

P1303

Poster Session V

Infections in transplant recipients

CLONALITY AND VIRULENCE OF ISOLATES OF VRE IN STEM CELL TRANSPLANTED PATIENTS

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Objective:

Vancomycin-resistant enterococci (VRE) are an important agent of colonization and infection in hematology patients, especially those undergoing Hematopoietic Stem Cell Transplantation (HSCT). The objective of this study was to evaluate the clonality and virulence of VRE isolates of HSCT patients within 6 years.

Methods:

From 64 HSCT patients, 72 clinical isolates were evaluated. PCR was performed for resistance genes *vanA*, *vanB* and for virulence genes (*esp*, *asa1*, *ge/E*, *cylA* and *hyl*). Minimum inhibitory concentration (MIC) was performed by microdilution for vancomycin, teicoplanin, gentamicin (HLAR), streptomycin (HLAR) and linezolid. Clonality of VRE isolates was characterized by Pulsed Field Gel Electrophoresis (PFGE). Demographic and clinical data were analyzed by Epiinfo.

Results:

Sixty-four patients, age ranged from 1 to 70 years old, were included in this study. The average of total hospitalization time was 39 days and the period between colonization and VRE first infection was around 13 days. A total of 34 (52%) infected patients died and the infection occurred within the first 40 days. Of 72 clinical isolates, 47% were obtained from allogeneic transplant patients and 70 (97.2%) were identified as *E. faecium* and only 2 (2.8%) *E. faecalis*. VRE infection isolates 49 (89.1%) were obtained from blood and colonization isolates 6 (10.9%) from feces, sputum and urine. All isolates were positives for PCR *vanA* gene. There is a predominant clone named clone A in 23 (46.9%) of isolates causing infection and in none of colonized. All VRE isolates were positive for *esp* gene including infection and colonization. Isolates belonging to clone A showed 83% positivity for *asa1* gene and 87% for gene *ge/E*. PFGE analysis and the distribution of virulence genes of all VRE isolates are shown in table 1. None isolates were positive for *cylA* and *hyl* genes. All isolates were resistant to vancomycin (MIC >32µg/mL) and 80.5% showed resistance for streptomycin (MIC >1000µg/mL). Gentamicyn and teicoplanin resistance were detected in 12.5% (MIC >500 µg/mL) and 86.1% (MIC >32µg/mL), respectively. Only one isolate showed resistance to linezolid (MIC 8µg/mL).

Table 1 - Distribution of PFGE profiles and virulence genes of 55 VRE isolates.

Clonality	PCR for virulence genes					
	Infection %			Colonization %		
	(n=49)			(n=6)		
	<i>esp</i>	<i>asa1</i>	<i>ge/E</i>	<i>esp</i>	<i>asa1</i>	<i>ge/E</i>
Clone A	47	39	41	0	0	0
Closely related	43	35	37	50	0	0
Possibly related	6	2	0	0	0	0
Different	4	4	4	50	33	17

Conclusion:

In our hospital, *E. faecium* was the most frequent specie identified. There is a predominant clone that harbored the virulence genes *esp*, *asa1*, *ge/E*, being responsible for the high mortality rate among patients in the unit. Colonized isolates were less virulent than these causing infections.