APPLICATION OF MALDI-TOF MS TO THE IDENTIFICATION OF DIALYSIS CATHETERS ASSOCIATED MICROORGANISMS

M. Martins¹, C. Santos¹, D. Machado¹, M. Maciel¹, N. Lima¹, O. Santos², A. Rodrigues², A. Cabrita², M.J. Carvalho², H. Silva², F. Silva², J. Queirós², A.M. Gomes³ and R. Oliveira¹

¹IBB-Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, Universidade do Minho, Campus de Gualtar, Braga, Portugal
²Nephrology Department, Centro Hospitalar do Porto - Hospital Santo António, Largo Abel Salazar, Porto, Portugal
³Department of Nephrology, Centro Hospitalar Vila Nova Gaia/Espinho, Rua Conceição Fernandes, Vila Nova de Gaia, Portugal
e-mail: roliveira@deb.uminho.pt

It has been estimated that 80% of the human infections are associated with biofilms. These microbial communities develop associated with surfaces, such as catheters, and contribute to the chronicity and spreading of the infections and device loss. To date, the conclusive diagnosis of catheter-associated infection relies on the removal of the device, culture of associated microorganisms and their subsequent identification. The objective of this work was to evaluate the usefulness of culturomics associated with matrix-assisted laser desorption/ionisation - time of flight mass spectrometry (MALDI-TOF MS) for the detection and identification of dialysis catheter associated microorganisms. A prospective observational study was carried out on catheters explanted from adult patients on renal replacement therapy with peritoneal dialysis (PD) and haemodialysis (HD). During a five-month period different segments of PD and HD catheters were analysed. Specifically, the samples were cultured on blood agar and the subsequent identification of the isolated microorganisms was performed using selective/differential culture media and MALDI-TOF MS. A total of 54 PD and 22 HD catheters were analysed. The frequency of microbial recovery, defined as a positive culture in at least one segment of the catheter, was found to be 44% for PD catheters and 77% for HD catheters. Polymicrobial cultures were only identified on PD catheters (20% of the positive cultures). Seventy-nine isolates were analysed by MALDI-TOF MS: 77.2% were identified at the species level, comprising eight genera and 10 species; 6.3% were identified at the genus level, comprising Corynebacterium and Sphingomonas bacteria; 16.5% were not identified. The non-identified isolates (11 from PD and 2 from HD) included gram-positive (n= 9), gram-negative (n= 2) and fungal (n= 2) species, as determined by presumptive identification. Our results show that MALDI-TOF MS is a powerful method for the identification of catheter-associated bacteria, particularly derived from HD.

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