

ASM Microbe 2016, 16 al 20 de junio de 2016, Boston, EEUU.

Colonization with CA-MRSA ST5-SCC*mecIV* and ST30-SCC*mecIV* Clones in Healthy Horses from Argentina

Author Block: P. Gagetti¹, G. Giacoboni², C. Lopez³, M. Kienast², M. Maldonado⁴, D. Faccione¹, **A. Corso**¹; ¹Antimicrobial Div. Natl. Reference Lab. INEI-ANLIS "Dr. Malbran", Buenos Aires, Argentina, ²Faculty of Vet. Sci, UNLP, Buenos Aires, Argentina, ³Faculty of Vet. Sci, UBA, Buenos Aires, Argentina, ⁴Antimicrobial Div. Natl. Reference Lab. INEI-ANLIS, Buenos Aires, Argentina

Abstract:

The emergence of MRSA in horses, pet animals and productive livestock has risen worldwide. Colonized horses may transmit MRSA to other horses and people. We evaluated the MRSA nasal colonization in horses from Argentina, characterized the resistance profile and the clonal relation between isolates

Methods: During May, September and October of 2015, 96 healthy thoroughbreds horses belonging to the La Plata Race track were screened for MRSA. Swabs were taken from nasal vestibulum and plated on chromogenic agar (CHROMagar™ MRSA). Nine suspicious strains were confirmed as *S. aureus* by conventional tests. Antibiotic susceptibility were done by disk diffusion test (CLSI M100S25). D-test was performed to evaluate inducible or constitutive MLSb-phenotype. Detection of macrolide resistance genes *ermA* and *msrA*, *mecA* and PVL were performed by PCR, SCC*mec* type was determined by multiplex PCR, and molecular typing by *SmaI* PFGE and MLST

Results: Nine strains were resistant to ceftaxime and *mecA* positive. The prevalence of MRSA was 9.4% (9/96). All were susceptible to ceftaroline, gentamicin, ciprofloxacin, tetracycline, chloramphenicol, trimethoprim-sulfamethoxazol, rifampin, teicoplanin, linezolid and nitrofurantoin, but seven (78%) were resistant to erythromycin and clindamycin. All MRSA isolates carried the SCC*mecIV*. Two clonal types were observed by PFGE. Most of them (7/9) belonged to clonal type A the already described ST5-SCC*mecIV* responsible of the emergence of community associated MRSA in human infections in our country between 2000-08. All MRSA ST5-SCC*mecIV* were PVL negative, showed inducible MLSb phenotype, carried the *ermA* gene and were negative to *msrA* gene. Isolates from clone B (2/9) were PVL positive and belonged to ST30-SCC*mecIV* (South West Pacific clone), responsible for the half of the CA-MRSA infections in humans in our country nowadays

Conclusions: This is the first study of prevalence of nasal MRSA colonization in healthy horses from Argentina. All the strains belonged to ST5-SCC*mecIV* or ST30-SCC*mecIV*, the two dominant community-associated clones in Argentina