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Microbiome Modulation and Machine Learning in Preventing Chronic Obstructive Pulmonary Disease Readmission

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Abstract

Chronic Obstructive Pulmonary Disease (COPD) is among the major global concerns of mortality and morbidity, affecting millions of people worldwide. It is a progressive pulmonary disease including symptoms like chest tightness, wheezing, coughing, and shortness of breath. COPD is a multifactorial respiratory condition influenced by various risk factors. These risk factors include tobacco smoking, environmental air pollution, occupational exposures, occupational exposures, genetic factors, and other comorbidities. Another factor that appears to play important role in the development and recurrence of COPD is lung microbiota dysbiosis. This dysbiosis is believed to contribute to chronic inflammation, impaired host defense mechanisms, increased mucus production, and treatment response in COPD patients. To delve deeper, the research in the field is oriented toward understanding the association between COPD and microbial Dysbiosis. The biomarkers associated with the microbiome are being used for diagnosis of the disease. This study brings forth to readers the application of Machine learning (ML) and Deep learning (DL) tools in the detection of the disease by extracting meaningful information from clinically relevant COPD data generated by various diagnostic techniques such as CT scans, spirometry, acute exacerbations, and several other COPD risk factors. Although ML and DL techniques have been applied extensively in the literature for the prediction of COPD readmission, microbial dysbiosis data has not been used for this prediction. The focus of this study is to highlight the latest research related to microbial dysbiosis in COPD and explore the possibility of applying AI tools for novel diagnostics and therapeutic strategies.

Keywords: COPD, Readmission, Machine Learning, Microbial Dysbiosis.

Introduction

Chronic Obstructive Pulmonary Disease (COPD) refers to a progressive lung disease characterized by a group of different disorders that obstruct airways and possess difficulties in breathing. Persistent bronchitis and emphysema are the two common disorders of COPD including wheezing, chest tightness, coughing, shortness of breath, and other respiratory symptoms. Chronic bronchitis involves irritation and inflammation of the bronchial tubes leading to increased mucus production and coughing. Emphysema, on the other hand, involves the enlargement of the lungs' air sacs due to the deterioration of their walls resulting in reduced lung elasticity and impaired gas exchange (1, 2). WHO reports COPD among the top 10 global causes of morbidity and mortality having a substantial negative impact on people's quality of life, healthcare systems, and society (3). Globally, ~384 million individuals are estimated to live with COPD, and the numbers continue to rise. Approximately 3 million fatalities are attributed to COPD each year, making it the third most prevalent cause of mortality, after stroke and ischemic heart disease. Furthermore, it is projected that COPD will become a preeminent cause of disability worldwide by 2030. Regional variations in COPD prevalence and mortality rates exist, with higher rates observed in low- and middle-income countries. However, developed nations also bear a significant burden of COPD due to the high prevalence of smoking and exposure to other risk factors. In the United States alone, it is estimated that over 16 million adults have been diagnosed with COPD, and millions more are undiagnosed or in the early stages of the disease. COPD not only affects a person's health but has economic implications as well; since direct and indirect costs associated with COPD management and treatment are substantial. According to the American Lung Association,

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COPD is estimated to cost the United States economy over $50 billion annually in healthcare expenditures and productivity losses (2, 4). In India, COPD ranks second in terms of death with distinct prevalence rates in different parts of Indian states and regions (5). The recent data from a few Indian states including West Bengal, Delhi, Tamil Nadu and the Urban area of Hyderabad shows 24.06 %, 10.10 %, 9 % and 11 % prevalence of COPD respectively (6–8). In 2021, Ashwani *et al.,* conducted a systematic review and meta-analysis of 23 studies with a total of 80,138 participants from 2000 to 2020 reporting the average prevalence of COPD in India to be 7.0 % (9). Another study performed by 8,569 individuals also found a similar prevalence rate of 7.4 % and recorded that males have a higher burden of the disease (10). Although the prevalence found in this study was lower than the global prevalence ranging from 10.7 % to 12.1 %, various research indicates that a significant proportion, ranging from 50 % to 90 %, of individuals with COPD are not diagnosed due to the limited availability or accessibility of spirometers or trained healthcare providers capable of identifying the condition. A cross-sectional community survey conducted with 5420 individuals from Pune, an Indian state, shows only 0.9 % (49/5420) people were aware of the term "COPD" and hence reveal the incredibly low level of COPD awareness in the Indian populace (11). This emphasizes the necessity for widespread mass awareness campaigns across the country. Actually, COPD is a multifactorial respiratory condition influenced by various risk factors. Understanding the percentage data associated with these risk factors is essential for effective prevention and management strategies. These risk factors include tobacco smoking, environmental air pollution, occupational exposures, genetic factors and other comorbidities (Figure 1). Tobacco smoking is widely recognized as the primary risk factor for COPD, contributing to a significant percentage of cases globally. Numerous studies have consistently shown a strong association between smoking and COPD development. According to WHO, approximately 70 % of COPD cases are attributed to Tobacco smoking in developing countries whereas it accounts for 30-40 % of COPD cases in low- and middle-income countries (12). Environmental air pollution, including indoor and outdoor pollutants, is another significant risk factor for COPD. The percentage data associated with air pollution can vary depending on geographical location and population density. Approximately 25 % of COPD cases worldwide are attributed to ambient air pollution (13). Additionally, exposure to indoor air pollution from biomass fuels has been found to contribute to approximately 19 % of COPD cases in low-income countries (14).

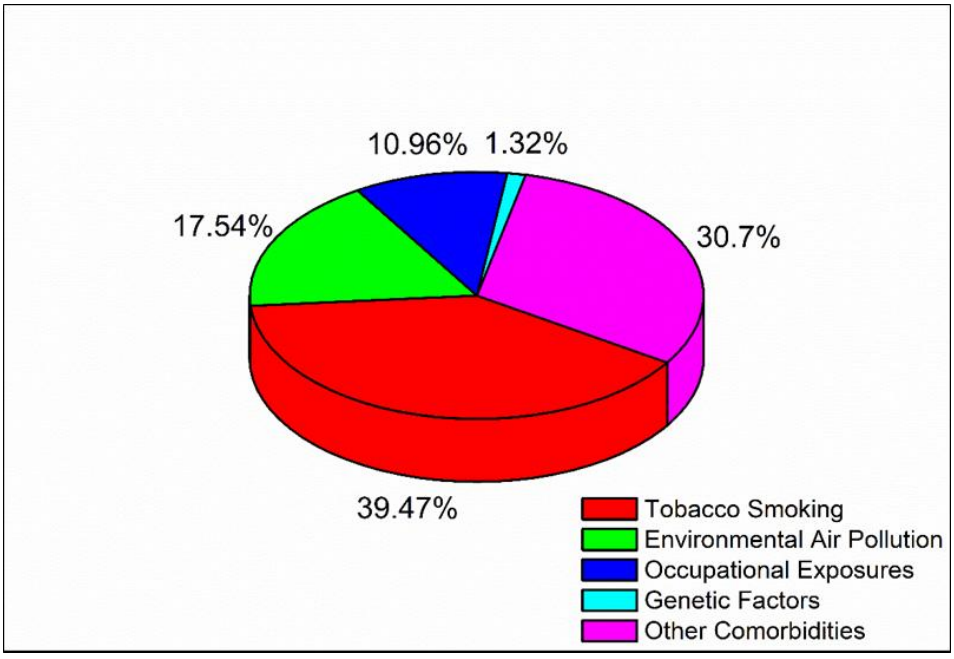

Figure 1: Percentage Distribution of Various Risk Factors Associated with COPD

The diagnostic criteria for COPD involve the presence of symptoms, obstructive airflow limitation, and a documented history of exposure to a known risk factor. If a patient is asymptomatic and/or lacks physiological signs of the disease, COPD cannot be diagnosed, presenting an inherent drawback that may lead to misdiagnosis. Assessing symptoms is challenging due to subjectivity in the patient's perception, and initial symptoms can overlap with other common illnesses, becoming significant only in later stages (15, 16). A multidimensional scoring BODE index comprising of Body-Mass Index (BMI), Obstruction, Dyspnoea, and Exercise Capacity is used to predict mortality in patients diagnosed with COPD (17). Spirometers, or Pulmonary Function Tests, are other common diagnostic techniques for assessing lung capacities in COPD patients. However, even with the inclusion of new criteria for determining at-risk patients for readmission like the Hospital Readmissions Reduction Penalty, the readmission rate has not decreased. It stays clinically challenging to identify patients at high risk and to prescribe a specific therapeutic regimen tailored to their needs. Therefore, this calls for a need to develop new tools for the prediction of COPD outcomes (18), where ML tools can play a pivotal role in selecting essential features for early COPD diagnosis. Machine learning techniques have been increasingly employed in the diagnosis of COPD. These tools leverage diverse data sources, including clinical records, imaging data, and patient history, to identify patterns and features indicative of COPD. One key advantage of machine learning in COPD diagnosis lies in its ability to handle complex and multifactorial data, allowing for the identification of subtle patterns that may be challenging for traditional diagnostic tools. Moreover, machine learning models can continuously adapt and learn from new data, enhancing their diagnostic capabilities over time. This dynamic and data-driven approach contrasts with the static nature of traditional diagnostic criteria, providing a more personalized and accurate diagnosis for individual patients. Integration of machine learning tools in COPD diagnosis offers a promising avenue for overcoming the limitations of traditional diagnostic methods. By leveraging advanced algorithms and diverse data sources, machine learning enhances the accuracy and efficiency of COPD diagnosis, ultimately improving patient outcomes.

Microbial Dysbiosis in COPD

Microbial dysbiosis refers to a disturbance in the composition and functionality of the microbial communities that reside within the respiratory and gastrointestinal tracts. The lungs and gut harbour a diverse array of microorganisms, including bacteria, viruses, fungi, and archaea. These communities form complex ecological networks and play essential roles in maintaining health and modulating immune responses (19). In the context of COPD, microbial dysbiosis mainly refers to an alteration in the lung microbiome, characterized by changes in the relative abundance and diversity of microbial species. Although it was always thought that the lungs were sterile, recent studies employing cutting-edge molecular techniques have shown that healthy humans have a rich population of bacteria, viruses, fungus, and other microbes living in their lungs (20, 21). However, the dysbiosis of gut (22) and oral (23) is also seen in people with COPD and may play a role in the emergence and aggravation of the condition due to increased abundance of potentially pathogenic bacteria, decreased microbial diversity, shifts in microbial composition and impact on inflammation and immune response.

Lung Microbial Dysbiosis and COPD

In COPD, the lung microbiome undergoes dysbiosis, characterized by changes in the types and relative abundance of microorganisms. This dysbiosis is influenced by various factors such as chronic inflammation, exposure to environmental pollutants (such as cigarette smoke), and respiratory infections. The dysbiosis observed in COPD has been linked to several detrimental effects. It can trigger abnormal immune responses and chronic inflammation in the airways, contributing to lung tissue damage and progressive airflow limitation. Dysbiosis may also impair the host's ability to effectively defend against respiratory infections, leading to recurrent exacerbations. Furthermore, dysbiosis can affect mucus production and clearance mechanisms in the airways, leading to increased mucus production, impaired clearance, and airway obstruction. These changes can further exacerbate symptoms and contribute to disease

progression in COPD (20). The human lungs have a high concentration of oxygen which allows a number of aerobic microbes to colonize it including several bacteria, fungi and even viruses (20,24). The lungs, which are typically considered free of any normal bacteria, are actually now known to contain a diverse and sparse population of microorganisms. These microorganisms, known as the lung microbiota, have been found to potentially play a role in maintaining the immune balance within the lungs and influencing the body's response to pathogens (25). According to a study the low density of the lung microbiota estimated to be around 10^3–10^5 colony-forming units per gram of lung tissue in mice, and ~ 2.2 $\times 10^3$ cells per square centimetre of lung in humans, may contribute to good health and well-being (26). The specific composition of the lung microbiota is influenced by various factors such as the immigration and elimination of bacteria, as well as the local conditions that support their growth. The most commonly observed bacterial phyla in the lungs include Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria. Compared to bacteria, fungi and viruses are less likely to colonise the lungs, but they can still exist in isolated amounts. Lung tissue has been found to include fungi including *Penicillium Candida, Aspergillus, Eurotium, Cryptococcus, Cladosporium and Malassezia.* (20, 21, 26). Evidence from various research shows the cruciality of lung microbiota in the onset and advancements of COPD. The lung microbial dysbiosis is characterized by reduction in the normal microbiota and development of pathogenic microorganisms. Majorly, an expansion of pathogenic organisms including *Haemophilus*, *Corynebacterium*, *Leptolyngbya*, *Capnocytophaga*, *Curvibacter*, *Afipia*, *Moraxella*, *Neisseria*, *and Undibacterium* were observed in case of COPD (27). The examination of microbiomes from different samples of COPD patients gives better understanding of lung microbial dysbiosis (28). The observations of lung tissues samples shows the abundance of *Firmicutes*, *Burkholderia* genus, *Lactobacillus* (29), *Flavobacterium* spp., *Prevotella* spp., *Haemophilus influenzae*, *Porphyromona*, *Bacteroidales*, *Dialister*, *Elizabethkingia meningoseptica* (30), *Neisseria, Corynebacterium*, *Staphylococcus*, *Rothia*, *Alloiococcus* and *Veillonella* (31). The increase in the abundance of these pathogenic bacteria was directly found to be associated with the pathogenesis, progression and exacerbation of COPD (32, 33).

Gut Microbial Dysbiosis and COPD

Apart from the respiratory microbiota, the gut microbiota also plays a vital role in COPD pathogenesis. The gut-lung axis, a bidirectional communication system between the gut and lungs, influences various aspects of immune regulation and inflammation. Studies have shown that COPD patients have an altered gut microbial composition, marked by alterations in the number of particular bacterial taxa and a decrease in diversity. These alterations are associated with systemic inflammation and impaired immune responses (24, 27, 28).

Lung-Gut Axis in COPD

Gut-lung axis refers to the communication that occurs between bacteria in the gut and lung (27). The onset and course of COPD are significantly influenced by the lung-gut axis. The interactions between the lungs and the gut have implications for the immune response, inflammation, and microbial composition, all of which contribute to COPD pathogenesis. The lung-gut axis involves bidirectional communication between the immune systems of the lungs and the gut. The gut, being a major site of immune activity and harboring a diverse microbial community, can contribute to systemic inflammation through the lung-gut axis. Both the lung and gut microbiota play crucial roles in immune regulation and overall health. The disturbance of gut-lung microbiota were found to be linked with various respiratory and gut diseases such as cystic fibrosis, asthma, ulcerative colitis, COPD, and Crohn's disease (34). The various factors associated with gut-lung microbial dysbiosis include tobacco smoking exposures, malnutrition, antibiotics and steroid treatments (27,35). A study of 15 patients with acute exacerbation of COPD, revealed the dynamic change in the gut-lung microorganisms during disease where antibiotic and steroid treatments were found to differentially affect the gut-lung microbiota, ultimately helping in the progression of the disease (35). The major abundance of microorganisms in the gut of healthy and COPD individuals were listed in Table 1. Understanding the association between the gut and lung

microbiota, highlighting its potential as a biomarker, and maybe pointing it as a target for future respiratory treatments, may depend on the application of culture-independent techniques to influence the gut and lung microbiota on COPD.

Oral Microbial Dysbiosis and COPD

Oral microbial dysbiosis refers to an imbalance or disruption in the normal composition and diversity of microorganisms in the oral cavity. This dysbiosis can have implications for various aspects of oral and systemic health, including its potential role in the development and progression of COPD. The oral cavity harbors a complex and diverse microbial community, which includes both commensal and potentially pathogenic bacteria. In individuals with poor oral hygiene or oral health conditions such as periodontitis, the oral microbiota can become dysbiotic, with an overgrowth of pathogenic bacteria. These pathogenic bacteria can be aspirated into the lower respiratory tract, potentially contributing to the inflammation and infection observed in COPD. Dysbiotic oral microbiota and the resulting periodontal disease can lead to chronic inflammation in the oral cavity. This local inflammation can stimulate a systemic inflammatory response, which can contribute to the systemic inflammation observed in COPD. The systemic inflammation may worsen COPD symptoms and contribute to the progression of the disease. Dysbiotic oral microbiota and periodontal disease can influence the composition and diversity of the lung microbiota (23, 36). Aspiration of oral pathogens can introduce these microorganisms into the lungs, potentially altering the lung microbial community. Changes in the lung microbiota have been associated with increased inflammation and exacerbations in COPD. COPD and oral health conditions, such as periodontitis, share common risk factors such as smoking, poor nutrition, and systemic inflammation. These shared risk factors may contribute to both oral microbial dysbiosis and the onset or progression of COPD. Recognizing the association between oral microbial dysbiosis and COPD highlights the importance of oral health in the management of COPD (37, 38). The distribution of microorganisms in the oral cavity of healthy and COPD individuals are listed in Table 1.

Table 1: Site specific Micro Biome Abundant in Healthy Versus COPD Individuals

Organ	Normal Micro biome	Micro biome in COPD	References
Lung	*Staphylococcus epidermidis*, *Corynebacterium* spp. (diphtheroids), *Propionibacterium* spp., *Haemophilus* spp, *Fusobacterium*, *Staphylococcus aureus, Moraxella*, *Veillonella*, *Eikenella, Streptococcus Prevotella*, and *Pseudomonas* **Fungi:** *Saccharomyces cerevisiae*, *Malassezia restricta*, and *Candida albicans*	*Streptococcus*, *Moraxella*, *Proteobacteria, H. infuenzae* and *Pseudomonas*	(24), (26), (28), (29), (31)
Gut	*Firmicutes, Bacteroides distasonis, Bacteroides uniformis, Fusobacteria, Actinobacteria, Proteobacteria, Verrucomicrobia, Enterococcus casseliflavus, E. avium, Eubacterium ramulus, Clostridium coccides, C. orbiscinden, Bifidobacterium infantis, B. longum, L. plantarum, L. casei, L. acidophilus, L. gasseri Butyrivibrio species, Peptostreptococcus and E. coli,*	*Firmicutes, Desulfovibrionales, family Victivallaceae, Marvinbryantia, Enterobacteria, C. perfringens, C. difficile, Neisseria, Haemophilus, Moraxella, Peptococcaceae, family, Bifidobacterium, and Lactobacillus.*	(22), (24), (27), (28), (30)
Oral	*Saccharibacteria, Actinobacteria,*	*Fusobacterium, Veillonella,*	(23), (37), (38)

Gracilibacteria, Proteobacteria, Bacteroidetes, Chlamydiae, Chloroflexi, Spirochaetes, Synergistetes, Saccharibacteria, and Fusobacteria.	*Rothia, Actinomyces, Campylobacter, Johnsonella, Catonella, Porphyromonas canis, P. intermedia, Johnsonella ignava and Catonella morbi*

Machine Learning and COPD

In recent years, various tools have been applied for the diagnosis, continuous management, readmission, acute respiratory failure, and mortality in COPD patients. Some studies are done on extensive population size, but others lack validation due to small cohorts. Nevertheless, many attempts have been made to predict various outcomes related to this disease. For the diagnosis of COPD patients, respiratory audio data was used in 126 patients for healthy participants and participants with COPD. Using Convolutional Neural Networks (CNN), they were able to distinguish healthy individuals from patients with an ROC of 0.92 (39). While there have been many well-established risk factors for readmission risk, they have not been useful in predicting risk for COPD readmission (18). This calls for a need to develop new methods to assess risk factors for readmission in COPD. For detecting a 90-day risk of readmission rate of patients, demographics, vitals, lab tests, medicines, and other clinical factors were used as features for distinguishing between the two groups of 3238 patients by Random Forests with a Receiver Operating Characteristic (ROC) of 0.73 (40). To detect whether patients were managed according to WHO GOLD Standards, clinical features like smoking history, pre and post-bronchodilator FEVI scores were used. SVM-RFE provided an ROC Score of 0.987 in differentiating the two cohorts from a total of 203 patients (41). Apart from this, COPD patients are at high risk of respiratory failure, ventilator dependence, and also mortality after hospitalization. Records of 5061 patients of COPD were collected and the risk for each of these categories was predicted, using multiple features like age, gender, BMI, vitals, temperature, pulse and other clinical factors. Evaluation with seven different machine learning algorithms showed XGBoost for mortality detection (ROC: 0.817), Random Forest for acute Respiratory failure (ROC: 0.804) and LightGBM for Ventilator dependence (ROC: 0.809) (42). Table 2 summarizes all tools that are available in the literature for the prediction of different outcomes in COPD (40, 42–48). To the best of our knowledge, there has been no use of ML/DL tools in COPD using microbial dysbiosis, even when it has been characterized as a major factor in COPD patients who are readmitted.

Table 2: Summary of Tools for Prediction of Various Outcomes in COPD using ML/DL

Predictor	Article/ Author	Details	Features Used	Techniques Used	Results	Cohort
Readmission	36299799 (40)	The authors developed a model to predict 90 day risk of readmission for AECOPD.	Demographics, vital signs, lab results, medications, comorbidities and other clinical factors	Random Forests	ROC= 0.73	Total of 3238 patients were evaluated out of which 1103 were readmitted and 2142 were not readmitted.

	36177924 (43)	Prediction of 30-day readmission risk in elderly patients with an exacerbation of COPD	Age, education, smoking history, diabetes and other heart related comorbidities, no. of times of hospitalization of AECOPD, seasonal factors and other risk factors.	Logistic Regression	Accuracy= 85.25% ROC=0.814	A total of 1,120 patients were investigated, including 879 non-readmission patients and 241 readmission patients.
				Back Propagation Neural Network	Accuracy = 80.65% ROC = 0.775	
				Support vector machines	Accuracy = 88.57% ROC= 0.858	
	30787351 (44)	Readmission after 30 days for patients with COPD	HOSPITAL score, LACE index, age, gender, (LOS), admissions in the previous year and other data driven features		ROC= 0.653	67771 patients admitted for COPD in the Geisinger Health System
Mortality	34943632 (42)	A model was developed for the prediction of the mortality of COPD patients in hospital	A combination of 28 clinical features was used: age, gender, BMI, SPO2 etc	XGBoost	ROC=0.817	5061 patients from 3 hospitals were selected out of which 4100 were alive and 961 died.
	32353417 (45)	Mortality of patients is predicted. The model is available at the web server at: https://cdnm.shinyapps.io/cgmortalityapp/.	30 features including clinical data, spirometry and imaging data was used	Random Survival Forest	C-Index>0.7	2632 patients from COPDGene database and 1268 participants from ECLIPSES were included. (46)

	15144 (46)	Mortality of the patients was predicted using CT images	CT images + six-minute walk distance	CNN+ Random Survival Forest	3 year survival = 0.8878 5 year survival = 0.8411	Data from 344 patients was taken from Korean Obstructive Lung disease cohort. 102 patients were chosen for external validation.
Acute Respiratory Failure	34943632 (42)	A model was developed to predict acute respiratory failure in hospital	Combination of 28 clinical features was used	Random Forest	ROC=0.804	5061 patients from 3 hospitals were selected out of which 4580 experienced Acute Respiratory Failure and 481 did not.
Ventilator Dependence	34943632 (42)	A model was developed to predict acute ventilator dependence in hospital	Combination of 28 clinical features was used	LightGBM	ROC=0.809	5061 patients from 3 hospitals were selected out of which 3980 experienced ventilator dependence and 1081 did not
Continuous Management	33177815 (47)	Differentiation of patients on whether their continuous management has been according to WHO GOLD standards.	Parameters included smoking, mMRC score, forced vital capacity, and FEV1	SVM-RFE	ROC=0.987	203 patients were evaluated with only 15 in the managed group
Diagnosis	33817019 (39)	Using CNN to detect COPD and its severity using respiratory audio data	Respiratory audio data is used.	CNN	Enhanced ICBHI Score to 93%	The cohort is 126 patients. Respiratory audio for patients healthy vs patients with

					ailments was chosen.
22018532 (48)	Using Forced Oscillations for diagnosis of COPD	7 features using forced oscillation measurements of patients	KNN, SVM, LBNC	ROC= 1	50 volunteers such that 25 healthy and 25 with COPD were selected for this study.

Discussion

This review sheds light on the intricate relationship between COPD and microbial dysbiosis and pivotal role it plays in disease pathogenesis and progression. Ample literature exists to suggest that dysbiosis of the lung, gut, lung-gut axis and oral cavity, contributing to chronic inflammation, impaired immune response thereby accelerating disease trajectory. The traditional techniques and criteria lead to the misdiagnosis of COPD individuals, leveraging machine learning tools for the diagnosis, continuous management, readmission, ventilator dependence, acute respiratory failure, and mortality of COPD individuals has shown potential. Microbial dysbiosis is a major contributor to COPD. Even though various ML Tools have been applied to predict various outcomes of COPD disease, to our knowledge, no ML/DL study has been performed that uses the human microbiome to predict diagnosis or readmission. The human gut microbiome, which consists of microbial communities inhabiting the intestinal tract, emerges as a significant factor in human diseases. Machine learning tools have shown good results in both the prediction and therapeutics of many diseases. Within the context of Colorectal Carcinoma (CRC), Thomas *et al.,* have investigated the link between gut microbiome and CRC (49). The study could differentiate between CRC and healthy controls through the help of their gut microbiome profile using Random Forests with Area under the Curve (AUC) score of 0.84. In their study, they reported the link between the microbial pathways producing trimethylamine (TMA) from choline; the associated choline trimethylaminelyase gene is abundant and overexpressed in the gut microbiome of CRC patients. The variants associated with CRC mostly originate from *H. hathewayi*, *C. aspargiforme*, *K. oxytoca* and *E. coli*. This work represents a significant advancement in establishing the relationship between microbial dysbiosis and diseases. In another study Wang *et al.,* conducted a systematic review consolidating the research on microbial dysbiosis and Irritative Bowel Syndrome (IBS), establishing a connection between gut microbial dysbiosis and IBS (50). Individuals with IBS exhibited lower populations of bacterial genera such as Lactobacillus and *Bifidobacterium*, alongside higher populations of harmful pathogenic bacteria like *Enterobacteriaceae* and *E. coli* compared to healthy controls. ML and DL tools have also aided in the development of Non-invasive tools for multi-class diagnosis based on the faecal microbiome. Recently, a study has shown multi-class classification of 9 major diseases including CRC and IBS, Cardiovascular diseases, Crohn's disease, ulcerative colitis and Post-Acute Covid-19 syndrome using Random Forests with AUC from 0.9 to 0.99 in independent datasets (51). The use of ML tools for the prediction of disease outcomes using microbial dysbiosis has been well-established in the literature. However, the use of these ML/DL techniques has not been explored with respect to COPD. The current research on microbial dysbiosis associated with disease pathogenesis and progression allows a new avenue to be explored for the detection of diseases, especially COPD through gut microbiome data and machine learning models. A non-invasive technique which can be employed with other diagnostic tools for better diagnosis of the disease. Such endeavours hold the potential to revolutionize COPD diagnosis by facilitating timely intervention and improving patient outcomes. Researchers and scientists equipped with the knowledge, resources and expertise in the domain of machine learning should leverage the microbiome data available for detecting COPD.

Conclusion

Understanding the role of microbial dysbiosis in COPD is an active area of research, as it may have implications for the development of new therapeutic strategies. Restoring a healthy lung microbiome through interventions such as probiotics or targeted antimicrobial approaches is being explored as a potential avenue for managing COPD. However, further research is needed to fully understand the complex interactions between microbial dysbiosis, the host immune response, and COPD pathogenesis. Continued studies will help shed light on the mechanisms underlying dysbiosis and its impact on disease progression, ultimately paving the way for improved diagnostic and therapeutic approaches for COPD. In recent years, the application of ML/DL tools in the medical field has evolved rapidly, and is being implemented in screening and diagnosis, classification and assessment, management and monitoring, as well as in rate of readmission of COPD patients, which has been summarized in the review. Further, explosion in the vast availability of gut microbial data is too massive to be analyzed using conventional methods. Therefore, ML and DL tools offer effective solutions and should remain the focus of further research and development in preventing COPD readmissions through microbial modulation. These tools could be further utilized for analyzing different responses to treatment, providing therapeutic guidance for specific phenotypes required in precision medicine, and establishing a management system for COPD.

Abbreviations

COPD: Chronic Obstructive Pulmonary Disease; ML: Machine learning; DL: Deep learning; AI: Artificial Intelligence, IBS: Irritative Bowel Syndrome; CRC: Colorectal Carcinoma; BMI: Body-Mass Index; CNN: Convolutional Neural Networks; ROC: Receiver Operating Characteristic; AUC: Area Under the Curve.

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Author Contributions

Dr. Vibha Gupta and Dikscha Sapra conceptualized and designed the study. Monika Antil, Malika Kapoor, Kushal Gupta, and Dikscha Sapra were involved in data acquisition, date organization and interpretation. Monika Antil, Malika Kapoor, Kushal Gupta, and Dikscha Sapra drafted the manuscript and Dr. Vibha Gupta and Dikscha Sapra performed the critical revision of the manuscript.

Conflict of Interest

The authors have no conflicts of interest, either financial or commercial.

Ethics Approval

Ethical approval is not required for this review paper, as it does not involve direct experimentation with human or animal subjects.

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