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Microbiological Patterns of Community Acquired Pneumonia

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Abstract

Background: To study the microbiological pattern in patients admitted with community acquired pneumonia at GHCCD, Visakhapatnam.

Methods: 30 patients clinically diagnosed to have Community acquired pneumonia were included in the study. Patients sputum was collected and subjected to gram stain and culture sensitivity.

Results: Out of 30 patients 53% were males and 47% were females. The most common age group in this study is 41-60 years. Unilateral Involvent of lung in seen in 77% and bilateral in 23 %. Lower lobes are commonly involved followed by middle/lingular and upper lobes. Among alcoholics, diabetics, COPD, lower lobe is commonly involved than other lobes. Klebsiella is the most commonly isolated organism. Among diabetics, klebsiella is most commonly isolated followed by E.coli, pneumococcus, pseudomonas. Among alcoholics and COPD, klebsiella is most common followed by pseudomonas , pneumococcus, acinitobacter .Lower lobes are commonly involved among its with comorbidites like diabetes, COPD and alcoholics.

Among its with lower lobe pneumonia Klebsiella is commonly isolated followed by pneumococcus.

Conclusion: The most common organism isolated was Klebsiella. Most common lobe involved Lower lobe. Most common organism in alcoholics and smokers was Klebsiella.

Keywords: Community acquired pneumonia, Klebsiella, Culture sensitivity

Introduction

Infectious Diseases Society of America (IDSA) defines Community Acquired Pneumonia as "an acute infection of the pulmonary parenchyma that is associated with at least some symptoms of acute infection, accompanied by the presence of an acute infiltrate on a chest radiograph or auscultatory findings consistent with pneumonia in a patient not hospitalized or residing in a long-term care facility for more than 14 days before onset of symptoms"^{[1,2].}

Pneumonia infection is the result of a complex process where the lower respiratory tract suffers the invasion of an infective microorganism^{[3].}

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It is important to know the role of the pathogenic microorganism in the etiology of a pneumonia infection in order to provide adequate clinical and therapeutic management of the patient. Globally, Streptococcus pneumoniae (pneumococcus) is the most common pathogen causing community-acquired pneumonia

Aims And Objectives

To study the microbiological pattern in patients admitted with community acquired pneumonia at GHCCD, Visakhapatnam, Andhra pradesh.

Materials And Methods

This is a prospective study comprising of 30 patients who are clinically diagnosed to have community acquired pneumonia who got admitted in the Department of Pulmonary Medicine, Govt. Hospital for Chest and Communicable Diseases (GHCCD) affiliated to Andhra Medical College(AMC), Visakhapatnam.

A) inclusion criteria

Adults with clinically diagnosed to have community acquired pneumonia who are admitted in our hospital.

B)Inclusion criteria:

Patients < 18 years of age, those who satisfied the criteria for a healthcare-associated pneumonia, HIV +, patients on immunosuppressive therapy.

C)sample collection:

Patients sputum was collected and subjected to gram stain and culture sensitivity.

Results

Age Distribution



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Age distribution: out of 30 patients the most common age groups were 41-60 followed by >60 years.

Sex Distribution







Lung involvement:out of 30 patients unilateral involvement was seen in 77% and bilateral in 23%.

Number of lobes



Number of lobes

Out of 30 patients, morethan 1 lobe(60%) is most commonly involved followed by single lobe(40%).

Lobe involvement

Out of 30 patients lower lobe most commonly involved followed by middle & lingular lobe.



Microbiology



Microbiology:

Out of 30 patients, most commonly involved organism was Klebsiella followed by candia, pseudomonas& pneumococcus.

Diabetes

Lobe involvement



Among diabetics.most commonly lower lobe followed by middle lobe.

Microbiology in diabetics



Among diabetics, most common organisms were klebsiella

followed by candida.

Alcoholics

Lobe involvement



Among alcoholics, lower lobe is most commonly involved followed by middle lobe.

Microbiology in alcoholics



Among alcoholics, most common organism were klebsiella followed by pseudomonas, candida.

COPD





Among COPD patients ,lower lobe was most commonly involved followed by middle lobe.

Microbiology



Among COPD patients,klebsiella was most common followed by pseudomonas.

Lower Lobe Pneumonia

Involvement



Lower lobe was most common in biomass fuel exposures followed by alcoholics, smokers.

Microbiology



Lower lobe pneumonia was most commonly caused by klebsiella followed by pneumococcus,candida.

Discussion

The most common age group in this study was 41-60 years.

Unilateral Involvent of lung in seen in 77% and bilateral in 23%.

Lower lobes are commonly involved followed by middle/lingular and upper lobes.

Among alcoholics, diabetics, copd lower lobe is commonly involved than other lobes.

Klebsiella is the most commonly isolated organism in this study Streptococcus pneumoniae has been identified as the commonest organism causing CAP all over the world, but some studies, over the last 30 years, have reported higher incidence of gram- negative organisms among culture-positive pneumonias ^[4-6] which may be due to introduction of pneumococcal vaccine.

Among diabetics klebsiella is most commonly isolated followed by E.coli,pneumococcus,pseudomonas.

Among alcoholics and COPD, klebsiella is most common followed by pseudomonas ,pneumococcus,acinitobacter Lower lobes are commonly involved among its with comorbidites like diabetes,copd and alcoholics.

Among its with lower lobe pneumonia Klebsiella is commonly isolated followed by pneumococcus.

Conclusion

The most common organism isolated was Klebsiella. Most common lobe involved Lower lobe.

Most common organism in alcoholics and smokers was Klebsiella.

Microbiological profile of CAP varies geographically.

There is a need to conduct regular prevalence and antibiogram studies to develop empirical guidelines for treatment of CAP in that particular region.

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