

Impact of epidemiological environment on the efficacy of serial routine respiratory surveillance cultures

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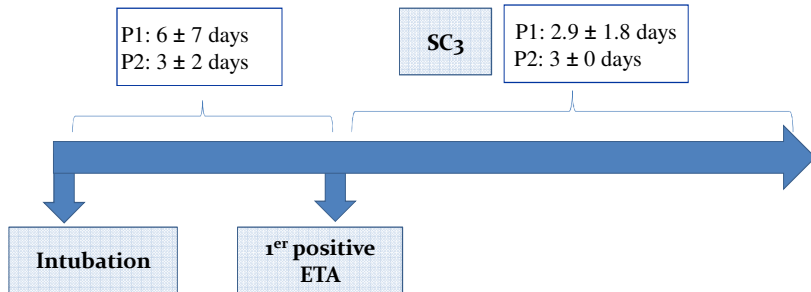
INTRODUCTION

Ventilator-associated pneumonia (VAP) is one of the most frequent nosocomial infections in the intensive care unit (ICU). Although its attributable mortality remains controversial, appropriate empirical antibiotic treatment seems to be determinant in hospital mortality. Therefore, efforts aimed at increasing the rate of appropriate antibiotic treatment could improve the outcome of critically ill patients.

RESULTS

440 patients with MV were followed

273 patients in the PERIOD 1 → 50 VAP in PERIOD 1 (18%)
167 patients in the PERIOD 2 → 21 VAP in PERIOD 2 (12.5%)



	Global (n 71)	Period 1 (n 50)	Period 2 (n 21)	p
Microorganisms in SC ² , n				0.069
A. baumannii	16 (22)	14 (28)	2 (9)	
P. aeruginosa	10 (14)	6 (12)	4 (18)	
Klebsiella spp.	6 (8)	2 (4)	4 (18)	
Other Enterobacteriaceae	8 (11)	4 (8)	4 (18)	
H. influenza	4 (6)	1 (2)	3 (14)	
S. aureus	8 (11)	5 (10)	3 (14)	
Other Gram positive cocci	6 (8)	6 (12)	1 (5)	
Fungi	8 (11)	7 (14)		

OBJECTIVES

Surveillance cultures (SC) has been postulated as a useful tool to predict ventilator-associated pneumonia (VAP) etiology and therefore to increase the rate of appropriate antibiotic therapy. Our aim was to assess SC prediction accuracy depending on the epidemiological environment of the intensive care unit

DESIGN AND SETTINGS

Prospective study performed in two periods and settings. The first study period (18 months) was carried out in a ICU with a high prevalence of multidrug resistant (MDR) microorganisms. The second study period (18 months) was carried out in a brand new hospital without epidemiological problems.

Consecutive patients receiving mechanical ventilation (MV) >48h were followed. Patients fulfilling VAP criteria were finally included.

SC obtained twice a week until VAP diagnosis or weaning from MV. Non-quantitative endotracheal aspirates (NQ-ETAs).

Bacterial identification using standard methods.



	Global (n 71)	Period 1 (n 50)	Period 2 (n 21)	p
Microorganisms, n				0.014
A. baumannii †	25 (35)	23 (46)	2 (9)	
P. aeruginosa †	18 (25)	14 (28)	4 (18)	
Enterobacteriaceae †	15 (21)	5 (10)	10 (48)	
S. aureus MR	1 (1)	1 (2)	3 (14)	
S. aureus MS	5 (7)	2 (4)	2 (9)	
Other cocci	3 (4)	3 (6)		
H. influenza	3 (4)	1 (2)		
Aspergillus spp.	1 (1)	1 (2)		
MDR⁴ microorganisms	28 (39)	24 (48)	4 (19)	0.033

	Global (n 71)	Period 1 (n 50)	Period 2 (n 21)	p
Age	60 ± 15	59 ± 15	63 ± 15	0.287
Sex, male	34(48)	29(58)	5(24)	0.146
APACHE II at admission	24 ± 8	22 ± 7	28 ± 8	0.005
SOFA at admission	10 ± 3	10 ± 3	9.9 ± 3	0.790

	SC1	SC2	SC3
VAP etiology predicted by SC			
Global	33%	62%	80%
Period 1	32%	57%	80%
Period 2	33%	75%	81%

	Global (n 71)	Period 1 (n 50)	Period 2 (n 21)	p
Appropriate antibiotic coverage	42 (59)	26 (52)	16 (76)	0.031
VAP etiology predicted by SC	57 (80)	40 (80)	17 (81)	0.744
Increase of % appropriate antibiotic using SC	21%	28%	5%	

S/E / PPV/PNV MR *A. baumannii*:
83%/98%/95%/92%

S/E / PPV/PNV MR *P. aeruginosa*:
56%/100%/100%/87%

CONCLUSIONS

Surveillance cultures were able to predict VAP etiology regardless the prevalence of MDR microorganisms. However, in an epidemiological environment with a high prevalence of MDR microorganisms SC may significantly increase the rate of appropriate antibiotic therapy for VAP.