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Overview of CF lung pathophysiology



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Abstract

Defects of the cystic fibrosis (CF) transmembrane conductance regulator (CFTR) protein affect the homeostasis of chloride, bicarbonate, sodium, and water in the airway surface liquid, influencing the mucus composition and viscosity, which induces a severe condition of infection and inflammation along the whole life of CF patients. The introduction of CFTR modulators, novel drugs directly intervening to rescue the function of CFTR protein, opens a new era of experimental research. The review summarizes the most recent advancements to understand the characteristics of the infective and inflammatory pathology of CF lungs.

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Keywords

Cystic fibrosis, CFTR modulators, Pseudomonas aeruginosa, Staphylococcus aureus, Lung inflammation, Reactive oxygen species.

Abbreviations

CF. Cystic Fibrosis: CFTR. Cystic Fibrosis Transmembrane conductance Regulator; IL-8, Interleukin 8; P aeruginosa, Pseudomonas aeruginosa; ENaC, Epithelium Sodium Channel; ASL, Airway Surface Liquid; BALF, Bronchoalveolar Lavage Fluid; PMN, PolyMorphonuclear Neutrophil; PTEN, phosphatase and tensin homolog deleted in chromosome 10.

Introduction

CF is a genetic disease caused by mutations of the cystic fibrosis transmembrane conductance regulator (CFTR) gene, localized on chromosome 7, which was correctly predicted as an ion transporter since the gene discovery [1-3]. More than 2000 CFTR gene variants have been identified so far, a few hundred being confirmed as disease causing mutations [4*].

In order to provide an operational synopsis of the effects of such a wide series of CFTR gene variants on CFTR biology, CFTR mutations have been categorized into six major classes depending on their main pathologic effects on CFTR protein, namely, Class I: absence of protein, Class II: protein trafficking defect, Class III: no function, Class IV: reduced function, Class V: reduced protein, Class VI: reduced protein stability [for review see the study by Bell et al. [5]].

As a result of CFTR protein mutations, CF disease affects the function of several organs, mainly exocrine pancreas, liver, intestinal tract, salivary glands, male reproductive organ, sweat glands, being the pathology in the respiratory tract the main cause of morbidity and reduction of life expectancy [6*]. Since the milestone of the CFTR gene discovery in 1989, tremendous progresses have been made in understanding the basic CF defect. This allowed to develop and apply novel drugs, termed "CFTR modulators," which act directly on the mutated protein by rescuing at least in part its defective function [7*]. In spite of these exciting therapeutic improvements, which make CF disease entering the era of the novel CFTR modulator Trikafta [8,9], different questions remain unanswered on CF lung pathophysiology.

Defective CFTR protein affects ion and fluid homeostasis in the respiratory mucosa

CFTR protein has been confirmed as an ATPdependent, protein kinase A and C regulated, transporter of chloride and bicarbonate [10,11]. These ions are secreted from the apical membrane of different kinds of epithelial cells composing the airway mucosa and submucosa. The cell types that express CFTR gene/ protein is a hot field of research. For example, recent single cell RNA-sequencing studies revealed CFTR-rich pulmonary ionocytes [12,13]. Furthermore, more recent studies on proximal and distal airways in control and CF airway epithelia suggest that secretory cells (but not ciliated cells, which had been previously considered as dominant CFTR-expressing cells [14]) are the dominant CFTR-expressing cell type [15**,16]. In addition to direct ion transport, CFTR inhibits the activation of the epithelial sodium channel (ENaC) [17] and regulates other chloride channels [18]. Because of defective chloride and bicarbonate secretion and excessive sodium reabsorption, it is logically expected that the airway surface liquid (ASL) residing on top of the apical membranes of the epithelium of the CF airways should be altered. However, the equilibrium between different phases of fluid secretion and absorption made this issue extensively debated for years, with contradictory results due to the complexity of the *in vivo* measurements of the physic-chemical parameters of ASL in CF patients [19]. Although still under scrutiny, the prevalent consensus now considers that the ASL of CF lungs is dehydrated and more acidic in respect to non-CF ASL [20].

Impaired ASL homeostasis affects the biology of CF airway mucosa

The ASL consists of a hydro-gel mucus layer with gelforming mucins constituting a mesh that traps dust and microorganisms. These are rapidly transported from distal airways to trachea by ciliary beating, the mucociliary clearance being considered the very basic innate defense mechanism in the lungs. The pH and the relative content of mucins and water in ASL is critical for the viscosity of the mucin hydrogel [20]. In CF, dehydration reduces the periciliary liquid and increases the viscosity of the mucin hydrogel mesh, which reduces the frequency of the muco-ciliary beating mechanism [21^{**}]. Besides the reduced hydration, bronchoalveolar lavage fluid (BALF) obtained from young CF patients revealed increased concentration of mucins (MUC) 5B and 5AC [22**], although it is not clarified whether this depends on the primary CFTR defect or it results from a mechanism secondary to the advanced stages of the CF lung pathology. Interestingly, markers of inflammation were found elevated either in presence or in absence of bacterial infection [22**]. Thus, altered physicochemical properties of mucus in CF ASL are considered an upstream initiating, and later amplifying, pathogenic mechanism in between defective ion transport and the infective/inflammatory process [21**,22**].

The onset of CF lung disease has been demonstrated since the early months of the life of CF infants, even in the absence of overt respiratory symptoms, as the bronchioles of CF infants has been found filled with polymorphonuclear neutrophils (PMN) [23]. Lung disease starts from a clinically asymptomatic phase that is followed by recurrent, and lately, chronic bacterial infections, associated with inflammation, conditions leading to damages of the bronchial walls, with dilations (bronchiectasis) filled with mucopurulent sputum. A huge number of microorganisms and PMNs in lumen constitutes an infective/inflammatory condition leading to progressively severe obstructive respiratory insufficiency [23]. CF lung pathology could be summarized with the two key points of infection and inflammation: 1) recurrent infections with *Haemophilus influenzae* in childhood and with *Staphylococcus aureus* (*S. aureus*) in early life are progressively substituted in adulthood with recurrent infection with *Pseudomonas aeruginosa* (*P. aeruginosa*), which lately chronically infects CF airways; 2) CF cellular and humoral immune defenses, that are inefficient in clearing bacterial infections, mount an "exaggerated" inflammatory response characterized by a huge amount of PMNs filling the airway lumen. Both recurrent and chronic infection and exaggerated inflammation contribute to bronchial wall tissue damage and progressive airway flow obstruction, leading to progressively severe respiratory insufficiency.

CF airways mucosa as a pro-infective milieu

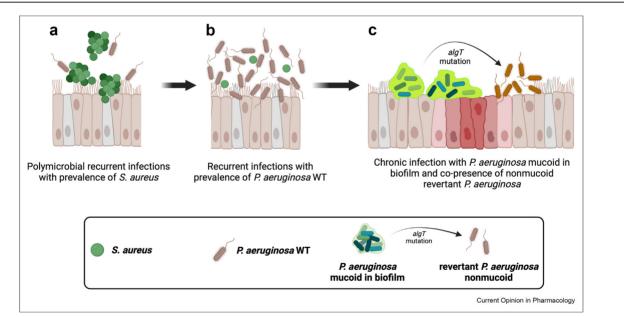
As mentioned, impaired muco-ciliary clearance and mucus abnormality is widely believed to constitute the favorable milieu for CF lung infections [21**,22**]. Although CF infections are polymicrobial along the whole life, including *H. influenzae*, Stenotrophomonas maltophilia, Achromobacter xylosoxidans, Nontuberculous mycobacteria, different fungi (e.g. Aspergillus and Candida species) and viruses (e.g. rhinovirus, influenza virus, respiratory syncytial virus) and other microorganisms, the main attention in clinics and research has been focused on S. aureus and P. aeruginosa, considered the major infectious effectors of CF lung tissue damage [24]. Predominance of S. aureus in lung expectorate early in life of CF patients has been related to a CFspecific defective immune response dependent on reduced pH in CF ASL, which favors survival of this bacterium [25]. In CF adults, *P. aeruginosa* becomes the predominant infection agent overtaking S. aureus, possibly by inducing the host secretion of the bactericidal enzyme type-IIA-secreted phospholipase A2, which kills S. aureus with limited lytic effects on P. aeruginosa [26], although coexistence of both microorganisms persists in CF adults [27].

The reason why *P. aeruginosa*, a ubiquitous environmental opportunistic microorganism causing disease almost only in immunocompromised individuals, becomes the predominant infectious agents in CF adults is still unknown, unless we consider the general hypothesis of CF as a mucosal immunodeficiency condition [28]. In this respect, it has been reported the association of the tumor suppressor phosphatase and tensin homolog deleted in chromosome 10 (PTEN) with defective CFTR, the latter acting as scaffold protein for PTEN. The CFTR-PTEN association induces mitochondrial metabolic dysfunction by increasing the release of itaconate and succinate, a condition promoting a selective advantage for P. aeruginosa infection in CF [29,30**]]. This mechanism could also be favored by the inhibition of the bacterial killing of CF macrophages exposed to the protease LasB, one of the virulence factors released by *P. aeruginosa* [31].

Evolution and adaptation of *P. aeruginosa* infection

Free flowing flagellated and piliated, so termed "wild type" or "environmental" or "planktonic", P. aeruginosa strains start infecting CF patients at a median age of one vear [32]. During childhood, P. aeruginosa infections are recurrent and in principle antibiotics at high doses could eradicate them. Soon or later, P. aeruginosa infecting CF adults undergoes several genomic mutations leading to a flagellum- and pili-deprived nonmotile "mucoid" phenotype, an evolution intervening in CF patients at the median age of thirteen years [32]. Bacterium mutated with mucoid phenotype lives much better protected than wild-type planktonic one from mucosal anti-microbial peptides, innate and adaptive host immune system, and antibiotics while encapsulated in biofilms. The protecting effect on P. aeruginosa is thought to be dependent on at least three major exopolysaccharides produced by the bacterium itself, namely alginate, Pel and Psl, which sustain the antimicrobial tolerance [33]. Different a condition which practically impedes bacterial eradication and is considered a true irreversible chronic infection. The role of the huge amount of reactive oxygen species (ROS) and redox unbalance in CF airway mucosa in producing a series of mutations in the genome of *P. aeruginosa*, leading to mucoid phenotype, has been extensively studied [for summary see the study by Malhotra et al. [34**]]. Relevantly to pathophysiology and pharmacology, entering the irreversible stage of the chronic *P. aeruginosa* infection does not mean that all CF bronchial tree is irreversibly and exclusively infected by the mucoid strains growing in biofilms. Actually, mucoid P. aeruginosa is known since long time to be instable in CF lung in vivo and to revert frequently back to planktonic form, because of accumulation of new genomic mutations. The switch from mucoid to nonmucoid, and again back to mucoid phenotypes, is assumed as a frequent process in vivo CF lung [35-37]. Interestingly, as recently reported by analyses of BALF obtained selectively from 6 pulmonary lobes of CF patients, different lung areas are infected at the same time by mucoid or by planktonic non-mucoid, again by mucoid/non-mucoid mixed strains [38**], suggesting to us a "leopard skin spots" heterogeneous model of *P. aeruginosa* infection in adult C6F lungs (Figure 1). Importantly, the heterogeneous type of P. aeruginosa phenotypes, co-existing in the same lung of chronically infected CF patients, leads to different

Figure 1



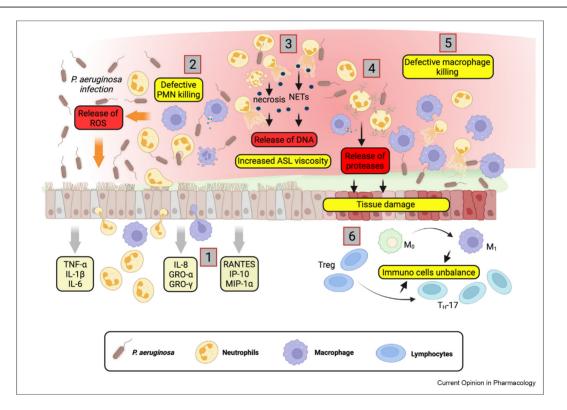
Evolution of bacterial infection in CF lung. The basic defect of *CFTR* leading to altered ASL with more viscous and acidic mucus favors bacterial infections since the early years of life of CF patients [17**,18**]. (a) During childhood, recurrent bacterial infections are mainly polymicrobial with *S. aureus* becoming progressively prevalent, possibly due to the acidic ASL environment [25]; (b) During adolescence, *P. aeruginosa*, which is present in CF airways since the early years of life, eradicates the *S. aureus* infection, possibly by action of a specific phospholipase providing selective advantage [26]; (c) During adulthood, the genome of wild type *P. aeruginosa* undergoes a series of mutations, possibly dependent on the CF pro-oxidative milieu of the ASL, loosing flagellum and pili and secreting alginate to build a biofilm, inside which it results more protected from the host immune responses and antibiotics [32]. The mutant *P. aeruginosa* recurrent infection thus evolves as a chronic one, sustained by the presence of mucoid strains. These mucoid strains further evolve towards revertant nonmucoid strains expressing flagellum and pili [34**,35–38]. The lungs of chronically infected CF patients therefore harbor at the same time *P. aeruginosa* mucoid strains in biofilms, nonmucoid revertant with flagellum and pili and mixed phenotypes, resembling a "leopard-like skin heterogeneous model" of infection and inflammation [34**]. Graph created with BioRender.com.

degrees of inflammatory/immune response among the different lobes [38**]. These findings contradict the scenario of a topographically homogeneous infective phenotype, corresponding to a homogeneous immune response in whole CF lung. In addition, the heterogeneity of chronic P. aeruginosa infection seems to best fit the previously advanced hypothesis that exacerbations, periodically affecting chronically infected CF patients and severely worsening their lung function, reflect most likely the spread of the disease from more infected to less/not-infected areas of the same lung, rather than being dependent on an intensification of the bacterial load [39]. This hypothesis on the main mechanism of CF infective exacerbations is, in our opinion, more easily explained by the co-presence of motile, planktonic bacteria, not only mucoid bacteria strictly confined in biofilms firmly adherent to bronchial walls.

Figure 2

The CF inflammatory response is ineffective and harmful

Whether the innate immune inflammatory response in CF lungs precedes or follows the bacterial infection has been debated for years. Although contradictory reports are presented, which leave this issue still unsettled, bacterial infection intervenes very early in CF life, either inducing or amplifying a series of host inflammatory responses modulated by different mucosal cell components [40,41] (Figure 2). CF mucosal epithelium is not a simple physical barrier to protect the airway mucosa from penetrating microorganisms but is known to orchestrate the strong chemotactic process driving PMNs in the CF lumen [42]. The huge amount of PMNs filling CF mucosa are inefficient in avoiding *P. aeruginosa* chronic infection but their presence, continuously activated by bacterial products, results in a



Key features of the host immune response in CF airway mucosa. Graphical summary of the hallmarks of the mucosal host response in advanced CF airways disease. 1) CF bronchial epithelium exposed to pathogen activated molecular patterns (PAMPs) activates the expression of pro-inflammatory cytokines (TNF- α , IL-1 β , IL-6) and chemokines recruiting PMNs (IL-8, GRO- α/γ) and mononuclear immune cells (RANTES, IP-10, MIP-1 α) mainly, but not exclusively, through MyD88-dependent toll-like receptors 2, 4, and 5 signaling [42]; 2) CF PMNs present a defective bacterial killing in respect to *P. aeruginosa* and their continuous stimulation by bacterial PAMPs induce massive release of reactive oxygen species (ROS), which contribute to unbalance the redox equilibrium of CF ASL towards a pro-oxidative status [41], which affects CFTR protein stability [65]; 3) huge amount of PMN DNA derived from Neutrophil Extracellular Traps (NETs) and PMN hypoxic necrosis further worsen the viscosity of CF ASL [44*,45]; 4) besides ROS and DNA, CF PMNs exposed to continuous bacterial stimulation release a series of proteases, first of all neutrophil elastase, which contribute to bronchial wall damage and dilation resulting in bronchiectasis, anatomical niches favoring bacterial stasis, thus recurrent bacterial exacerbations; 5) CF macrophages present defective *P. aeruginosa* killing and defective removal of dead neutrophils, the latter being a critical process that is necessary to reestablish tissue homeostasis [47]. Moreover, they contribute to release of ROS in CF ASL and are implicated in selecting an environment favoring *P. aeruginosa* chronic infection [29–31,48–50]; 6) as a result of M₁ preferential polarization of CF macrophages, a T cell unbalanced pattern has been found, where T_H-17 pro-inflammatory cells are prevalent of Treg cells [54–56]. Graph created with BioRender.com.

series harmful effects, such as: 1) the release of ROS. contributing to a pronounced pro-oxidative redox unbalance [43]; 2) the spread of DNA on mucosal surface, both from PMN necrosis and release of neutrophil extracellular traps, which further increase ASL viscosity and are associated with lung disease severity [44*]; 3) the exocytosis of proteases, which contribute to damage the fibers of the extracellular matrix of the bronchial walls and to amplify the inflammatory response, with very limited effect on bacterial killing [45]. Overall, the presence of a huge number of activated neutrophils is thought to have a critical role in CF lung pathology, thus the neutralization of neutrophil elastase or the fine regulation of recruitment of these cells in the airway lumen by the chemokine IL-8/CXCL8 are considered relevant therapeutic targets [46]. Besides neutrophils, CFTR mutations are implicated in immune functions of macrophages, which show reduced efficiency in removing dead neutrophils [47], a critical process to reestablish tissue homeostasis. Macrophages are gaining a critical role in further explaining the defective CF host response to *P. aeruginosa* and to sustain a proinflammatory status by preferential polarization to M1 phenotype [47-52]. Although M1 polarization of macrophages is mainly applicable to *in vitro* investigation with limited translation into *in vivo* setting [53], a possible consequence of CF macrophage dysfunction and M1 polarization has been also suggested as regards an imbalance of anti-inflammatory regulation of the adaptive immune branch, where a reduced Tregs cells presence has been observed in CF patients and accompanied by preferential increments of Th-17 cells (the latter actively involved in PMNs recruitment in CF bronchi [54,55]), an imbalance that does not seem corrected by CFTR modulators [56].

Entering the era of the novel CFTR modulator Trikafta, CF lung pathophysiology should consider not only its effects on chronic infection and inflammation on bronchial tissue damage, but also on the efficiency of rescue of mutant CFTR in CF patients treated with CFTR modulators. Several reports consistently indicate that the rescue by CFTR modulators of the most common F508del-mutated CFTR protein in bronchial epithelial cells is strongly reduced by planktonic P. aeruginosa [57-64], the proposed mechanisms including quorum sensing [62], LasB protease [63], the interference with expression of the CFTR scaffolding protein NHERF1 [59]. In parallel, the ROS abundantly released in the CFASL inflammatory milieu, as a result of activated PMNs by bacterial infections, have been shown to strongly reduce wild type and F508del-CFTR expression through a mixed lineage kinase-3 dependent activation inducing CFTR proteolysis [65]. In contrast, it has been reported that the supernatant obtained from mucopurulent material (SMM) of CF lungs augments *in vitro* the rescue of F508del-CFTR by CFTR modulators $[66^{**}]$, a recent finding that will open a series of further investigations.

Conclusions

A defect in muco-ciliary clearance of the airways due to viscous respiratory mucus has been suggested since the early clinical identification of cystic fibrosis (CF), originally termed "mucoviscidosis." CFTR gene identification and the intense clinical and experimental research have confirmed the role of altered airway mucus in the onset of inflammation and infection, although the final answer revealing the mechanism of the selectivity of *P. aeruginosa* is still debated. In the years, a condition of relative deficiency of CF mucosal defenses is gaining consensus, as either CFTR defects seem to involve directly or indirectly the bacterial killing efficiency of CF PMNs and macrophages. The chronic infective/inflammatory condition has implications not only on bronchial wall damage but also on the efficiency of novel CFTR modulators. Whether the cascade of events starting from CFTR ion transport defects down to chronic infection and inflammation is becoming consistently clear, that the novel CFTR modulators will be per se sufficient to completely revert lung infection and inflammation of adult CF patients to a reasonably stable respiratory function is presently under scrutiny.

Author contributions

Conceptualization: GC, AR, MB. Data curation and formal analysis: GC, AR, MB, PP, RG. Methodology: GC, AR, MB. Writing - original draft: GC. Writing - review and editing: GC, AR, MB, PP, RG. All authors read and approved the final manuscript.

Availability of data and material

Not applicable.

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Ethics approval and consent to participate Not applicable

Conflict of interest statement

GC, AR, MB, PP, RG report no conflict of interest.

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A state of the art of the mucus alterations in the airway surface liquid of patients with CF, analyzing different biochemical and physiological aspects, with implications towards clinical therapeutics.

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Here the report of the analyses of the ASL composition, inflammatory and infectivity markers in the bronchoalveolar lavage fluids (BALFs) obtained from 46 preschool children with CF and 16 non-CF diseased controls enrolled in the Australian Respiratory Early Surveillance Team (AREST) for CF study. Due to its invasiveness, the study is one of the few available reporting results from *ex vivo* sampling of young CF patients. The results focus on the role of CF airway mucus in relation to both infection and inflammation and provides further hints on the origin of the inflammatory process and its dependence on bacterial infection.

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This paper completes a series of previous observations which identify CFTR protein as a scaffold protein for PTEN. Defective CFTR therefore

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This review provides an excellent presentation of different key aspects of *P. aeruginosa* CF lung infection mainly, but non-exclusively, from the microorganism side. It includes the evasion of innate immunity, the adaptation during chronic infection evolution, the mechanisms of mutagenesis and alginate biofilm synthesis, the mucoid conversion with instability and its nonmucoid reversion, the heterogeneity of *P. aeruginosa* phenotypes in the CF chronically infected lung.

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Malhotra and Coll. study a cohort of 14 adults CF patients chronically colonized with *P. aeruginosa* performing in each patient a bronchoalveolar lavage in 6 different lobes to isolate and characterize bacterial phenotypes and the degree of inflammatory response in different areas of their lungs. Results demonstrate the heterogeneity of *P. aeruginosa* phenotype during chronic colonization by finding in different regional areas either mucoid or nonmucoid strains together with mixed colonies in the same patient. Interestingly, the different phenotypes were found associated with different degrees of inflammatory response, as studied by measuring the concentration of the classical cyto-chemokines found in CF lungs (e.g. TNF-alpha and IL-8). The article provides strong *ex vivo* proof of the heterogeneity of infective/inflammatory status in each adult CF patient chronically infected with *P.aeruginosa*.

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This investigation tests the effect of the supernatant of mucopurulent material (SMM), a pool of sputum extracted from different adult CF lungs, filtered from living bacteria, which contains a large series of molecules, on F508del-CFTR rescue with CFTR modulators on CF airway epithelia grown polarized at the air-liquid interface *in vitro*. The results 1) exclude that novel generation CFTR modulators has antiinflammatory effect by reducing the expression and release of the pro-inflammatory mediator IL-8 (CXCL8) from CF epithelium and 2) show that F508del-CFTR rescue is augmented by the SMM. The article opens a new perspective and suggests investigation on the underlying mechanisms activated by SMM and how to reconcile them with previous reports showing the opposite effects observed with living *P. aeruginosa* on rescue of mutated F508del-CFTR operated by CFTR modulators.