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Research Article

ALLERGIC AIRWAY DISEASES: ROLE OF MICROBIOTA AND ENVIRONMENTS

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ABSTRACT

A prospective study on 220 patients were clinically diagnosed with COPD were included in the study. Early morning sputum samples were collected within 24 hours of admission in sterile bottle after an antiseptic oral rinse. Identification and its antibiogram from the sputum samples were done by the standard conventional methods. The quality of the sputum was assessed by Bartlett's grading. The microbiological quality of the patients working environment was assessed by determining the concentrations and composition of bacteria and fungi present in the outdoor air using six stage Anderson's air sampler. Study findings revealed that pathogenic bacterial organisms were found in 50 to 80% of patients with COPD during exacerbations. The major causative organisms are *Staphylococcus aureus*, *Klebsiellapneumoniae*, *Streptococcus pyogenus*, *E.coli* and *Pseudomonas aerogenosa* and the common fungal allergens are *Aspergillusfumigatus*, *Candida albicans*, *Penicillium*and *Rhizobium* are found to be predominant organisms in causing allergic airway diseases. The findings of the present study shows clear evidence for presence of pathogenic microbiota in environment and cause allergic airway disease like COPD among the field working individuals.

INTRODUCTION

People are exposed to aeroallergens in various settings, both at home and at work. Fungi are ubiquitous airborne allergens and are important causes of human diseases, especially in the upper and lower respiratory tracts. The concentration of allergens in the environment varies, depending on various factors including climate, vegetation, and air quality.[1] Bacterial infections are the most common observable cause of acute exacerbation and death in COPD. Acute exacerbation is characterized by increase in cough, dyspnoea and alteration in type and amount of sputum production.[2,3] Pathogenic bacterial organisms are found in 50 to 80% of patients with COPD during exacerbations. Respiratory disease caused by micro-organisms, is a major global public health problem that affects millions of people each year and ranks as the second leading cause of death from an infectious disease worldwide, with 8-6 million new cases and 1.3 million deaths in 2012.[4,5]

The outdoor allergens are predominantly constituted by pollens and fungal spores. Many of these fungal spores are lesser than 10 microns in diameter and their deposition into lower airways is common.The indoor allergens are represented by allergens from dust mites, cockroaches and pets.[6,7] Bacteria and fungi from human environment may cause allergic reactions. They are associated with number of allergic diseases in humans including allergic rhinitis, bronchial asthma and allergic bronchopulmonary mycoses resulting from exposure to spores. Recent studies of the respiratory tract micro biota using sputum samples and mixtures of saliva and pharyngeal secretions indicate changes and possible associations with pulmonary infections. Bacterial infections are the most common observable cause of acute exacerbation and death is COPD.[8,9]Isolation and susceptibility testing of organisms make diagnosis to be established and also make drug selection more rational.[10-12] This study was undertaken to determine the role of environment in causing allergic airway disease

MATERIALS AND METHODS

Collection of clinical samples

The present study is an institutional based cross sectional study. 220 patients for clinically diagnosed with COPD were included in the study. All the patients were positive allergic skin tests of S.S. Institute of Medical Sciences and Research Centre, Davangere between January 2013 to January 2014. Early

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morning sputum samples were collected from all above patients were instructed to collect deep coughed sputum samples into a sterile container with a screw cap.

These samples were streaked on MHA, MacConkey agar and Blood agar incubated at 37°C for 48 hours. Organisms were identified based on colony morphology and standard biochemical tests with antibiogram. Identification of the organisms and its antibiogram from the sputum samples were done by the standard conventional methods. The quality of the sputum was assessed by Bartlett's grading. (William M.J. and Firegold S.M. 1982)

Identification of organisms from environmental study

Bacteriological examination of above patient's working environment was done. Anderson's six stage sampler for sampling of airborne bacteria and fungi in working environment was used. Anderson's sampler is a multi-stage, multi orifice cascade impacter that automatically separate particles based on size from 10 mm and above to 0.3 mm in diameter. Procedures for sampling was done as per manufacturers' instruction.

The plates were incubated at room temperature for 24-48 hours for bacterial count and for 5 to 7 days for fungal count. The airborne bacterial and fungal concentrations were calculated and expressed as colony forming units per cubic meter of air (Cfu/m^3).Isolation, identification of the organisms from patients working environment were done by standard conventional techniques.

RESULTS

A total of 220 clinical samples from patients suffering from pulmonary infections among different age groups from both male and female were collected from S.S Institute of Medical Sciences and Research Centre, Davangere.

Among 220 clinical samples, the most common bacterial species isolated from patient's are *Staphylococcus aureus*i.e in 58 samples, *Klebsiellapneumonia* 88 samples, *Streptococcus pyogenus*32 samples, *E.coli*15 samples and *Pseudomonsaerogenosa*22 samples respectively (Table 1).

Table 1 Bacteria species identified in clinical samples

Bacteria spp. Identified	Clinical samples	
	No.of samples	**Percentage**
Staphylococcus aureus	58	26.36
Klebsiella pneumonia	88	40.00
Streptococcus pyogenus	32	14.54
E.Coli	15	6.81
Pseudomonas aerogenosa	27	12.27

Among 220 clinical samples, the most common fungi species isolated from patient's are*Aspergillusfumigatus*120 samples, *Candida albicans*60 samples and *Penicillium species*40 samples respectively (Table 2).

Table 2 Fungi species identified in clinical samples

Fungi spp. Identified	Clinical samples	
	No.of samples	**Percentage**
Aspergillusfumigatus	120	54.55
Candida albicans	60	27.27
Penicillium spp.	40	18.18

The most common bacteria species identified from patients working environment are *Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pyogenus* and *Pseudomonas aerogenosa* (Table 3).

Table 3 Bacteria species identified from patients working environment using Anderson's air sampler

Bacterial organisms	Percentage
Staphylococcus aureus	40.91
Klebsiella pneumonia	31.82
Streptococcus pyogenus	13.64
Pseudomonas aerogenosa	13.64

The common fungi species identified from patients working environment are *Aspergillusfumigatus*, *Rhizobium*, *Candida albicans* and *Penicillium*(Table 4).

Table 4 Fungi species identified from patients working environment using Anderson's air sampler

Fungi spp. Identified	Percentage
Aspergillusfumigatus	36.36
Rhizobium	27.27
Candida albicans	22.73
Penicillium spp.	13.64

The organism isolated from both patients' clinical samples and patients working environment is a particular field were identified and listed as follows (Table 5). In paddy and maize field *Staphylococcus aureus* was identified, in groundnut and maize dust *Aspergillusfumigatus,* in cotton field *Penicillium spp.* in rice field *Aspergillusfumigatus* and *Klebsiella pneumonia* identified.

Table 5 Organism isolated from both patients clinical samples and patients working environment

Agricultural market Field	% organisms from clinical samples		% organisms from environment samples	
	Organism	**%**	**Organism**	**%**
Paddy	S.aureus E.Coli	55.0 24.2	S. aureus	31.5
Maize	S.aureus Kl. Pneumonia	26.4 66.0	S. aureus	31.56
Groundnut	Aspergillus	55.0	Aspergillus Rhizobium	27.6 5.9
Maize dust	Kl. Pneumonia S. Pyogenus	48.4 22.0	Aspergillus	31.56
Cotton	Penicillium C.albican	44.0 33.0	Penicillium	8.1
Rice	Aspergillus Kl. Pneumonia	26.4 39.6	Aspergillus Kl. Pneumonia	51.2 23.67

The count of culturable bacteria was observed in the range of 1560 to 17060 cfu/m^3 with an average count of 7120.48 Cfu/m^3 and the fungal load ranged from 220 to 1560 Cfu/m^3 with an average count of 776.19 Cfu/m^3.

DISCUSSION

COPD remains among one of the commonest disease of elderly population with the increase in life expectancy, the prevalence of COPD is increasing. Though a progressive disease, acute exacerbation can account for significant increase in the morbidity and mortality of these patients. The bacteriological profile COPD is constantly changing with advanced diagnostic techniques. In most previous studies airway infection seems to be the first cause of decompensationand accounts for 80-90% of cases whom triggering factor can be demonstrated[2,3,5].

Positive cultures of the sputum was seen in 220 patients. 27 (12.27%) of patients were positive for *Pseudomonas aerogenosa* that is consistent with the study by Griffth DE, Muzerek GH *et al*, have also found that traditional pathogens *KlebsiellaPneumoniae* were 88 (40%) are declining its importance, while newer pathogens such as *E.coli*15(6.81%) *Streptococcus pyogenus*32(14.54%) and *Staphylococcus aureus*58(26.36%) are becoming important and *Aspergillusfumigatus* were 120(54.55%), *Penicillium* were 40(18.18%), and *Candida albicans* were 60(27%) respectively, which is consistent with study by Herberty Reynolds who have found these organisms are responsible for acute exacerbation of COPD.[13-15]

The average bacterial count during working days (Monday to Saturday) varied between 6456 to 8410 Cfu/m^{3}and weekend count was 3973.33 Cfu/m^3. The weekend bacterial concentration were significantly higher than counts on the working days[18,20]. A total of 91% gram positive bacteria were found, at agricultural market sites, respectively. It was previously demonstrated that gram positive bacteria have greater resistance and survival ability in atmosphere than gram negative bacteria under strong sunlight. *Bacillus, Microccous, Microbacterium, Pseudomonas* and *Staphylococcus aureus* were previously reported as the dominant bacteria in outdoor environment from different parts of the world.[19,20]

The working days count averaged between 760 to 1000 Cfu/m^3 and weekend count was 466.67 Cfu/m^3. The weekend fungal concentration was significantly lower from working days. The working days counts averaged between 503.33 to 653.33 Cfu/m^3 and weekend count was 806.67 Cfu/m^3. Many of the fungal species identified in the atmosphere like *Alternia, Aspergillusfumigatus, Aspergillus, flavus, Aspergillusniger, Penicillium* and *Rhizobium* are common known to outdoor environment[20,21]. The daily fungal spore concentration is associated with increase in number of emergency visit and hospital admission due to exacerbation is asthma attacks. In most of the cases appropriate antibiotics and antifungal improved the clinical condition of most of the patients.

CONCLUSION

The role of specific microbial species in the pathogenesis of airway disease like COPD has been much studied over the past two decades in different way in different settings. Despite of ongoing debate, the present study significantly proves there are bacterial and fungal spores are abundant in nature and much evidence is now available to show that bacteria and fungi can cause atopic clinical illnesses. Assessing patient's clinical samples and also their working environment plays a very key role in effective treatment of illness conditions. Aerobiological studies and control of environmental factors can reduce the burden of allergy in human beings and can reduce the patient's hospital stay also. More, such studies from India may help in better understanding of the condition which can lead to proper diagnosis and management of such airway diseases.

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References

1. Aaron Fernstrom and Michael Goldblatt. Aerobiology and its role in the transmission of infectious diseases. *Scientific Research and Essays* 2012; 67(25):30-40.
2. Akihiko Tanaka, Megumi Jirno, Kuniaki Hirai, Yoshito Miyata, Hiroko Mizuma, Munehiro Yamaguchi, ShirOhta, Yoshio Watanabe, Mayumi Yamamoto, ShirtaroSuzuji, Takuya Yokor, Mitsuru Adachi and Hironori Sagara. Longitudinal increase in total IgE levels in patients with adult asthma: An association with poor asthma control. *Journal of Microbiology*2014; 15:144.
3. Anupama N, Vishnu Sharma M,Nagaraja HS and Ramesh BhatM. The serum immunoglobulin level reflects the severity of bronchial asthma. *Journal of Antimicrobial Chemotherapy* 2005 December; 18(3): 35-40.
4. Fletcher L.A., Noakes C.J., Beggs C.B. and Sleigh P.A. The importance of bio-aerosols in hospital infectious and the potential for control using Germicidal Ultraviolet Irradiation. *Journal of Investigating Allergol Clinical Immunology*.2006; 16(6): 357-63
5. Gurjeet Singh, Raksha A.D., Urhekar. Candidal infection, Epidemiology, Pathogenesis and Recent Advances for Diagnosis. 2013; 1(1):34-8.
6. Luz Elena Botero., Luisa Delgado-Serrano., Martha Lucia Cepeda., Jose Ricardo Bustos., Juan Manual Anzola., Patricia Del Portillo., Jaime Robledo and Maria Mercedes Zambrano. Respiratory tract clinical sample selection for microbiota analysis is patients with pulmonary tuberculosis. *Asian Pacific Journal of Tropical Disease* 2014; 2:29.
7. Makut M.D., Nyam M., Shelu L., AnzakuSJ. A survey of the microflora of the outdoor air environment of Keffi Metropolis, Nasarawa State, Nigeria. *African Journal of Microbiology and Research*; 2014; 8(27):2650-55.
8. Karuppasamy C., Lalsanglura Ralte, Kannan R., and Saravanakumar. A preliminary assessment of aero fungal allergens from the wards of civil hospital Aizawl. *Asian Pacific Journal of Allergy and Immunology* 2013; 4(3):13-22.
9. Kuriakose J.S., and Miller R.L., Environmental epigenetics and allergic diseases: Recent Advances. 2010; 40:1602-10.
10. Manjunath N.S., Dayanand S., Jagannath K.V., Basavarajappa K.G and Rangaswamy B.E. Prevalence of human pyogenic skin infections Bacterial Pathogens and their Antibiotic Susceptibility Profile 2013;1(1):37-42.
11. Neelkamal Chaudhary and Kikeren A. Marr. Impact of Aspergillusfumigatus in allergic airway diseases. Journal of Antimicrobial Chemotherapy2011; 1:4.

12. Padma Srikanth, SuchithraSudharsanam, Ralf Steirberg. Bio-aerosols in indoor environment: Composition, Health. Effects & Analysis 2008; 26(4):302-12.
13. Pramod Kumar, PawanMohar AK, God DV, Kamboj and Om Kumar. Aero-microbiological study on distribution pattern of bacteria and fungi during weekdays at two different locations in urban atmosphere of Gwalior, Central India. 2011; 6(25): 5435-41.
14. Rangaswamy Be, YogithaSeema AM, Jayasimha VL. Bacteriological study of infection in allergic airway disease. Indian J Aerobiol 2013; 26 (No.1&2):65-70.
15. Robert K. Bush, and Jay M. Portroy. The role and abatement of fungal allergens in allergic diseases. EurRespir J 2001; 12:107-09.
16. Rodolfo J. Dennis, Luis Caraballo, Elizabeth Garcia, Maria X. Rojas, Martin A, Rondon, Adriana Perez, Gustavo Aristizabal, Augusto Penaranda, Ana M. Barragan, VelkyAhumada& Silvia Jimenez. Prevalence of asthma and other allergic conditions in Colombia 2009 – 2010; a cross – sectional study. Am J RespirCrit Care Med 2012; 12:17-20.
17. Sathavahara Chowdary V, Lakshmi Prasanna, Sangram V, Sudha Rani, Vinay Kumar EC. Role of fungi (Molds) in allergic airway disease – An analysis in a South Indian otolaryngology center. Indian J Allergy Asthma Immunol 2011; 25(2):67-78.
18. Senthil Velsivasakthivel and Natarajan Nandini. Airborne multiple drug resistant bacteria isolated from concentrated municipal solid waste dumping site of Bangalore, Karnataka, India. International Research Journal of Environment Sciences 2014; 3(10):43-6.
19. Shahnawaz A, Saleem SM, Mushtaq S. Lone Shah, Sonaullah Tariq Bhat, Bhat GH, Nabi Dhobi. Bacteriological profile in acute exacerbation of chronic obstructive pulmonary disease (COPD). Thai Journal of Physiological Sciences 2003; 10(3):55-60.
20. Shiv Shankar Gautam, Navneet, Sanjay Kumar, Prabhat. Screening of antibacterial activity of Nepeta Ciliaris Benth. Against Respiratory Tract Pathogens 2012; 8(1):100-3.
21. Sichletidis L, Tsiotsios I, Gavriilidis S, Chlors D, Gioulekas D, Kottakis I, Pataka A. The effects of environmental pollution on the respiratory system of children in Western Macedonia, Greece. J Invest AllergolClinImmunol 2005; 15(2):117-23.

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