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Abstract (publication only)

**Genetic lineages, resistance and virulence factors of *Staphylococcus aureus* isolates from nasal samples of healthy companion animals in Tunisia**

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**Objective:** To study the carriage rate, resistance mechanisms, virulence traits and genetic lineages of nasal *S. aureus* of healthy companion animals in Tunisia. **Methods:** Nasal swabs of healthy animals (100 dogs and 30 cats) were obtained in National School of Veterinary Medicine and several veterinary clinics that receive animals from all Tunisia (2010-2011). Samples were inoculated into Baird Parker and ORSAB plates for *S. aureus* and methicillin-resistant *S. aureus* (MRSA) recovery, respectively. Isolates were identified by biochemical methods and nuc-gene PCR. Antibiotic susceptibility profile to 18 antibiotics was determined by disk diffusion method. The presence of 9 resistance genes (*tetL*, *tetM*, *tetK*, *blaZ*, *ermA*, *ermB*, *ermC*, *msrA* and *ant(6)-Ia*), 18 staphylococcal enterotoxin genes and *lukF/lukS-PV* (encoding Panton-Valentine leucocidin, PVL), *lukE-lukD*, *lukM*, *eta*, *etb* and *tsst1* genes were studied by PCR. *S. aureus* isolates were typed (*spa*, *agr*, MLST and SmaI-PFGE). **Results:** Six *S. aureus* were detected (one/sample) from the 130 tested samples (4.6%), representing 4% in dogs and 6.6% in cats. All *S. aureus* were methicillin-susceptible (MSSA). Four different *spa*-types (*t189*, *t279*, *t582* and *t701*) and four sequence-types (ST6 (CC6), ST15 (CC15) and ST188 (CC22), including a new sequence-type named ST2121 (CC30)) were identified among our MSSA isolates. They were ascribed to *agr* type I (4 isolates), II (1) and III (1). MSSA isolates showed susceptibility to the tested antibiotics with the following exceptions (% of resistance, resistance gene): penicillin (100%, *blaZ*), tetracycline (16.6%, *tetM*), erythromycin (16.6%, *ermA*), streptomycin (16.6%, *ant(6)-Ia*) and ciprofloxacin (16.6%). Virulence genes carried by MSSA were (number of isolates): *lukF/lukS-PV* (2, from cats), *hla* (6), *hld* (6), *hly* (4), *lukED* (5), *sea* (3), *ser* (3), *sei* (2), *see* (2), *ser* (1), *hlg* (1), *hlgv*(1) and a variant of *egc*-cluster-like [*sen-sem-sei-seu-seg*] (1, from dog). The remaining virulence genes tested were negative among our isolates. **Conclusions:** The nares of healthy companion animals could be a reservoir of PVL-positive community-associated-MSSA with implications in public health.