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<td>Leung, Janice; University of British Columbia, Medicine; Tiew, Pei Yee; Singapore General Hospital, Respiratory and Critical Care Medicine; Mac Aogáin, Micheál; Nanyang Technological University, Lee Kong Chian School of Medicine; Budden, Kurtis; University of Newcastle, Priority Research Centre for Healthy Lungs; Yong, Valerie Fei Lee; Nanyang Technological University, Lee Kong Chian School of Medicine; Thomas, Sangeeta; Nanyang Technological University, Lee Kong Chian School of Medicine; Pethe, Kevin; Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore, Translational Respiratory Research Laboratory; Hansbro, Philip; The University of Newcastle, Centre for Asthma &amp; Respiratory Disease; Hunter Medical Research Institute, Vaccines, Infection, Viruses &amp; Asthma; Chotirmall, Sanjay; Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore, Translational Respiratory Research Laboratory</td>
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THE ROLE OF ACUTE AND CHRONIC RESPIRATORY COLONISATION AND INFECTIONS IN THE PATHOGENESIS OF COPD

*Janice M. Leung¹ MD, *Tiew Pei Yee² MD, Micheál Mac Aogáin³ PhD, Kurtis F. Budden⁴ PhD, Valerie Yong Fei Lee³ BSc, Sangeeta S. Thomas³ MD, Kevin Pethe³ PhD, Philip M. Hansbro⁴ PhD and Sanjay H. Chotirmall⁴ MD PhD

¹Centre for Heart Lung Innovation and Division of Respiratory Medicine, St Paul’s Hospital, University of British Columbia, Vancouver, British Columbia, Canada; ²Department of Respiratory and Critical Care Medicine, Singapore General Hospital, Singapore; ³Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore; ⁴Priority Research Centre for Healthy Lungs, University of Newcastle and Hunter Medical Research Institute, Newcastle, Australia.

*Joint 1st authors

Correspondence to: Assistant Professor Sanjay Haresh Chotirmall, Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore

E-mail: schotirmall@ntu.edu.sg

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ABBREVIATIONS: COPD: Chronic obstructive pulmonary disease; AECOPD: acute exacerbation of chronic obstructive pulmonary disease; IPA: Invasive pulmonary aspergillosis; IA: Invasive aspergillosis; Th2: T-helper 2; Ig: Immunoglobulin; PAMP: pathogen-associated molecular pattern; PRR: pattern recognition receptors; NE: neutrophil elastase; LTB4: leukotriene B4; MMP: matrix metalloproteinase; MPO: myeloperoxidase; PPM: potentially pathogenic microorganisms; NTHi: Non-typeable *Haemophilus influenzae*; NTM: Non-tuberculous mycobacteria; E1A: Adenovirus early region 1A; ICAM-1: Intercellular Adhesion Molecule 1; ROS: Reactive oxygen species NF-κB; TNF: Tumour necrosis factor; RSV: respiratory syncytial virus; ICS: inhaled corticosteroid; LABA: long acting β2-agonist; MDR; multi-drug resistance.
ABSTRACT

Chronic obstructive pulmonary disease (COPD) is a major global concern, increasingly so in the context of aging populations. The role of infections in disease pathogenesis and progression, is known to be important yet the mechanisms involved remain to be fully elucidated. While COPD pathogens such as *Haemophilus influenzae*, *Moraxella catarrhalis* and *Streptococcus pneumoniae*, are strongly associated with acute exacerbations of COPD (AECOPD), the clinical relevance of these pathogens in stable COPD patients remains unclear. Immune responses in stable and colonised COPD patients are comparable to those detected in AECOPD, supporting a role for chronic colonization in COPD pathogenesis through perpetuation of deleterious immune responses. Advances in molecular diagnostics and metagenomics now allow the assessment of microbe-COPD interactions with unprecedented personalisation and precision, revealing changes in microbiota associated with the COPD disease state. As microbial changes associated with AECOPD, disease severity and therapeutic intervention become apparent, a renewed focus has been placed on the microbiology of COPD and the characterisation of the lung microbiome in both its acute and chronic states. Characterisation of bacterial, viral and fungal microbiota as part of the lung microbiome has the potential to reveal previously unrecognised prognostic markers of COPD that predict disease outcome or infection susceptibility. Addressing such knowledge gaps will ultimately lead to a more complete understanding of the microbe-host interplay in COPD. This will permit clearer distinctions between acute and chronic infection and more granular patient stratification that will enable better management of these features and of COPD.
1. INTRODUCTION

The role of microbes and infection in obstructive lung disease was first proposed in the 1950s by the British hypothesis. This states that recurrent infection and mucus hypersecretion were the primary causes of progressive airways obstruction in smokers. However, subsequent studies failed to detect significant associations between infection and lung function decline and consequently, exposure to noxious particles and gases were advanced as the principal causes of COPD.¹ A wealth of evidence shows that the isolation of bacteria, viruses and fungi in the airways of stable COPD patients is in fact significant and has implications for disease pathogenesis, progression and treatment. This places a renewed emphasis on microorganisms isolated from the COPD lung, driving us to revisit the original British hypothesis.² Advances in diagnostic technologies now permit a more accurate detection of specific pathogens in COPD while molecular studies shed light on the immune response elicited by COPD-associated microorganisms. Metagenomic studies have revealed microbial consortia in both healthy and diseased individuals, helping to define pathogenic and beneficial microbes associated with various disease states. This has major implications for our understanding of COPD and its therapy, particularly in the face of antibiotic-mediated lung dysbiosis during therapy. Therefore, both acute and chronic infections are linked to COPD disease progression and exist as components of overarching lung microbiome architecture, which is modulated during therapeutic intervention. Characterising this dynamic interaction between microbes, therapy and disease states is now a central focus in COPD research. Further, the emergence of antibiotic resistance in COPD-associated pathogens is also a growing international concern and greater emphasis on antimicrobial stewardship and rational therapies is of increasing importance. Ultimately, the role
of microbes and infection in COPD may reveal novel prognostic markers of disease which in turn provide scope for more focused interventions and novel therapeutic approaches.

2. ACUTE INFECTION IN COPD: VIRAL AND BACTERIAL SUPERINFECTION AND THEIR ROLE IN COPD EXACERBATION

Periodic worsening of respiratory symptoms in patients with COPD are known as acute exacerbations (AECOPD). They can have marked effects on lung function, quality of life, and health socioeconomic burden. The exact nature and cause of these events can often be difficult to establish clinically, but in general infections are largely blamed, with up to 80% of AECOPD linked to either bacterial or viral pathogens.\(^3\),\(^4\) Because a certain subset of COPD patients have frequent exacerbations, the concept of inherent susceptibility to acute infection in COPD subsequently triggering AECOPD events has been developed. Several studies have now demonstrated that COPD patients feature impaired innate immunity, the first line of defence against infection. Alveolar macrophages resident in the airways provide the key initial response to bacteria by both recognising and removing harmful pathogens through phagocytosis, but in COPD, these functions may be impaired. Recently, Berenson et al. investigated Toll-like receptor (TLR) expression and responses in alveolar macrophages collected from exacerbation-prone and exacerbation-free COPD patients.\(^5\) In response to exposure to common COPD-related pathogens including *Moraxella catarrhalis*, *Streptococcus pneumoniae*, and *Haemophilus influenzae*, alveolar macrophages from exacerbation-prone patients had diminished TLR2 expression and cytokine responses. Similarly, alveolar macrophages from COPD patients appear to phagocytose *H. influenzae* and *S. pneumonia* poorly compared to those of control patients yet they still release reactive oxygen species (ROS).\(^6\),\(^7\) Together, these studies suggest that COPD
patients have impaired responses to bacterial colonisation and infection which in turn increases susceptibility to AECOPD and promotes oxidative stress response (Figure 1).

Defects in innate immunity may also play a role in increased susceptibility to viruses. Recognition of viral infection by the innate immune system is essential for coordinating an effective antiviral response in the airways, yet in patients and mice with COPD, the cascade from recognition to response falters. This involves increases in phosphatidylinositol 3-kinase responses and impaired anti-viral stress granule formation and type I IFN signalling. In the healthy host, pathogen recognition by TLR3 triggers interferon (IFN) pathways that then can hinder viral replication and mediate the adaptive immune responses. In epithelial cells, constitutive type I IFNs are critical for protection. In these cells and lung fibroblasts exposed to cigarette smoke, responses are reduced and even stimulation with IFN-β yields a diminished antiviral response.

Furthermore, mucociliary clearance, which is key for the removal of virus from the airways, appears to be perturbed in COPD. Cigarette smoke exposure reduces both the number and length of cilia, while goblet cell hyperplasia in COPD leads to more viscous mucus in the airways, further impeding proper ciliary motion. In mouse models, respiratory viruses themselves can induce mucus hypersecretion, contributing to the inability to clear the virus from the airway.

Of the 80% of exacerbations with an infectious cause, approximately half are bacterial in origin while approximately 30% are viral. Numerous studies have been performed to classify the most common pathogens implicated in AECOPD using sputum samples to identify bacteria and nasopharyngeal swabs to identify viruses. In a landmark 2002 study, Sethi et al., traced longitudinal sputum cultures in 81 moderate-to-severe COPD patients during both times of
clinical stability and exacerbation.\textsuperscript{16} Interestingly, the acquisition of a new strain of bacteria (discovered through molecular typing) was highly associated with the development of an AECOPD. The relative risk of an exacerbation varied with each new species: 1.69 for \textit{H. influenzae}, 1.77 for \textit{S. pneumoniae}, and 2.96 for \textit{M. catarrhalis}. Since then, more sensitive quantitative PCR methods of identifying bacteria relative to standard culture methods have enabled better quantification and typing of bacterial strains during exacerbations. In one study, while species such as \textit{H. influenzae} and \textit{S. pneumonia} were identified in stable states, their relative loads, determined by PCR were considerably higher during exacerbations ($10^8$ versus $10^7$ cfu/mL for both species).\textsuperscript{17} The most prevalent species identified during exacerbation was \textit{S. pneumoniae}, followed by \textit{H. influenzae}, \textit{M. catarrhalis}, and \textit{Legionella pneumophila}. In more severe COPD patients (FEV1 $<$50% predicted), \textit{Pseudomonas aeruginosa} was also frequently encountered as a cause of exacerbations (Table 1).\textsuperscript{18} \textit{P. aeruginosa} infections appear to portend a worse prognosis with higher 30- and 90-day mortality rates compared with exacerbations not associated with this bacterium.\textsuperscript{19}

Viruses implicated in the development of AECOPD include respiratory syncytial virus (RSV), rhinovirus, human metapneumovirus, influenza, parainfluenza, adenovirus, and coronavirus.\textsuperscript{20-22} A meta-analysis of nineteen studies (totalling 1,728 patients) evaluated the pooled prevalence of respiratory viruses in AECOPD and found that rhino-/enteroviruses were the most commonly encountered virus (16%), followed by RSV (10%), and influenza (8%). Of lesser prevalence were coronaviruses (4%), parainfluenza (3%), human metapneumovirus (3%), and adenovirus (2%).\textsuperscript{23} Co-infection with two or more viruses has also been reported,\textsuperscript{24} with one study noting
that in their cohort, only the patients with viral co-infections were severe enough to be admitted to the hospital for their exacerbations.\textsuperscript{21}

While simultaneous bacterial and viral pathogens have been detected during acute exacerbations, it remains unclear whether these co-infections carry any greater risk for poor outcomes in comparison to single infections.\textsuperscript{25} They indeed may simply represent more severe disease as other studies have detected.\textsuperscript{26, 27} More compelling is the notion of “superinfection,” where an acute viral infection in COPD may set up the necessary microenvironment in the lung for a subsequent bacterial infection, or \textit{vice versa}. In an experimental rhinovirus infection, where COPD and control patients were nasally inoculated with low doses of rhinovirus, only COPD patients developed significant increases in sputum bacterial load post-viral infection.\textsuperscript{28} While sputum viral loads peaked between days 5 and 9 post-inoculation, bacterial loads peaked later around day 15, confirming that in these studies viral infection can promote bacterial superinfection. Subjects who ultimately developed secondary bacterial infections had lower baseline FEV\textsubscript{1} compared to those who remained free from secondary infections. A plausible mechanism was suggested whereby rhinovirus infection induces neutrophil elastase production, which then degrades the antimicrobial peptides elafin and secretory leukoprotease inhibitor, both of which may be important in protecting subjects from bacterial infections\textsuperscript{28}. These data suggest that AECOPD events thought to be bacterially induced may in fact have been preceded by an initial viral infection. Moreover, greater vigilance for superinfections in patients with more severe lung function may be warranted.
3. CHRONIC INFECTION IN COPD

3.1 Role in COPD Pathogenesis

Microorganisms are commonly detected in the airways in stable COPD and are considered ‘colonisers’ in the absence of acute infective symptoms (Table 1). However, the term colonisation in this context may be debated, as the microorganisms identified in stable COPD are not necessarily benign. Collective evidence favours the vicious cycle hypothesis whereby an inciting event (e.g. smoking) leads to an impaired innate immune response and resultant bacterial colonisation. This in turn promotes airway and systemic inflammation leading to COPD progression. As airway inflammation persists despite smoking cessation, the presence of a persistent stimulus - independent of cigarette smoke - is consistent with a role for colonising bacteria in the pathogenesis of COPD.

Recognition of pathogen-associated molecular patterns (PAMPs), by pattern recognition receptors (PRRs) expressed on epithelial and innate immune cells, activates signal transduction pathways including nuclear factor-kB, p38 mitogen activated protein kinases, phosphoinositide-3-kinase and interferon regulatory factors. This results in the production of pro-inflammatory mediators such as cytokines and chemokines. In turn, the recruitment of neutrophils to the airways ensues, a feature characteristic of bacterially-colonised COPD patients. Neutrophils are anti-infective and have recently been found to have modulatory functions. In COPD, neutrophils are intrinsically altered with abnormal host defence functions, and have unusual chemotactic behaviour and migratory structure. Activated neutrophils cause lung destruction and emphysematous change through the release of oxygen radicals and proteolytic enzymes, including neutrophil elastase (NE) that reduces ciliary function, induces epithelial damage and is
a potent stimulator of mucin production. The resulting mucus production and impaired mucociliary clearance leads to further bacterial colonisation and airway obstruction. Additionally, increased levels of airway inflammatory markers such as IL-6, IL-8, IL-1β, TNF-α, leukotriene B4 (LTB4), matrix metalloproteinase (MMP), myeloperoxidase (MPO) and NE are found in stable COPD patients with bacterial colonisation compared to those without, strongly implicating the colonised state with a deleterious immune response. Such persistent inflammation is associated with increased daily symptoms, exacerbations and mortality. Defective phagocytosis is also characteristic of COPD particularly that of alveolar and monocyte-derived macrophages, which in turn likely contributes to chronic bacterial colonisation and infective exacerbations. This is clearly evidenced by the observed impaired phagocytosis of *H. influenzae* and *M. catarrhalis* with increasing COPD severity. In addition, alveolar macrophage surface receptors (TLR-2, TLR-4 and scavenger receptor (MARCO)) that respond to intracellular signalling and phagocytosis, are seen to be diminished in both COPD and smokers. Chronic bacterial colonisation also activates adaptive immune responses, with the development of B-cell lymphoid follicles and production of mucosal IgA and serum IgG antibody including strain-specific IgG antibody against bacterial colonisers, a phenomenon characteristic of the COPD airway. Increases in lymphoid follicles have been noted in the small airways of patients with severe COPD, possibly secondary to chronic airway infection. Thus, impaired innate immune responses likely contribute to microbial airway colonisation while the activation of adaptive immunity suggests a state of heightened immune surveillance associated with lung function decline in established COPD.
3.2 Bacterial Infection and Colonisation

Potentially pathogenic microorganisms (PPM) have been isolated in up to 74% of stable COPD patients. The commonest PPMs identified include *H. influenzae*, *Moraxella catarrhalis*, *S. pneumonia*, *P. aeruginosa* and *C. pneumonia* similar to the culprit repertoire in AECOPD and severe asthma. Bacterial colonisation is, however, a dynamic process with alterations in pathogen type, load and strain over time. Increases in bacterial load and changes in species are associated with greater lung function decline and airway inflammation.

Non-typeable *H. influenzae* (NTHi) is the most common bacteria isolated in both the stable state and during AECOPD. It alone accounts for up to half of all bacteria isolated in the lower airways of stable COPD patients. The differing cell surface proteins facilitate bacterial adhesion to the respiratory mucosa including outer membrane proteins P2 and P5 that bind to mucin, and adhesin (HMW1 and HMW2) which adhere to the epithelial and extracellular matrix. Lipooligosaccharide, a key component of the NTHi cell wall, and the outer membrane protein P6, are potent immunomodulators for macrophages leading to increased phagocytosis and cytokine secretion, including IL-8 and TNF-α which drive neutrophil recruitment. Given the defective phagocytic ability of the COPD alveolar macrophage, a failure of bacterial clearance potentially leads to the state of persistent infection. Furthermore, NTHi is uniquely able to survive intracellularly within the alveolar macrophages. Through its secreted proteases, it cleaves IgA and in turn protects against IgA-mediated cytotoxicity. Where persistent, COPD NTHi infection of the lower airway results in increased inflammation with elevated IL-8, IL-1β, MPO, TNF-α and MMP-9 detectable in patient samples. Critically, the organisms’
immunoevasive ability causes chronic airway inflammation which in turn correlates with poorer health status and lung function.\textsuperscript{58, 59}

\textit{Moraxella catarrhalis}, the second most prevalent colonising organism in stable COPD (seen in 2-22.5\%), has been shown in previous studies to be linked to a heightened airway inflammation (IL-8, TNF-\(\alpha\) and NE).\textsuperscript{46, 60, 61} In contrast to NTHi,\textsuperscript{62} this bacterium is cleared after a relatively short colonisation period and the development of immune responses that are protective against the homologous strain.\textsuperscript{42}

\textit{Streptococcus pneumoniae} is another important bacterial organism (7.5-17\%) in stable COPD.\textsuperscript{60} Its polysaccharide capsule reduces the effectiveness of host defence mechanisms, which normally cause its clearance, leading to its airway persistence and colonisation. In turn, this is associated with increased exacerbations, emphysema, lower diffusion capacity and pneumonia.\textsuperscript{63}

The role of \textit{Pseudomonas aeruginosa} in COPD pathogenesis is underscored by its frequent isolation in patients with more severe disease.\textsuperscript{58, 64} Two types of \textit{Pseudomonas}-related infection are described in the COPD setting: short-term colonisation followed by clearance and long-term persistent colonisation.\textsuperscript{65} Risk factors for \textit{Pseudomonas} isolation in COPD include bronchiectasis, antibiotic exposure, previous hospitalisation, steroid use, and worse BODE index.\textsuperscript{64} The mucoid phenotype is most likely to cause persistent colonisation and, amongst \textit{P. aeruginosa} positive COPD patients, there is a significant association between colonisation and disease severity.\textsuperscript{65} Despite this, a nested case control study comparing mortality showed no
difference in relation to *Pseudomonas* status in stable COPD however, in AECOPD, recent work has re-affirmed this organisms association with higher COPD mortality rates.\textsuperscript{66, 67}

Finally, chronic *C. pneumoniae* infection in COPD has been brought to light by a number of observational studies. Through its induction of a cytokine response (TNF-\(\alpha\), IL-1\(\beta\), IL-6, IFN-\(\alpha\)), airway inflammation and critical airway remodelling ensues. Prevalence varies widely (0-65%) likely attributable to the lack of samples collected, standardization in applied microbiological methodology and lack of diagnostic testing in routine use.\textsuperscript{68, 69} Despite this, serum *C. pneumoniae* specific IgG and IgA antibody levels are found in higher titres in COPD when compared to a control group. Furthermore, a statistically significant association between chronic *C. pneumoniae* infection and COPD has been established.\textsuperscript{70} Employing combinations of both PCR and serological testing reveal that chronic *C. pneumoniae* infection is associated with more severe COPD, faster lung function declines and, importantly, exacerbations.\textsuperscript{68} These relationships however are not clear cut as a separate study of 110 COPD patients showed no association between *Chlamydia pneumoniae* and either COPD exacerbation frequency or FEV\(_1\).\textsuperscript{71} In this latter study, IgG titers were used to define chronic *C. pneumoniae* infection which may explain the observed disparity. Furthermore, it is likely that *Chlamydia pneumoniae* resides in the lower respiratory tract and sampling needs to occur from this site. Standardisation and validation of reproducible and robust diagnostic tests to clearly define *C. pneumoniae* infection in COPD is necessary and will likely clarify existing differences observed in our current evidence base.
3.3 Tuberculosis (TB) and Non-Tuberculous Mycobacteria (NTM)

Mycobacterial disease, both nontuberculous (NTM) and tuberculous (TB), has long been associated with COPD, whether thought to be related to an inability to clear these chronic pathogens in the setting of structurally damaged lung or potentially the concurrent burden of bronchiectasis increasingly appreciated in COPD. Studies of NTM in COPD cohorts have revealed that roughly a fifth of COPD patients culture NTM in their sputum. Moreover, in 126 COPD patients undergoing lung volume reduction surgery, histologic evidence of mycobacterial disease (necrotizing granulomas) occurred in 14 (11%) patients, 8 of whom had acid-fast bacilli (AFB)-positive stains. Conversely, COPD appears to be a major comorbidity in patients with NTM, with estimates of prevalence ranging from 24 to 79%. Not merely an innocent bystander, NTM infections in COPD portend a worse prognosis with more frequent exacerbations and a more rapid decline in FEV1. However, long-term, prospective studies on the impact of NTM on COPD mortality and anti-mycobacterial treatment outcomes in COPD have yet to be performed.

The relationship between TB and COPD dates back to 1955 when Anno and Tomashesfki first described airflow obstruction and air trapping in patients with TB. Since then, the link between TB and COPD has largely focused on COPD as a sequela of TB infection, a risk that consistently appears to be independent of smoking histories. The proportion of COPD patients found to harbor a history of TB are listed in Table 2, while worldwide estimates of the prevalence of airflow obstruction in cohorts of TB patients are listed in Table 3. Patients with a history of TB carry anywhere from a 1.8 (worldwide estimate) to 8.9 (South Africa) times overall risk of developing COPD. In particular, TB remains an important risk factor for COPD in non-
smokers, with TB patients carrying an estimated 1.3 to 5.8 times the risk of developing COPD compared to those without TB.\textsuperscript{84-87} Likewise, COPD patients are at higher risk of developing TB. In Pakistan, for instance, 7.5\% of COPD patients were found to have TB-positive sputum cultures.\textsuperscript{88} Even in non-endemic regions, for example in Sweden, COPD patients carry a three times higher likelihood of developing active TB, conferring a two-fold higher risk of death compared to COPD patients without TB.\textsuperscript{89}

Why TB may predispose individuals to COPD, and vice versa, is a matter of some speculation, as outlined in Figure 2. Both conditions share a number of common risk factors, including cigarette smoking and biomass fuel exposure. In addition, the spread of human immunodeficiency virus (HIV) has triggered not just a resurgence in TB rates, but also an accelerated form of COPD affecting HIV patients as early as in their 30s and 40s. Recent interest in the role of vitamin D in airways diseases and pulmonary infections has suggested that certain vitamin D-binding protein polymorphisms may also predispose patients to both COPD and TB. Once contracted, TB may set the stage for future COPD by activating matrix metalloproteinases. Destruction of the extracellular matrix and caseous necrosis are critical to the formation of cavitary lesions by which TB can then propagate and aerosolize. At the same time, however, the upregulation of MMPs may also help to trigger emphysema, as multiple studies have shown an increase in MMP-1, -2, -8, and -9 in emphysematous lung tissue. The ensuing lung remodeling may result in significant airways disease. Conversely, COPD itself may promote subsequent TB infection by impairing immune responses and ciliary function, two key defences against pathogenic microbes. Innate immune dysregulation against pathogens such as \textit{H. influenzae} and \textit{S. pneumoniae} have been well-documented in COPD; while similar work in TB has yet to be
confirmed. The phagocytic disruption observed in COPD may indeed hold validity for TB as well. Cigarette smoke-exposed mice have for instance been shown to demonstrate impaired macrophage responses to TB in comparison to control mice. These injuries may be in part mediated by chronic exposure to inhaled corticosteroids.

3.4 Fungal Infection and Colonisation

The clinical significance of fungal infections in COPD is poorly understood and likely underestimated. Fungal colonisation is observed in severe COPD patients. Whether such colonisation is a marker of advanced COPD or contributes to disease progression remains to be studied. *Aspergillus* spp. are frequently isolated from the airways of COPD patients during exacerbations (16.6%) and even during follow up (14.1%).\(^{90, 91}\) In an observational study, positive *Aspergillus* cultures in COPD patients were associated with increased sputum cell counts.\(^{92}\) The incidence of AECOPD in the preceding year and concomitant bacterial pathogen isolation were associated with increased *Aspergillus* detection. Positive *Aspergillus* cultures in COPD patients are associated with increased sputum neutrophils suggesting the presence of host immune response in relation to the organism\(^{92}\).

Up to 8-15% of COPD patients have hypersensitivity to *Aspergillus*, with associated reduced lung function.\(^{93, 94}\) Whether the use of antifungals may mitigate such declines in pulmonary function remains to be studied. Isolation of *Aspergillus* in the airway may represent temporary passage, benign carriage or be an early sign of invasive pulmonary aspergillosis (IPA), especially with high steroid use for recurrent exacerbations conferring host immunosuppression. Increasing evidence suggests that COPD patients are at risk of IPA with resulting high mortality rates; up to 22% of COPD patients with detection of *Aspergillus* in airway culture had IPA.\(^{95}\) Innate immune
responses play an important role in _Aspergillus_ clearance mechanisms. Inhaled _Aspergillus_ conidia bind to surface receptors within terminal airways via galactomannan, which enhance uptake by alveolar macrophages and dendritic cells leading to a cascade of immune responses. Recruitment of neutrophils and alveolar macrophages leads to ingestion, phagolysosomal degradation and killing of the fungal conidia. Toll like receptor-2 and -4 dependent signals further contribute to host recognition and the inflammatory response to both _Aspergillus_ conidia and hyphae.96 Steroids therefore interfere with alveolar macrophage function, thereby increasing the risk of IPA through this and other defective innate immune responses in COPD including functionally abnormal neutrophils and toll like receptors.97

_Pneumocystis jirovecii_ is another opportunistic fungal pathogen of the COPD lung (8-85% of cases).98-101 _Pneumocystis_ colonisation is described in 36.7% of severe COPD patients (Gold stage IV) compared to 5.3% of those with milder disease (Gold stages 0-III). Colonisation is associated with severe airflow obstruction independent of smoking.99, 102 Increased systemic inflammation (IL-8, TNF-α, IL-6)100, 102 and proteases (MMP-12) responsible for parenchymal destruction and emphysema in COPD have been found in higher concentrations in COPD patients colonised with _Pneumocystis_. This suggests that the organism is unlikely an innocent bystander and may contribute to disease pathogenesis and progression. An up-regulation of chemokine ligands (CXCL9, CXCL10, CXCL11) of the CXCR3 receptor predominantly expressed on activated Th1 lymphocytes is also observed and may prime Th1 inflammatory pathways contributing to the progression of COPD in these cases.101
3.5 Viral Infections

Although respiratory viruses are associated with asthma and COPD and cause acute cell damage, release of ROS and activation of NF-κB, their significance in stable COPD is less well understood (Table 1). Adenovirus DNA is detectable in lung tissue of stable COPD patients and when compared to healthy smokers, a 5-40-fold increase in adenovirus E1A expression is observed in patients with emphysema. \(^{103, 104}\) In animal models, even latent adenovirus infection amplified the inflammatory responses (increased CD8 cells, macrophages and neutrophils) and emphysematous destruction, \(^{105}\) and increased IL-8 and ICAM-1 expression are also described in human epithelial cell transfection with adenovirus E1A genes. \(^{106, 107}\) Respiratory syncytial virus is also common in stable COPD with prevalence rates of up to 33\%. \(^{108-110}\) An RNA virus of the Paramyxoviridae family and a common cause of acute respiratory tract infections, its presence in stable COPD is unsurprisingly linked to higher levels of both airway and systemic inflammation. \(^{108, 109}\)

4. THE ROLE OF THE MICROBIOME IN COPD PATHOGENESIS AND PROGRESSION

There is an emerging role for the microbiome in both stable and during exacerbations of COPD that has been recently reviewed elsewhere \(^{111-119}\).

While most research has focused on the bacteriome, viruses (virome) and fungi (mycobiome) are also important constituents of the microbiome. The respiratory tract contains genetic material from eukaryotic viruses such as anelloviruses, herpesviruses and papillomaviruses, as well as retroviruses that may establish persistent asymptomatic infections, and bacteriophages, which
dominate the virome.\textsuperscript{120-123} In the lung, the virome is highly variable between individuals and is strongly influenced by environmental conditions such as oxygen availability.\textsuperscript{122} Unfortunately, in many studies a large proportion of sequencing reads are not matched to a reference genome and it is unclear whether the identified viruses are commensal or a latent infection. Given these difficulties, it is challenging to directly compare the entire virome in COPD patients and healthy subjects. Nevertheless, COPD patients have increased total viral load, as well as an increased prevalence or abundance of influenza, cytomegalovirus and Epstein-Barr virus.\textsuperscript{124-126} Ultimately, the role of acute viral infection including rhinovirus, RSV and influenza, which clearly contribute to inflammation, pathology and exacerbations of COPD,\textsuperscript{23, 127, 128} remains to be fully elucidated. As previously described, latent adenoviral infection is associated with increased inflammation and alveolar destruction\textsuperscript{129} while total and influenza-specific viral loads of COPD patients without symptoms of infection correlated with inflammatory cell numbers in the airways.\textsuperscript{126} Moreover, human rhinovirus-encoded proteinase 2a has been proposed to elicit a duel Th1/Th2 response in COPD patients through its impact on dendritic cell maturation, thereby driving inflammation, allergy and airway obstruction.\textsuperscript{127}

Although fungi are only detectable at low abundance in healthy individuals, several members of the mycobiome are consistently identified in the lower respiratory tract, including \textit{Cladosporium} and \textit{Aspergillus} spp.\textsuperscript{95, 130} Moreover, the outgrowth of \textit{Aspergillus} can lead to IPA, with COPD the most common predisposing condition. Colonisation with \textit{Pneumocystis} was associated with COPD development and GOLD stage classification,\textsuperscript{99, 131} \textit{Pneumocystis} spp. are capable of inducing COPD-like disease in animal models both with and without cigarette smoke exposure.\textsuperscript{132, 133} In the oral cavity, smoking is associated with increased prevalence of \textit{Candida}
spp. as a consequence of the ability of cigarette smoke to increase the growth, adherence and immunostimulatory activity of *C. albicans*.\textsuperscript{134, 135} Cigarette smoke also increased the content of chitin in the cell wall of *C. albicans*. While it is not clear whether cigarette smoke causes similar changes in fungi that colonise the lung or if fungi in the oral cavity affect the lung through microaspiration, notably, the activity of chitotriosidase and the chitin binding protein YKL-40 are increased in the BAL and alveolar macrophages of COPD patients.\textsuperscript{136, 137} Even serum levels of YKL-40 and chitotriosidase are elevated in COPD patients and inversely correlate with lung function, indicating that host responses to fungal colonisation may contribute to COPD progression.\textsuperscript{138}

The bacterial microbiome, virome and mycobiome are not isolated and act in concert. Indeed, bacteria and phage populations are strongly correlated,\textsuperscript{120, 122} while eukaryotic viruses and fungi can affect bacterial growth.\textsuperscript{128, 130} Furthermore, the gastrointestinal microbiome interacts with the respiratory microbiota and plays a critical role in the development of several chronic respiratory diseases, and likely COPD (Figure 3).\textsuperscript{139}

5. THE EFFECT OF INFECTION ON COPD DISEASE PATHOGENESIS, PROGRESSION AND THERAPEUTICS

5.1 Antibiotic, bronchodilator and steroid use

The prominent role of bacteria in inciting acute COPD exacerbations has placed antibiotics at the forefront of COPD therapy. In 1987, Anthonisen *et al.*, reported a 13% increase in treatment success rate with antibiotic therapy compared to placebo, particularly in patients with increased dyspnea and sputum production and purulence.\textsuperscript{140} Since then, antibiotics covering pathogens
such as *H. influenzae*, *S. pneumoniae*, and *M. catarrhalis* have become mainstays of therapy and numerous trials have confirmed their beneficial effects.\textsuperscript{141-143} Nonetheless, the notion that all acute exacerbations must be treated with antibiotics has been called into question, given that not every exacerbation is the result of a bacterial infection. Efforts to better identify the subset of exacerbating COPD patients who may benefit from antibiotics have explored biomarkers such as procalcitonin,\textsuperscript{144, 145} C-reactive protein,\textsuperscript{146} and neutrophil CD64 expression,\textsuperscript{147} but few of these have yet made it into mainstream clinical decision algorithms.

The pleiotropic effects of antibiotics, particularly those of the macrolide class that also have anti-inflammatory properties led to their use in the prevention of exacerbations. Azithromycin, for instance, has not only antimicrobial activity against both Gram-positive and negative pathogens, but also anti-inflammatory and anti-viral effects.\textsuperscript{148-149} Treatment in stable COPD patients reduced severe exacerbations, and in a population of patients with frequent COPD exacerbations, chronic use of azithromycin resulted in a significantly longer time to first exacerbation and a reduced yearly exacerbation rate.\textsuperscript{150-151} Azithromycin was particularly effective in reducing exacerbations requiring both antibiotics and systemic corticosteroids and appeared to be more effective in older patients with milder disease.\textsuperscript{152} The long-term effects of chronic azithromycin therapy on the lung microbial community, however, are yet to be determined although initial reports suggest that while the overall bacterial burden remains stable, the alpha diversity of the lung decreases significantly.\textsuperscript{153} The implications of these changes are yet to be established.

While these therapies have proven beneficial for COPD patients, it is important to remember that other COPD treatments can have untoward microbial effects. Inhaled corticosteroids (ICS), for
instance, have been shown to increase the risk of both pneumonia and TB. In initial randomised controlled trials studying ICS and ICS-LABA combination drugs, a higher rate of pneumonia was noted in the ICS-containing treatment groups.\textsuperscript{154} Subsequent analyses, however, have specifically implicated fluticasone as the ICS most likely to increase the risk of pneumonia, as budesonide does not appear to confer as great a risk.\textsuperscript{155-158} Similarly, the risk for developing TB while on ICS therapy is significant in moderately to highly TB endemic areas. Research in Taiwan and South Korea has demonstrated an up to 25 times greater risk of developing TB while on ICS treatment, with a dose-dependent effect.\textsuperscript{159} Thus, in endemic areas, clinicians should be vigilant for the development of TB in COPD patients on ICS therapy. In addition to geographical distinctions, infection is not uniform in COPD, with changes in pathogen, strain and load over time\textsuperscript{16,46}. Different species trigger distinct inflammatory responses\textsuperscript{58}. Furthermore, host factors play an essential role in infection manifestation and outcome. This results in variable response to antibiotics treatment in COPD. Therapy such as long-term macrolides can be beneficial with reductions in exacerbation rates in a select group of patients with COPD\textsuperscript{160}. This effect has been linked to anti-inflammatory properties of macrolides likely explained by their impact on the microbiome, which, in turn, modulates immune tone. Culture independent molecular techniques have constructed a comprehensive analysis of the microbial community in the lower airway and yet how the complexities in interactions between the host, pathogen and the environment contribute to disease manifestation and progression in COPD is far from understood. Future studies are required to better define the contribution of infection in COPD pathogenesis and intervention studies incorporating antimicrobial and anti-inflammatory approaches in the treatment of COPD. The application of whole genome metagenomics in this context may uncover mechanisms beyond the scope of culture-based and amplicon sequencing.
approaches revealing precise genetic and metabolic pathways that intersect key immune responses contributing to disease progression.

5.2 COPD in the Asia-Pacific region

The differences in risk factor exposure, ethno-geography and genetic background in Asia result in distinct characteristics of Asian COPD, which is currently overlooked by existing COPD treatment guidelines. Many of the COPD risk factors, including indoor and outdoor air pollution, occupational exposure to dust and fumes, a history of repeated childhood respiratory tract infections, intrauterine growth retardation, pulmonary tuberculosis, and poor socioeconomic status factors, are observed at higher prevalence in the Asia-Pacific region. Of particular note is the higher prevalence of pulmonary tuberculosis among Asian COPD patients\textsuperscript{161}. Concomitant NTM, tuberculosis and bronchiectasis in COPD have been associated with higher risk of exacerbations, greater declines in pulmonary function and increased risk of mortality\textsuperscript{72, 74}. Furthermore Asia is an epicentre of antimicrobial resistance, with high prevalence of multi-drug resistance organisms, which include respiratory pathogens\textsuperscript{162}. Consequently, there may be differing in responses to antibiotic therapy during bacterial exacerbation of COPD and an array of variable organisms identified during AECOPD in the Asia-Pacific region. Gram-negative bacteria including \textit{Pseudomonas aeruginosa}, \textit{Klebsiella pneumoniae} and \textit{Acinetobacter} spp. were more common in AECOPD in Asia-Pacific\textsuperscript{163}. The distinction in risk factor exposure as compared to western cohorts, under-utilisation of spirometry, higher prevalence of tuberculosis, bronchiectasis and antibiotic resistance all pose unique challenges for better diagnosis and treatment of COPD particular to the Asia-Pacific region.
5.3 Emerging antimicrobial resistance in COPD: implications for disease pathogenesis and progression

The excessive mucus production in COPD patients is a fertile ground for the stimulation of chronic bacterial infection. Pulsed therapies of antibiotics are frequently used to control bacterial multiplication, which consequently promotes the development of antimicrobial resistance. Prolonged use of macrolides for the prophylaxis and treatment of COPD exacerbations has been shown to increase antimicrobial drug resistance in *H. influenzae*.\textsuperscript{164} The commonly used drug azithromycin has a long half-life of around 66 hours, which can lead to drug concentrations below the Minimum Inhibitory concentration for an extended period of time.\textsuperscript{165} This prolonged exposure to sub-inhibitory concentrations of the drug may be one of the reasons behind the increased resistance to macrolides. Indeed, a study by Desai *et al.*, on COPD patients with *S. pneumoniae* infection showed a correlation between exposure to macrolides and development of resistance.\textsuperscript{166} They advised for the use of alternative antibiotics in patients who have been taking macrolides in the previous six months.\textsuperscript{166} A 15-year longitudinal study conducted by Perrigrew *et al* concluded that fluoroquinolones represent the best choice for eradicating *H. influenzae* in COPD patients.\textsuperscript{164} In their study, none of the bacterial isolates developed resistance to fluoroquinolones.\textsuperscript{164} Even though *Pseudomonas aeruginosa* is a relatively uncommon cause of COPD exacerbations, its incidence is on the rise and the rapid emergence and spread of multi-drug resistance (MDR; defined by resistance to at least three antibiotic classes) is a serious cause for concern. A comparative study conducted in Spain has demonstrated that the carriage of MDR *P. aeruginosa* in COPD patients was associated with increased mortality rates and more recent work in AECOPD reveals a high burden of antibiotic resistance.\textsuperscript{167} The lung environment found in COPD patients is also favourable to the formation of biofilms, a mechanism by which
bacteria, particularly *P. aeruginosa* and *H. influenza*, evade antibiotic killing. In addition to limiting antimicrobial penetration, the biofilm triggers the emergence of relatively quiescent bacteria that become phenotypically drug resistant to most antibiotics, therefore increasing their persistence for prolonged periods of time.\(^{168}\) Currently, the most effective way of curbing antimicrobial resistance is to reduce the use of antibiotics by prescribing them only to patients with demonstrated pathological bacterial infection. In this respect, the use of sensitive markers of bacterial infection such as procalcitonin to guide the start of antibiotic therapy was shown to significantly reduce the use of antibiotics in COPD patients.\(^ {169}\) There is also the potential that the new therapies developed for steroid-resistant asthma may also be beneficial in COPD and possibly avoid the infection-inducing effects of ICS.\(^ {170}\)

5.4 Utility of mouse models and new translational techniques

The majority of studies described above are of the associations between infections and microbiomes with COPD in humans. These studies are limited by the type of samples that can be collected and typically the cross-sectional nature of study design. Mouse models of cigarette-smoke-induced experimental COPD that accurately recapitulate the hallmark features of the human disease have been generated.\(^ {171, 172}\) Chronic models that use only inhalational exposures drive the development of airway inflammation and remodelling, mucus hyper-secretion, emphysema and changes in lung function similar to those in humans.\(^ {171, 172}\) This can be achieved in a relative short time frame of eight weeks with exposures similar to those of a pack-a-day human smoker.\(^ {171}\) Importantly, these and other models have increased susceptibility to respiratory bacterial and viral infections that are relevant to those in humans described above.\(^ {8, 9, 34}\) They are being used to assess the mechanisms of the associations between infections,
microbiomes and COPD and have recently implicated roles for immune defects, microRNAs, mast cell proteases and many other factors. In combination with parallel ex vivo human sample and primary cell culture analysis, they provide powerful tools for exploring these associations and are valuable for testing new drugs.\textsuperscript{7-9, 41, 45, 150} Translatability into humans can be addressed by applying treatments specifically to those patients with alterations in drug targets. Through similar analysis of comparable similar tissues from mice and humans using similar techniques such as the interrogation of precision cut lung slices permit important therapeutic questions to be examined in future COPD studies.\textsuperscript{173-175}

6. CONCLUSIONS

Although the role of pathogenic microbes in AECOPD has been extensively investigated, their clinical significance in stable but colonised COPD patients remains less clear. The question of whether colonising microbes actively contribute to COPD disease pathogenesis and more importantly progression may be difficult to address with the current evidence base, given technical challenges in detecting these organisms and the subtlety of their association with disease over long periods of time. Nevertheless, immune responses observed in stable and colonised COPD patients reflect the corollary of those seen in AECOPD supporting a role for microbial colonisation in COPD pathogenesis most likely through a perpetuation of negative immune responses over time. Initial work has started to uncover changes in the lung microbiome associated with the COPD disease state and may reveal further variables to be considered in the investigation of microbe-COPD interactions. The parallel use of mouse models and interrogation of human samples ex vivo and in primary cell culture will likely progress mechanistic insights and drug development. Importantly however, other variables of microbiome composition may
confound pathogen-centric investigations of disease-microbe interactions and it is likely that large-scale studies will be required to address the current gaps in our knowledge of bacterial, viral and fungal microbiota and their association with COPD. Precipitous drops in the costs of DNA sequencing, coupled with the technological innovations in metagenomics, may soon bring such technology into the realm of routine diagnostics in COPD. This could allow for refined patient phenotyping and stratification that in turn will allow more focused and personalised therapy based on microbiology. Finally, the impact of antimicrobial therapy and the use of antibiotic prophylaxis on the respiratory microbiome provide further challenges. The extensive remodelling of the microbiome that occurs in response to COPD antibiotic treatment while recognised has unclear long-term consequences for patients.

7. ACKNOWLEDGEMENTS

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The Authors:

Janice M. Leung is a respirologist at St. Paul’s Hospital and the Centre for Heart Lung Innovation at the University of British Columbia in Vancouver, Canada. Her research and clinical interests are in HIV-related COPD. Her lab studies the small airway epithelium in HIV, focusing on DNA methylation, gene expression, and the microbiome. Tiew Pei Yee, MD, works at Singapore General Hospital and Changi General Hospital Respiratory and Critical Care Department with special interest in COPD. Dr. Micheál Mac Aogáin is a Visiting Research Fellow at the Lee Kong Chian School of Medicine with research interests in microbial genomics and the analysis of the microbiome in human health and disease. Kurtis F. Budden received his B. Biomedical Science (Honours) from The University of Newcastle, Australia. He is currently completing his PhD in Immunology and Microbiology under the supervision of Prof. Phil Hansbro where he is investigating the manipulation of microbiomes and utilisation of microbial products as new therapies for COPD. Valerie Yong Fei Lee is a Research Assistant in the Chotirmall Lab, Lee Kong
Chian School of Medicine, Singapore. Her research interests are in translational lung research in the context of hormonal influences on Pseudomonas aeruginosa. Dr Sangeeta Susan Thomas obtained her M.B.B.S from Government Medical College, Kozhikode; MD Microbiology from Christian Medical College, Vellore and Masters in Stem Cell Biology from University of Southern California. She is currently working on novel drug discovery platforms in Mycobacteria species under the supervision of Dr. Kevin Pethe at LKC School of Medicine, Singapore. Kevin Pethe is Associate Professor at the Lee Kong Chian School of Medicine and the School of Biological Sciences, Nanyang Technological University. His current research focuses on host-bacteria interaction and antibiotic drug development, with a focus on mycobacterial diseases and hospital-acquired bacterial infections. Professor Hansbro is chair in immunology and microbiology, and an NHMRC Principal Research Fellow at the Hunter Medical Research Institute and University of Newcastle, Australia and Associate Director of the Priority Research Centre for Lung Health there. His group has developed several novel mouse models of diseases (COPD, severe, steroid-insensitive asthma, early life infection & lung cancer) and studied them to further our understanding of pathogenesis and develop novel therapies. Sanjay H. Chotirmall is a Respiratory Clinician-Scientist, Assistant Professor of Molecular Medicine at the Lee Kong Chian School of Medicine, Nanyang Technological University and Honorary Senior Clinical Lecturer at Imperial College, London. He leads a translational respiratory research group that focuses on bacterial and fungal airway infection and the role of the microbiome in disease pathogenesis and progression in chronic respiratory disease.
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Table 1. Summary table of COPD disease state and associated microorganisms.

<table>
<thead>
<tr>
<th>COPD-associated organisms</th>
<th>Prevalence</th>
<th>Sample size (n)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AECOPD</td>
<td>Stable COPD</td>
<td></td>
</tr>
<tr>
<td><strong>Bacteria</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Haemophilus influenzae</em></td>
<td>26%</td>
<td>17-35%</td>
<td>410*</td>
</tr>
<tr>
<td><em>Streptococcus pneumoniae</em></td>
<td>25%</td>
<td>7.5-17%</td>
<td>442*</td>
</tr>
<tr>
<td><em>Moraxella catarrhalis</em></td>
<td>19%</td>
<td>2-22%</td>
<td>247*</td>
</tr>
<tr>
<td><em>Pseudomonas aeruginosa</em></td>
<td>13-29%</td>
<td>-</td>
<td>332*</td>
</tr>
<tr>
<td><em>Chlamydophila pneumoniae</em></td>
<td>24%</td>
<td>43%</td>
<td>141</td>
</tr>
<tr>
<td>Non-tuberculous mycobacteria</td>
<td>22%</td>
<td>-</td>
<td>73</td>
</tr>
<tr>
<td><strong>Viruses</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rhinovirus / Enterovirus</td>
<td>16%</td>
<td>-</td>
<td>1728</td>
</tr>
<tr>
<td>Respiratory syncytial virus</td>
<td>10%</td>
<td>-</td>
<td>1728</td>
</tr>
<tr>
<td>Influenza virus</td>
<td>8%</td>
<td>-</td>
<td>1728</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>2%</td>
<td>-</td>
<td>1728</td>
</tr>
<tr>
<td><strong>Fungi</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Aspergillus spp.</em></td>
<td>-</td>
<td>14%</td>
<td>141</td>
</tr>
<tr>
<td><em>Pneumocystis jirovecii</em></td>
<td>-</td>
<td>8-55%</td>
<td>137</td>
</tr>
</tbody>
</table>

*Cumulative sample size is reported for multiple studies.*
### Table 2: Tuberculosis as a Risk Factor for COPD

<table>
<thead>
<tr>
<th>Author</th>
<th>Year</th>
<th>Country</th>
<th>n</th>
<th>Definition of COPD</th>
<th>Proportion of COPD Patients with History of TB</th>
<th>Adjusted Odds Ratio (95% CI) for COPD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chan-Yeung M</td>
<td>2007</td>
<td>Hong Kong</td>
<td>289 COPD</td>
<td>FEV1/FVC &lt;70%</td>
<td>24 (8.3%)</td>
<td>1.52 (0.45-5.19)</td>
</tr>
<tr>
<td>Menezes AM</td>
<td>2007</td>
<td>Brazil, Chile, Mexico,</td>
<td>5,571</td>
<td>FEV1/FVC &lt;70%</td>
<td>Not provided</td>
<td>2.57 (1.69-3.93)</td>
</tr>
<tr>
<td>Caballero A</td>
<td>2008</td>
<td>Colombia</td>
<td>494 COPD</td>
<td>FEV1/FVC &lt;70%</td>
<td>62 (12.6%)</td>
<td>2.94 (1.58-5.49)</td>
</tr>
<tr>
<td>Lam KB</td>
<td>2010</td>
<td>China, BOLD (14 countries)</td>
<td>4,291 Controls</td>
<td>FEV1/FVC &lt;LLN</td>
<td>167 (32%)†</td>
<td>1.37 (1.13-1.67)†</td>
</tr>
<tr>
<td>Idolor LF</td>
<td>2011</td>
<td>Philippines</td>
<td>722</td>
<td>FEV1/FVC &lt;70%</td>
<td>15 (10.6%)</td>
<td>5.99 (0.82-44)</td>
</tr>
<tr>
<td>Danielsson P</td>
<td>2011</td>
<td>Sweden</td>
<td>86 COPD</td>
<td>FEV1/FVC &lt;70%</td>
<td>4 (4.7%)</td>
<td>5.99 (0.82-44)</td>
</tr>
<tr>
<td>Govender N</td>
<td>2011</td>
<td>South Africa</td>
<td>110 COPD</td>
<td>Pulmonologist diagnosis</td>
<td>17 (15%)</td>
<td>7.7-8.1</td>
</tr>
<tr>
<td>Lee SW</td>
<td>2011</td>
<td>South Korea</td>
<td>3,687</td>
<td>FEV1/FVC &lt;70%</td>
<td>FEV1/FVC &lt;70%; 82 (27.9%)</td>
<td>FEV1/FVC &lt;70%; 2.56 (1.84-3.56)</td>
</tr>
<tr>
<td>Hooper R</td>
<td>2012</td>
<td>BOLD (14 countries)</td>
<td>4,733</td>
<td>FEV1/FVC &lt;LLN</td>
<td>Not provided</td>
<td>1.72 (1.19-2.48)</td>
</tr>
<tr>
<td>Perez-Padilla R</td>
<td>2012</td>
<td>Brazil, Chile, Venezuela, Brazil, Uruguay, Mexico</td>
<td>2,278 never smokers</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>Not provided</td>
<td>5.82 (2.22-15.28)</td>
</tr>
<tr>
<td>Hwang YI</td>
<td>2014</td>
<td>South Korea</td>
<td>1,384</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>44 (29.5%)†</td>
<td>3.12 (2.01-4.67)†</td>
</tr>
<tr>
<td>Smith M</td>
<td>2014</td>
<td>China</td>
<td>317,399 never smokers</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>Not provided</td>
<td>Females 2.36 (2.06-2.71)</td>
</tr>
<tr>
<td>Amaral AF</td>
<td>2015</td>
<td>BOLD (14 countries)</td>
<td>18,644</td>
<td>FEV1&lt;FVC &lt;LLN</td>
<td>Not provided</td>
<td>Males 1.81 (1.40-2.34)</td>
</tr>
<tr>
<td>Chan TC</td>
<td>2015</td>
<td>Taiwan</td>
<td>96 COPD</td>
<td>ICD-9 or ICD-10 code</td>
<td>7 (7.3%)</td>
<td>Not provided</td>
</tr>
<tr>
<td>Jaganath D</td>
<td>2015</td>
<td>Peru</td>
<td>2,957</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>Not provided</td>
<td>Females 7.02 (3.63-13.59)</td>
</tr>
<tr>
<td>Jo YS</td>
<td>2015</td>
<td>South Korea</td>
<td>9,488</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>94 (12.6%)</td>
<td>Males 3.12 (2.02-4.83)</td>
</tr>
<tr>
<td>Lee SJ</td>
<td>2015</td>
<td>South Korea</td>
<td>3,473 never smokers</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>Not provided</td>
<td>2.55 (1.86-3.50)</td>
</tr>
<tr>
<td>Lee SH</td>
<td>2016</td>
<td>South Korea</td>
<td>15,063</td>
<td>FEV1&lt;FVC &lt;70%</td>
<td>Non-Smokers 81 (20.3%)*</td>
<td>Non-Smokers: 4.73 (3.63-6.17)</td>
</tr>
</tbody>
</table>

*GOLD II-IV patients only
#TB defined as radiographic evidence of prior, inactive TB
$BOLD = Burden of Obstructive Lung Disease Study
<table>
<thead>
<tr>
<th>Author</th>
<th>Year</th>
<th>Country</th>
<th>n</th>
<th>Definition of COPD</th>
<th>Prevalence of COPD in Patients with History of Tuberculosis</th>
</tr>
</thead>
<tbody>
<tr>
<td>Snider GL</td>
<td>1971</td>
<td>United States</td>
<td>1,403</td>
<td>FEV1/VC &lt;70%</td>
<td>589 (42%)</td>
</tr>
<tr>
<td>Willcox PA</td>
<td>1989</td>
<td>South Africa</td>
<td>71</td>
<td>FEV1/FVC &lt;70% and/or RV&gt;120%</td>
<td>48 (68%)</td>
</tr>
<tr>
<td>Plit ML</td>
<td>1998</td>
<td>South Africa</td>
<td>74</td>
<td>FEV1/FVC &lt;70%</td>
<td>21 (28%)</td>
</tr>
<tr>
<td>Ramos LM</td>
<td>2006</td>
<td>Brazil</td>
<td>50</td>
<td>Not provided</td>
<td>12 (24%)</td>
</tr>
<tr>
<td>Pasipanodya VG</td>
<td>2007</td>
<td>United States</td>
<td>107</td>
<td>FEV1/FVC &lt;70%</td>
<td>16 (15%)</td>
</tr>
<tr>
<td>Girdler-Brown BV</td>
<td>2008</td>
<td>Lesotho</td>
<td>184</td>
<td>FEV1/FVC &lt;70%</td>
<td>37 (20.1%)</td>
</tr>
<tr>
<td>Baig IM</td>
<td>2010</td>
<td>Pakistan</td>
<td>92</td>
<td>FEV1/FVC &lt;70%</td>
<td>26 (55.3%)</td>
</tr>
<tr>
<td>Rhee CK</td>
<td>2013</td>
<td>South Korea</td>
<td>595</td>
<td>FEV1/FVC &lt;70%</td>
<td>457 (76.8%)</td>
</tr>
<tr>
<td>De la Mora IL</td>
<td>2015</td>
<td>Mexico</td>
<td>70</td>
<td>FEV1/FVC &lt;70%</td>
<td>24 (34.3%)</td>
</tr>
<tr>
<td>Manji M</td>
<td>2016</td>
<td>Tanzania</td>
<td>501</td>
<td>FEV1/FVC &lt;70%</td>
<td>210 (42%)</td>
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Figure Legend

Figure 1: Microbial factors affecting COPD disease pathogenesis and progression. Pathogenic microbes associated with acute and chronic COPD infection influence disease progression. Increasingly, the role of the microbiome and its associated virome and mycobiome is recognised. As microbiome architecture is profoundly altered by COPD therapy, dynamic interaction between microbiology, infection and therapy likely occurs during COPD disease progression.

Figure 2: A proposed schematic of the interactions between COPD and TB. While both conditions share a number of risk factors, TB may contribute to the development of COPD through matrix-metalloproteinase-mediated lung remodelling. COPD may also contribute to TB infection by impairing immune responses, ciliary function, and through exposure to inhaled corticosteroids.

Figure 3: Role of the microbiome in COPD pathogenesis and progression. Bacteria, viruses and fungi enter the lung through breathing and microaspiration of oral microbes. In the healthy lung, homeostasis is achieved through an appropriate immune response and pathogen clearance. In COPD, an increased abundance of pathogenic organisms and oral taxa is seen in association with reduced overall bacterial diversity. Consequently, perpetuation of a deleterious immune response occurs with associated COPD progression. Host-microbe dialogue may also proceed via the gut-lung axis further exacerbating disease symptoms as demonstrated in other chronic respiratory disease states.
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233x201mm (150 x 150 DPI)
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