

**08. Healthcare-associated infections, infection prevention & control**

## 8a. Intravascular catheter-related infections

**Miguel Pinto <sup>1</sup>, Vitor Borges <sup>1</sup>, Maria Nascimento <sup>2</sup>, Filomena Martins <sup>3</sup>, Maria Ana Pessanha <sup>4</sup>, Isabel Faria <sup>4</sup>, Joao Rodrigues <sup>5</sup>, Rui Matias <sup>5</sup>, João Paulo Gomes <sup>1</sup>, Luisa Jordao <sup>2</sup>**

<sup>1</sup>Bioinformatics Unit, Department of Infectious Diseases, National Institute of Health Dr Ricardo Jorge - Lisboa (Portugal), <sup>2</sup>Unidade de Investigação & Desenvolvimento, Departamento de Saúde Ambiental, Instituto Nacional de Saude Dr Ricardo Jorge (INSA) - Lisboa (Portugal), <sup>3</sup>Direção do Programa de Prevenção e Controlo de Infeção e Resistência aos Antimicrobianos, Centro Hospitalar de Lisboa Ocidental (CHLO) - Lisboa (Portugal), <sup>4</sup>Laboratório de Microbiologia e Biologia Molecular do Serviço de Patologia Clínica, CHLO - Lisboa (Portugal), <sup>5</sup>Unidade Laboratorial Integrada de Microbiologia, Departamento de Doenças Infeciosas, INSA - Lisboa (Portugal)

**Background** Central venous catheter (CVC)-related bloodstream infection (CRBSI) is a huge public health concern with considerable impact on mortality and health costs. The emergence of antimicrobial resistant microorganisms associated or not with CVC colonization by biofilms makes the treatment of CRBSI even more challenging.

**Methods** A 3-year observational study enrolling 3 tertiary hospitals located in Lisbon (Portugal) was designed to identify the major etiological agents of 58 CRBSI, their ability to colonize CVCs and their antimicrobial resistance profiles. Etiological agents of CRBSI were identified by VITEK-2. Whole-genome sequencing was used to confirm CRBSI by the most prevalent etiological agents and characterize their resistome. CVC's colonization (namely by biofilm assembly) was monitored by scanning electron microscopy.

**Results** Staphylococci were the most prevalent causative agent (36/58, 62.0%), with *S. aureus* and coagulase negative *S. epidermidis* accounting for 24.1% and 36.2% of CRBSIs, respectively. Fifty-nine of 72 staphylococci isolates were methicillin resistant. Comparative genomic analysis of central venous catheters/ hemoculture pairs of isolates revealed genomic matches for 35 of 36 pairs and a good correlation between antibiotic susceptibility phenotype and the presence of antimicrobials resistance genetic determinants. CVC colonization was observed mainly in the catheter lumen and presented different phenotypes ranging from isolated attached microorganisms to mature biofilms. The latest phenotype, mature biofilms of *S. epidermidis* and *S. aureus* were found for 50.0% and 48.6% of the CVC, respectively. Nevertheless, no statistical significant association was established

between biofilm assembly and CRBSI highlighting the need for further studies to elucidate biofilms' role on this healthcare associated infection.

**Conclusions** Whole-genome sequencing proved to be a valuable tool to confirm CRBSI. Despite staphylococci biofilms identification on a considerable number of CVCs , no statistically significant association was found between CRBSI and biofilms.

**Keyword 1**

Catheter-related bloodstream infection

**Keyword 2**

Staphylococci

**Keyword 3**

Biofilms

**Conflicts of interest**

**Do you have any conflicts of interest to declare?**

I have no potential conflict of interest to report