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Original research article

Bacteriological profile of ventilator associated pneumonia

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Abstract

Attention to the microbiology of VAP has many additional benefits: it may inform the prognosis of individual patients, can allow clinicians to track trends in local antimicrobial resistance patterns, can provide insights into the pathogenesis of VAP, can aid the prompt recognition of local VAP outbreaks, and can suggest locally relevant infection-control and VAP prevention efforts. All adult Patients who develop VAP in critical care units as per defnation in inclusion criterias are investigated clinically, radiologically and bactriologically to determine presence of pneumonia. Clinical and diagnostic criteria were based on the Clinical Pulmonary Infection Score (CPIS). Patients who developed pneumonia within 48 hours or those who were admitted with pneumonia Age, sex, date of admission to ICU, date of initiating mechanical ventilation and mode of access to the patient airway were recorded. Indication of mechanical ventilation was noted. In Early VAP group, in majority of subjects organism isolated was Staphylococcus Aureus (38.9%) and in Late VAP group, in majority of subjects organism isolated was Klebsiella (36.9%). There was significant difference in Organism isolated between two groups.

Keywords: Ventilator associated pneumonia, bacteriological profile

Introduction

The awareness of the potential microbial causes of VAP and confirmation of the specific cause in an individual patient are essential to guide optimal antibiotic therapy. This is arguably the single most important management decision in the care of these patients, because inadequate initial antibiotic therapy leads to excess mortality and excessive antibiotic therapy increases treatment related complications and costs and leads to increased prevalence of antibiotic resistance[1].

Attention to the microbiology of VAP has many additional benefits: it may inform the prognosis of individual patients, can allow clinicians to track trends in local antimicrobial resistance patterns, can provide insights into the pathogenesis of VAP, can aid the prompt recognition of local VAP outbreaks, and can suggest locally relevant infection-control and VAP prevention efforts[2].

Feldman and colleagues[3] assessed the sequence of colonization in the oropharyngeal, gastrointestinal tract, lower respiratory tract and endotracheal tube in mechanically ventilated patients. They studied 10 patients on admission showed no evidence of infection and cultured the oropharynx, gastric content, the interior of airway tube and endotracheal secretions twice a day for 5 days. Nine patients becomes colonized the oropharynx was the first site at 36 hrs, followed by stomach at 48-60 hrs.Lower respiratory tract at 60-84 hrs. Organism was isolated from endotracheal tube at 48 hrs. but occurred at significant amount at 60 to 84 hrs.

Gram positive organism did not colonize in ET tube in significant amount, nososcomial pneumonia was diagnosed in 3 out of 10 patients. In two cases acinetobacter was responsible for VAP was first isolated from tracheal aspirate and from interior of ET tube(between 60 to 84 hrs) and at 96 hrs there was a clinical evidence of noscomial pneumonia. It was found oropharyngeal colonization was followed by gastric, lower respiratory tract &eventually ET colonization suggesting early colonization of oroopharynx may be important precursor for subsequent LRT colonization[4].

Methodology

All adult Patients who develop VAP in critical care units as per defnation in inclusion criterias are investigated clinically, radiologically and bactriologically to determine presence of pneumonia. Clinical and diagnostic criteria were based on the Clinical Pulmonary Infection Score (CPIS).

Patients who developed pneumonia within 48 hours or those who were admitted with pneumonia Age, sex, date of admission to ICU, date of initiating mechanical ventilation and mode of access to the patient airway were recorded. Indication of mechanical ventilation was noted.

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Study design
The study was prospective observational study.

Inclusion criteria
All the patients who are on mechanical ventilation for more than 48 hours irrespective of the cause.A total of 101 patients of both sexes, who were on mechanical ventilation for more than 48 hours were selected.
Clinical and diagnostic criteria were based on the Clinical Pulmonary Infection Score (CPIS). The CPIS originally proposed by Pugin and others helps in diagnosing VAP with a sensitivity of 72% and specificity of 80%.
It includes
1) New or progressive infiltrates in chest radiography.
2) At least two of the following four.
a) Hypothermia or hyperthermia.
b) Presence of purulent secretions.
c) Leucocytosis or leukopenia.
d) Decreasing oxygen saturation.

Exclusion criteria
- Patient already having pneumonia at the time of admission.
- Patient who developed pneumonia in first 48 hours of mechanical ventilation

Sample size: 101.

Sampling method
- All the eligible study subjects, satisfying inclusion and exclusion criteria were recruited into the study by convenient sampling.

Results

Table 1: Organism isolated distribution comparison between two groups

		Type of VAP					
		Early VAP		Late VAP		Total	
		Count	%	Count	%	Count	%
Organism	Acinetobacter	1	2.8%	8	12.3%	9	8.9%
	Citrobacter	4	11.1%	4	6.2%	8	7.9%
	E coli	2	5.6%	3	4.6%	5	5.0%
	Klebsiella	7	19.4%	24	36.9%	31	30.7%
	NFLB	3	8.3%	4	6.2%	7	6.9%
	NFNB	3	8.3%	9	13.8%	12	11.9%
	Provedencia Species	0	0.0%	1	1.5%	1	1.0%
	Pseudomonas	2	5.6%	6	9.2%	8	7.9%
	Staphylococcus Aureus	14	38.9%	6	9.2%	20	19.8%

χ 2 =17.41, df =8, p =0.026*

In Early VAP group, in majority of subjects organism isolated was Staphylococcus Aureus (38.9%) and in Late VAP group, in majority of subjects organism isolated was Klebsiella (36.9%). There was significant difference in Organism isolated between two groups.

Table 2: Sensitivity pattern distribution comparison between two groups

		Type of VAP					
		Early VAP		Late VAP		Total	
		Count	%	Count	%	Count	%
Sensitivity	Amikacin	11	30.6%	38	58.5%	49	48.5%
	Ampicillin	4	11.1%	0	0.0%	4	4.0%
	Ceftriaxone	1	2.8%	0	0.0%	1	1.0%
	Gentamycin	0	0.0%	1	1.5%	1	1.0%
	Imipenem	8	22.2%	7	10.8%	15	14.9%
	Levofloxacin	0	0.0%	2	3.1%	2	2.0%
	Linezolid	2	5.6%	1	1.5%	3	3.0%
	Minocycline	0	0.0%	1	1.5%	1	1.0%
	Pipercillin	10	27.8%	15	23.1%	25	24.8%

χ 2 =18.47, df =8, p =0.018*

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In Early VAP group, majority of subjects were sensitive for Amikacin (30.6%), Pieprcillin (27.8%) and others as shown in above table. In Late VAP group, majority of subjects were sensitive for Amikacin (58.5%), Pieprcillin (23.1%). There was significant difference in Sensitivity pattern between two groups.

Discussion

In majority of subjects organism isolated was Klebsiella (30.7.%) followed by staphyloccous aureus(19.8%),Non fermenting gram negative bacilli(11.9%).In Early VAP group, in majority of subjects organism isolated was Staphylococcus Aureus (38.9%) and in Late VAP group). There was significant difference in Organism isolated between two groups.

In a study done by ravi *et al.*[5] Klebsiella species which accounted for 38.3% of cases followed by gram negative non fermenters (18.3%) and Pseudomonas (11.7%). Organisms grown were similar in both early and late VAP. In study of geetika *et al.*[6] Acinetobacter species (66%), Pseudomonas aeruginosa (12%) and Klebsiella pneumoniae (10%) were the most common organisms VAP. In a study done by hina gadani *et al.*[7]the most common organism associated with VAP is Pseudomonas (43.24%), followed by *Klebsiella*18.91%). In Early VAP group, majority of subjects were sensitive for Amikacin (30.6%), Piepercillin (27.8%). In Late VAP group, majority of subjects were sensitive for Amikacin (58.5%), Piepercillin (23.1%).

Nosocomial gram negative bacterial pneumonia develop in hospitalized patients and are due to changes in bacterial flora, and colonization of the upper respiratory tract by gram negative bacilli is mediated by alteration in the surface properties of epithelial cells. In healthy individuals a film of fibronectin covers the epithelium lining the mucosa of the mouth and oropharynx and prevents the gram negative bacteria from adhering to the epithelial cells. This protective covering is lost in very ill individual, so that pathogenic gram negative organism adhere to the receptors present in the epithelial cells of the mucosa and soon colonize it. The number of bacterial receptors on both upper and lower airway epithelial cells is increased in many illnesses. The risk factors responsible for oropharyngeal colonization with gram negative bacteria include neutropenia, prior antibiotic therapy, alcoholism, azotemia, coma, diabetes, serious illness, hypertension, intubation, smoking and neutralization gastric acid[8].

The potential routes of infection, micro aspiration of a small volume of oropharyngeal secretions previously colonized with pathogenic bacteria is most common. Microaspiration is reported in even in healthy individuals during sleep. But it is the presence of pathogenic organism which are able to overwhelm the lower respiratory tract defences that is most important in development of pneumonia.

The incidence of aspiration increases when the gag reflex is impaired. If there is alteration in the level of consciousness,when certain devices such as nasogastric tube or endotracheal tube are used or if oesophageal disease is present.

Among mechanically ventilated patient additional routes of entry exist. The ET tube by pass host defences above the vocal cords and impairs lower tract defences such as cough and mucocillary clearance. Contaminated secretions can pool above the inflated ET cuff and are not easily removed by suctioning. The secretions can leak around the ET cuffs and directly enter the lower respiratory tract when there are changes in airway caliber during swallowing and breathing[8].

Conclusion

Klebsiella was the most common organism isolated (30.7%), Staphyloccocus Aureus (19.8%), Gram negative non fermenters in 11.9%. Majority were susceptible to amikacin(58.5%) and piperecillin and Tazobactam (23.1%).

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