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ORIGINAL ARTICLE

Bacteria in sputum of patients with chronic chest lesions in chest department of Beni-Suef University Hospital

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Abstract Pulmonary infection in chronic chest lesions (CCL) is poly-microbial and it is possible that anaerobic bacteria that are not detected by routine aerobic culture methods may be present in the airways mucus.

Introduction

Chronic, pulmonary infections remain the most prominent cause of the increased morbidity and mortality in CCL with more than 95% of deaths due to respiratory failure. The bacteria most frequently isolated from the sputum of patients with CCL and pulmonary infection by standard aerobic microbiological methods are Pseudomonas, *Staphylococcus aureus*, and *Burkholderia cepacia* complex.

Recently, it has been shown that there are steep oxygen gradients in the mucus of the patients with CCL leading to proliferation of Pseudomonas within hypoxic media that generates fully hypoxic (anaerobic) conditions in the lungs of patients with CCL with persistent respiratory infection [1]. Because of that there is the real possibility that CCL pulmonary infection is poly-microbial with anaerobic bacteria that are not detected by routine aerobic culture methods.

A number of studies have detected pathogenic anaerobic bacteria in significant numbers in the lungs of patients with CCL by culture [2].

Mainly Pseudomonas and *B. cepacia* complex are the principal anaerobic pathogens in lungs of patients with CCL such as pneumonia, lung abscesses, and emphysema in which aerobes and anaerobes were present in a poly-microbial nfection and were considered to be of significance [3].

The presence of anaerobes in the lungs of patients with CCL could be important because current antibiotic treatment targeting aerobic bacteria may be ineffective against anaerobic bacteria, which may result in a less optimal treatment outcome for patients [3].

In this study, we used strict anaerobic bacteriologic culture techniques to detect anaerobic bacteria in sputum and broncho-alveolar lavage fluid (BAL) to determine the susceptibility of these anaerobes to a range of antibiotics [3].

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Aim of the work

- To determine whether anaerobic bacteria are present in the sputum of patients with CCL and its role in pathogenesis of these lesions.
- To detect the antimicrobial susceptibility of anaerobic bacterial infection in CCL patients in Beni-Suef University Hospital.

Patients and methods

There are currently 100 adults attending the chest department in Beni-Suef University Hospital at the time of this study:

75 patients had chronic Pseudomonas infection.
10 patients had chronic *B. cepacia* complex infection.
15 infected by a number of different pathogens.
20 healthy volunteers (control).

All were clinically stable patients who were capable of expectorating sputum sample. Clinical stability was defined as no change in symptoms, FEV1 within 10% of best value in the previous 6 months, and no new antibiotic.

Collection of sputum samples from adult patients with CCL

Sputum samples were collected in sterile containers. After collection, all samples were transferred within 15 min to an anaerobic cabinet in the microbiology laboratory for processing.

Collection of BAL from patients with CCL

BAL samples were frozen within 5–10 min of collection and stored at −70 °C. When all samples had been collected, they were transported in dry ice at −70 °C to microbiology department for processing. Samples were subsequently thawed in the anaerobic cabinet at 37 °C before processing.

Results

Tables 1 and 2.

Discussion

This study provides evidence that the lungs of patients with CCL are not only chronically colonized with pathogens such as Pseudomonas, but also by a range of other bacterial species, many of which are anaerobes. A high percentage of the patients with stable CCL was examined to have numbers of anaerobes in sputum equal to or greater than those of Pseudomonas. In a number of samples, more than one anaerobic species was detected, indicating that the anaerobes exhibited far greater microbial diversity than previously associated with the lung of CCL. Furthermore, we detected similar anaerobic species in multiple samples collected from the same patients at different time points, which suggests persistence of these bacteria within the lung of those patients. These culture results support the results of many molecular studies, which indicated the presence of metabolically active bacterial community within the lung of patients with CCL [4].

The anaerobes detected by culture in the present study and previously by molecular methods were those that would normally be found colonizing the oropharynx [5]. It is possible, therefore, in patients with CCL who have impaired mucociliary clearance mechanisms, that these bacteria are carried from the oropharynx into the lower airways where they colonize the lung and potentially contribute to infection and lung damage. Furthermore, the anaerobes detected were similar to those found in other studies of anaerobic pulmonary infection, such as pneumonia, lung abscesses, and emphysema were aerobes and anaerobes were present in a poly-microbial infection and were considered to be of significance [3].

Colonization with Pseudomonas significantly increased the likelihood that anaerobic bacteria would be present in the sputum. This suggests that a preceding bacterial infection, with Pseudomonas renders airway secretions frankly anaerobic and creates the environment required for subsequent anaerobic infection. Consistent with this hypothesis is the observation

Table 1 Bacteria isolated by culture from the sputum of adult patients with chronic chest lesions.

Aerobic isolates			Anaerobic isolates		
Name	No of isolates from 100 sputum samples	% of isolates from 100 sputum samples	Name	No	% of isolates From 100 Sputum samples
1- *Pseudomonas aeruginosa*	100	100	1- prevotella	29	29
2- *B. cepacia* complex	20	20	2- Actinomyces	10	10
3- Rothia	3	3	3- Veillonella	7	7
4- Streptococcus	73	73	4- Propionibacterium	7	7
5- Staphylococcus	31	31	5- Peptostreptococcus	1	
6- Micrococcus	15	15	6- BuHeidia	1	
7- Neisseria	10	10	7- Bifidobacterium	1	
8- Bacillus	17	17	8- Gemella	1	
9- *E. coli*	8	8	9- Lactobacillus	1	
10 Stenotrophomonas	5	5	10- Fusiobacterium	1	
			11- Clostridium	1	
			12- Staphylococcus	1	
			13- Streptococcus	1	
Total	282	100	Total	62	100