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**Paper Poster Session**

**MRSA - one health worldwide**

**High frequency of *Staphylococcus aureus* detection in game animals with identification of *mecC* gene in MRSA isolates of wild rabbits**

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**Background:** The *mecC* gene represent and emerging mechanism implicated in methicillin resistance in *S. aureus* (MRSA), that has been recently detected in different animal species, but few data do exist in relation with game animals, that could enter into the food chain. The objective of this study was to analyse the prevalence of *S. aureus* in nasal samples of game animals and to characterize detected isolates

**Material/methods:** Nasal samples of 71 game animals (wild rabbits, 38; wild pigs, 17; deers, 9; mouflons, 4; hare, 2, and ibex, 1) were obtained after hunting process and they were inoculated in Manitol Salt agar and ORSAB agar plates (supplemmented with 2 mcg/ml oxacillin) for *S. aureus* and MRSA recovery, respectively. *S. aureus* isolates were identified by biochemical and molecular methods (detection of *nuc* gene). Susceptibility testing for 12 antimicrobials was performed according to EUCAST and detection of antimicrobial resistance genes by PCR. Molecular typing of all *S. aureus* isolates was performed by *spa*-typing and MLST typing was carried out in selected ones. The presence of *pvl*, *tsst*, *eta* and *etb* virulence genes was studied in *S. aureus* isolates. The Immune Evasion Cluster (IEC) genes were checked by PCR.

**Results:** *S. aureus* isolates were detected in 29.6% of game animals (59.5% in wild pigs; 44% in deers; 7.9% in wild rabbits; all mouflons and none hare or ibex). The three *S. aureus* strains from wild rabbits were MRSA and carried the *mecC* gene. They were typed as *spa* t843, associated to CC130, and they lacked virulence genes and also the IEC genes. The remaining 18 *S. aureus* recovered isolates were methicillin susceptible (MSSA). Three MSSA isolates of wild pigs and one of a deer were typed as t1535, associated to the lineage CC130. The remaining MSSA isolates were typed into other 9 different *spa* types associated to clonal complexes CC5, CC425 and CC522. None of the *S. aureus* recovered harboured the IEC genes and most of them lacked the virulence genes tested (except two *S. aureus* isolates of deer/wild pig which harboured the *tsst* gene) Three strains carried the *ermC* genes.

**Conclusions:** Wild pigs and deers are frequently colonized by MSSA. In addition, MRSA with the *mecC* gene have been detected in wild rabbits, what could have implications in public health because these animals could enter in the human food chain.