating CS-induced acquired CFTR dysfunction in COPD support this notion. Additionally, the authors suggest that *Pa* infection may similarly impact CFTR ion channel activity in both CF and COPD. Conversely, membrane-CFTR may regulate bacterial pathogenesis and inflammatory-apoptotic signaling (3, 8, 12). It is not clear if the decrease in membrane-CFTR (genetic or acquired) activity is sufficient to trigger chronic lung disease or whether it requires an additional stimulus such as subsequent *Pa* infection (CF/COPD) and/or CS exposure (COPD).

The current study uses a carcinoma cell line and an acute infection animal model to clearly demonstrate the role of neutrophil elastase and calpains in CFTR dysfunction, suggesting an additional mechanism whereby neutrophil elastase contributes to the pathogenesis of CF lung disease. The chief function of neutrophils in host defense is to restrain and destroy invading microbial pathogens (16). Neutrophils accomplish this task by binding and internalizing the pathogens via a complex process termed phagocytosis, eventually killing the organisms through the combined actions of potent antimicrobial compounds including reactive oxygen and nitrogen species, antimicrobial peptides, and proteinases such as elastase that are delivered to the nascent phagosome (17). Although these antimicrobial functions are usually performed without injury to host tissues, in pathological circumstances such as during progressive bacterial infection, these potent antimicrobial compounds can be released extracellularly where they can induce a spectrum of responses in host cells ranging from activation to injury and death. Unregulated release of these neutrophil-derived cytotoxic compounds, particularly elastase, is believed to contribute to inflammatory injury to the gastrointestinal tract (18) and lungs (19, 20).

As indicated by their name, proteinases were originally identified as protein-degrading enzymes that can degrade a diverse range of substrates including various components of the extracellular matrix such as collagen (collagenases) and elastin (elastases) (21). In contrast to the widely held view that proteinases function primarily as simple degradative enzymes, it is now appreciated that proteinases control diverse physiological processes including immune responses, cell proliferation and death, wound repair, digestive processes, and recycling of critical proteins and organelles (22, 23). With respect to inflammatory processes, proteinases such as elastase and matrix metalloproteinases are able to activate cytokines, growth factors, and cell surface receptors by limited proteolytic processing (24). In contrast to signal transduction pathways initiated by traditional receptor–ligand interactions, proteinase-mediated signals are transmitted through the cleavage of protein substrates resulting in their activation, inactivation, or alteration of function (22). One example of such proteinase-mediated signaling relevant to inflammatory lung diseases involves proteinase-activated receptors (PARs) such as PAR-1, which can be activated by limited proteolytic cleavage by elastase, resulting in apoptosis of lung epithelial cells (25). Notably, elastase-mediated apoptosis of lung epithelial cells has been implicated in the pathogenesis of the acute respiratory distress syndrome (26, 27) and COPD (28).

In addition to PARs, neutrophil elastase has been shown to degrade numerous receptors involved in control of innate and adaptive immune responses such as CD2, CD4, and CD8 on T lymphocytes (29), and phagocytic receptors such as CD16 (30) expressed by neutrophils and macrophages. Neutrophil elastase is able to degrade

receptors that are involved in recognition and clearance of apoptotic cells, which has significant implications for the resolution of neutrophilic inflammation in diseases such as CF (31). Neutrophil elastase also can directly cleave and activate the epithelial sodium channel, thus altering fluid and electrolyte transport across the pulmonary epithelium, a process that results in mucous dehydration and contributes to the pathogenesis of CF lung disease (32, 33).

In the current study, Le Gars and colleagues describe a novel mechanism by which neutrophil elastase induces proteolytic cleavage of CFTR (7). The authors demonstrate that the CFTR protein is degraded in a neutrophil elastase–dependent manner. Unexpectedly, as opposed to direct degradation of CFTR by neutrophil elastase, the authors describe a mechanism whereby neutrophil elastase activates intracellular calpains that, in turn, are directly responsible for the proteolytic degradation of CFTR. Notably, this proteolytic degradation of CFTR abrogates the chloride transport function of the CFTR protein, which has crucial pathophysiological consequences for inflammatory lung diseases such as CF and COPD as described above. Importantly, the authors demonstrate the importance of this pathway in an animal model of bacterial lung infection, underscoring the relevance of this pathway to more complex model systems. These observations have important implications for the pathogenesis of CF as well as COPD. Hence, as discussed above, further studies are warranted to determine if a decrease in functional membrane-CFTR (via genetic mutation or CS exposure) and/or *Pa* infection (via neutrophil elastase and calpains) is a critical step(s) in the initiation of chronic inflammatory responses in the lung contributing to the pathogenesis of obstructive lung disease.

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The Elusive “Gold” Standard for Detecting *Mycobacterium tuberculosis* Infection

When introduced in 2001, IFN- γ release assays (IGRAs) were seen as a potential breakthrough in tuberculosis (TB) control because they could be completed with one patient visit and because they might avoid the subjectivity and variability

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associated with placing and reading the tuberculin skin test (TST) (1). Variability of the TST has been well described in both qualitative and quantitative terms during its long history of use (2). However, increased test–retest reliability of IGRAs compared with TST has been difficult to demonstrate. Lack of a gold standard for diagnosing *Mycobacterium tuberculosis* infection, the potential for TST to boost subsequent TST and IGRA results, the complexity of IGRAs, and the shortcomings of statistical methods limit assessment and comparisons between the tests. IGRA variability has been assessed in relatively few studies, and in most cases using different “yardsticks.”