

Prevalence and Molecular Epidemiology of *Staphylococcus aureus* in European Wildlife †

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Abstract: Staphylococci can be found on the skin and mucous membranes of people and several animal species. In addition, due to their ubiquity in surviving in adverse environmental conditions, staphylococci have also been found in dust, air, soil, water, plants and environmental surfaces. Nevertheless, studies describing the *Staphylococcus aureus* distribution, prevalence, antimicrobial resistance and genetic lineages in environmental niches are scarce. Due to the zoonotic potential of *S. aureus* and their ability to easily acquire antimicrobial resistance, it is important to study these bacteria in all environmental compartments, including free-living animals. Some studies have reported the presence *S. aureus* in several different species of wild animals, such as, among others, in hares, deer, foxes, mice, mountain goats, kangaroos, hedgehogs, bears, wild boars, beavers, squirrels, shrews, bats, minks, raccoons, seals, apes, as well as in different species of birds. *S. aureus* present a great diversity of genetic lineages, of which some have been previously associated with humans and livestock. The majority of methicillin-resistant *S. aureus* (MRSA) strains isolated from wild animals harbor the *mecC* gene, which is a homologue of the more common *mecA* gene (responsible for the methicillin resistance). Unlike, *mecC*-positive MRSA strains, which are sensible to all antimicrobial agents, *mecA*-MRSA isolates present resistance to other classes of antibiotics and several virulence factors. Wild animals may be overlooked as a transmission vector of antibiotic resistant bacteria and monitoring the presence of antimicrobial resistance species, in this particular case, *S. aureus*, in wildlife could lead to a better understand of the epidemiology of *staphylococci* infections.

Keywords: *Staphylococcus aureus*; wildlife; antibiotic resistance; molecular epidemiology

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