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Poster Session VI

Zoonotic antimicrobial resistance

EVOLUTION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS (MRSA) ST398 ISOLATES INFECTING OR COLONIZING PATIENTS IN A SPANISH HOSPITAL: GENOTYPES AND CLINICAL FEATURES.

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Objectives: The first isolate belonging to the MRSA-ST398 clone was identified in the Hospital Universitari de Bellvitge (HUB) in 2003. From this data to 2009, 11 patients (pts) were infected or colonized by this clone. In the 2010-2011 period, isolates of MRSA-ST398 clone increased to 22 cases. The aim of this study was to analyze the prevalence and the molecular features of the current MRSA-ST398 isolates, identified in HUB from January 2012 to June 2013.

Methods: Tetracycline resistant (Tet-R) MRSA isolates from single pts were screened by *Sma*I-pulsed field gel electrophoresis (PFGE). Nontypable MRSA strains by *Sma*I (NT-*Sma*I) were re-analysed by *Apa*I-PFGE. Molecular typing including *SCCmec*, *agr*, MLST and DNA microarray hybridization were performed for all NT-*Sma*I isolates.

Results: Among 33 Tet-R MRSA isolated during the 2012-2013 period, 11 (33%) NT-*Sma*I isolates belonging to the MRSA-ST398 clone were found. No difference between gender was observed (man, n=6; women, n=5) and the mean age was 54 years (range 33 to 72). In 8 pts (73%; 8/11), MRSA-ST398 was associated with colonization. Three pts (27%; 3/11) were infected: two skin and soft tissues infections and one surgical bone infection. The most frequent underlying diseases (46%; 5/11) were cancer and obesity. Four unrelated pulsotypes (A-D) were provided by *Apa*I-PFGE, with type A in 8 of 11 isolates. All isolates were *agr*I and carried the *SCCmec* type V with the exception of one isolate that carried the *SCCmec* type IV. A total of 3 different *spa* types were detected: t011 (9/11), t1451 (1/11) and t899 (1/11).

Forty-six percent of the strains (5/11) showed resistance to 3 or more antibiotic classes, in addition to beta-lactams. Tet-R was mediated by both *tet*(M) and *tet*(K) genes in 8 isolates. Ciprofloxacin resistance was found in 8 isolates (73%; 8/11).

None of the strains carried PVL, enterotoxines, exfoliative toxins, *egc* cluster or *tst* genes. Genes carried on mobile genetic elements and involved in immune evasion such as *scn*, *sak* and *chp* were identified in a single isolate of *spa* type t899. All isolates carried genes codifying capsule type 5 and were positive for the *cna* gene.

Conclusion: The increasing isolation trend of MRSA-ST398 clone in the period 2003-2011 was discontinued during 2012-2013. No active transmission of this strain was detected in the HUB. Pts colonized or infected suffered underlying comorbidities. Isolates of MRSA-ST398 showed variable antibiotic resistance profiles and a low virulence gene content.