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Prospective observational study on the role of catheter colonization and multidrug-resistance associated with catheter-related bloodstream infections.

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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. The latest data reported for Portugal is shown in the table.

Microorganisms	Portugal (n= 380)	Total (n=7 929)
Coagulase-negative staphylococci	10.8	23.6
Enterococcus spp	7.9	14.9
S. aureus	9.7	12.0
Klebsiella spp	21.1	12.4
E. coli	6.3	9.2
P. aeruginosa	19.2	9.5
Enterobacter spp	10.0	8.3
Candida spp	6.8	4.5
Serratia spp	5.5	3.4
Acinetobacter spp	2.6	2.3

Adapted from Table 3: Number of isolates and percentages of the ten most frequently isolated microorganisms in ICU-acquired bloodstream infection (BSI) episodes by country, EU/ EEA, 2017, Healthcare-associated infections acquired in intensive care units - Annual Epidemiological Report 2019

Aim

A three-year observational study enrolling three tertiary hospitals located in Lisbon, Portugal, was designed to

- identify the major aetiological agents of CRBSI
- their ability to colonize CVCs and
- their antimicrobial resistance (AMR) profiles.

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Results:

3-years prospective study (March 2017- February 2020)

Etiological agent(s)	CRBSI [n (%)]			
	Hospital A	Hospital B	Hospital C	Overal
S. aureus	6 (40 %)	4 (28.5%)	4 (13.8%)	14 (24.1%)
S. epidermidis	3 (20%)	5 (35.7%)	13 (44.8%)	21 (36.2%)
S. haemolyticus		1 (7.1%)		1 (1.7%)
K. pneumoniae	3 (20%)	1 (7.1%)	6 (20.7%)	10 (17.2%)
P. aeruginosa			2 (6.9%)	2 (3.4%)
Enterococcus faecalis	1 (6.7%)			1 (1.7%)
Serratia marcescens	1 (6.7%)			1 (1.7%)
Candida glabrata			1 (3.4%)	1 (1.7%)
Candida parapsilosis		2 (14.3%)	1 (3.4%)	3 (5.1%)
K. pneumoniae, S. epidermidis			1 (3.4%)	1 (1.7%)
S. marcescens, E. faecalis		1 (6.7%)		1 (1.7%)
S. marcescens, P. aeruginosa	1 (6.7%)			1 (1.7%)
E. cloacae, C. parapsilosis			1 (3.4%)	1 (1.7%)
Total (n/ %)	15 (25.9%)	14 (24.1%)	29 (50.0%)	58 (100%)

S. aureus

MDR 64.3 %

Coagulase-negative staphylococci

MDR 95.5 %

Staphylococci 62.0 % CRBSIs

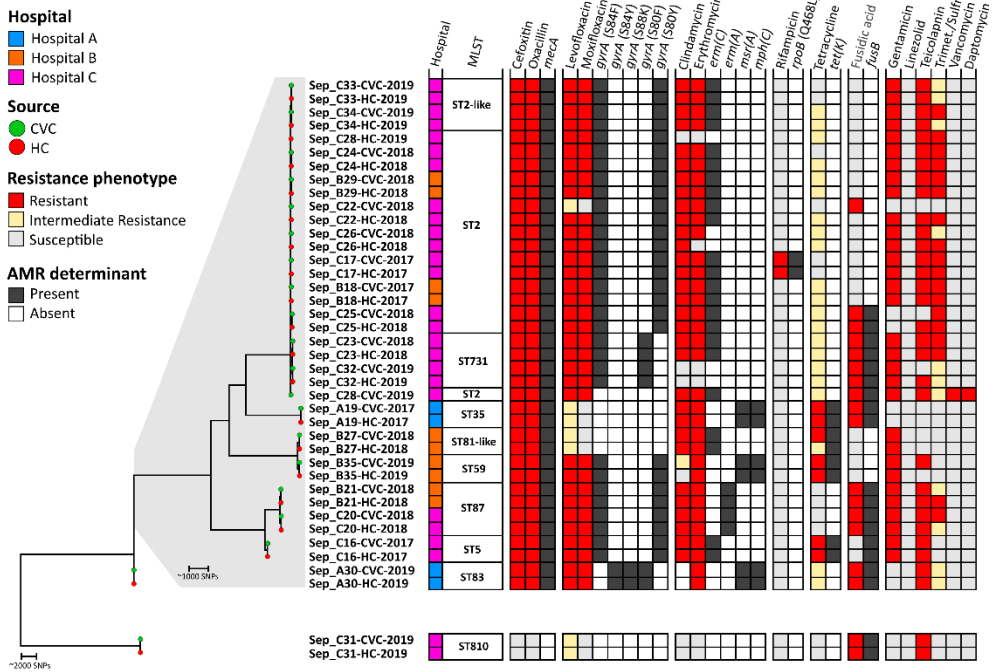
Polymicrobial infections 6.8 % CRBSIs

Most prevalent aetiological agents (Staphylococci):

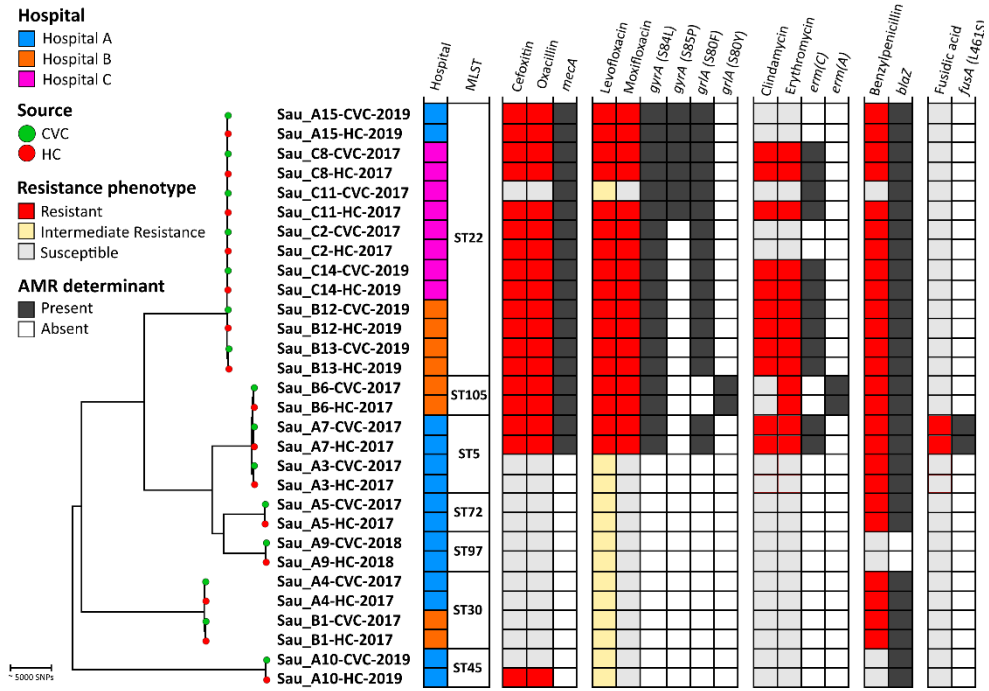
- **CVC/HC comparative genomics, AMR genotype-phenotype associations**
- **CVC screening for biofilms were performed.**

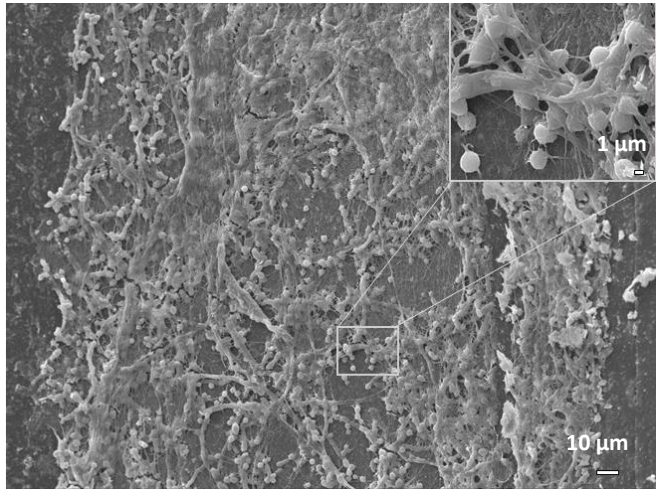
High rates of multidrug resistance (MDR)

Coagulase-negative staphylococci *S. epidermidis*

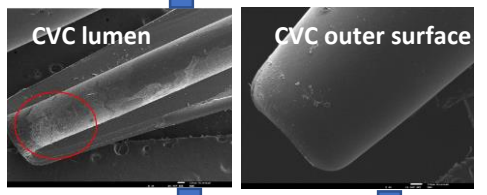


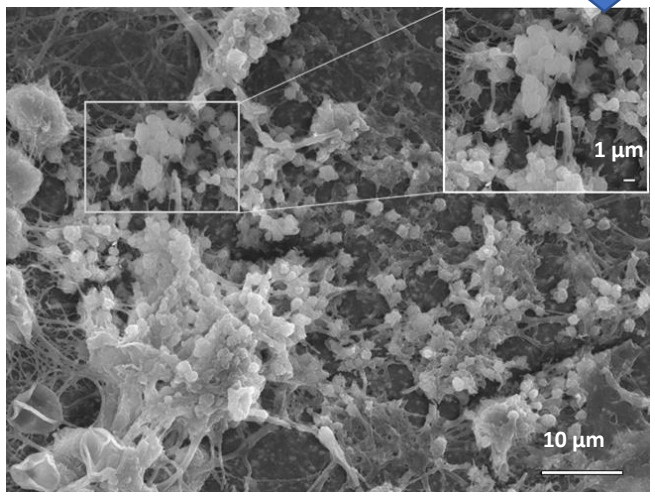
S. aureus

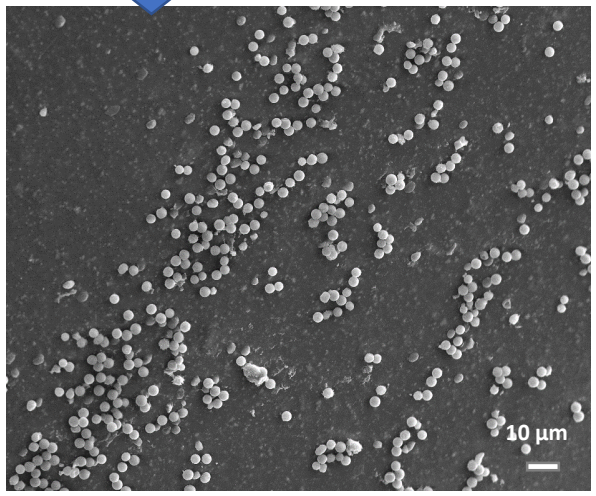




Biofilm positive: 50.0 %







Biofilm positive: 48.6 %

Comparative genomic analysis:

- Genomic matches found for 35/ 36 pairs CVC/HC

- Good correlation between antibiotic susceptibility phenotype and the presence of antimicrobials resistance genetic determinants.

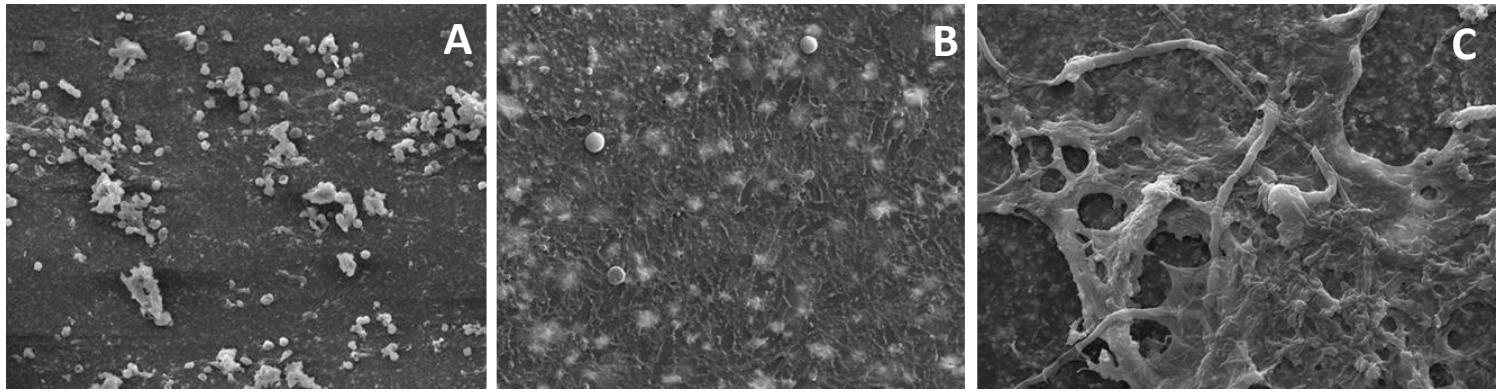
No statistical significant association established between biofilm assembly and CRBSI.

Final Remarks:

Whole-genome sequencing proved to be a valuable tool to confirm CRBSI.

Despite mature staphylococci biofilms were observed on a considerable number of CVCs , no statistically significant association was found between CRBSI and biofilms.

Early stage biofilms (A), isolated staphylococci attached to the CVC surface (B) and mature biofilms of other then the aetiological agent of CRBSI (C) were found.



More prospective *in vitro* and *in vivo* studies are required to clarify the role of biofilms on CRBSI and other foreign-bodies-related infections.

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