



12th International Meeting on Microbial  
Epidemiological Markers (IMMEM XII)  
Dubrovnik, Croatia  
18–21 September 2019

**228 Transmission of methicillin-resistant *Staphylococcus aureus* (MRSA) ST398 through the food chain in Portugal**

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**Background:** Livestock associated (LA) MRSA has rapidly emerged in food producing animals and belongs mainly to clonal complex 398. Pigs have been described as the main reservoir of ST398 MRSA. Until now, the molecular epidemiology of LA-MRSA and the transmission routes of MRSA ST398 along the food production chain are not well established in Portugal.

**Materials/methods:** In order to trace MRSA transmission through pig food production chain in slaughterhouses in Portugal, we studied 31 MRSA isolates collected from 75 samples in 2016 at a slaughterhouse in different days and different sites (live pigs, pork, equipment and workers). MRSA SRL354 isolated in 2016 from blood in a Portuguese hospital was used for comparative genome analysis. Antibiotic susceptibility testing was performed by disk diffusion and E-test. Biocide, toxin, virulence, antibiotic resistant genes and SCC $mec$  typing were performed by PCR. All isolates were characterized by PFGE and *spa* typing and representative strains were analyzed by WGS (Illumina NextSeq). Relatedness of the isolates was assessed by SNP and cgMLST using CSI phylogeny and chewBBACA, respectively.

**Results:** We found a high prevalence of MRSA in live pigs (60%), followed by workers (40%), equipment (38%) and meat (23%). All MRSA showed multidrug resistance profiles with high rates of resistance to tetracycline, clindamycin (100% each), erythromycin (76%), chloramphenicol (65%) and gentamicin (61%). We detected a high frequency of biocide resistance genes: *mepA* (87%), *sepA* (71%), *norA*, *lmrS* (61% each) and *qacAB* (52%) and virulence genes: *hly*, *hlg*, *sel* (65% each) and *sep* (55%). MRSA strains yielded identical PFGE profile and SNP analysis identified a high genetic relatedness between three strain-pairs from animal/worker (28 SNPs), meat/worker (55 SNPs) and equipment/meat (6 SNPs). The cgMLST analysis revealed that MRSA ST398 isolated from workers and pigs in the slaughterhouse were closely related (15 to 147 allelic differences) to MRSA SRL354 isolated in hospital, sharing the same *spa* type t011.

**Conclusions:** Our results suggest that ST398 MRSA is frequently transmitted from live pigs to the slaughterhouse environment. The possible relatedness with MRSA ST398 causing invasive disease in hospitals is worrisome, which emphasize the need for continuous surveillance in the slaughterhouses.

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