



**HUNGARIAN UNIVERSITY OF AGRICULTURE AND LIFE SCIENCES  
KAPOSVÁR CAMPUS  
INSTITUTE OF PHYSIOLOGY AND ANIMAL NUTRITION**

**One Health in Animal Science - Circulation of antimicrobial  
resistance between the domains of health**

**MASTER'S THESIS (MSC)**

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Animal Nutrition and Feed Safety MSc

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## SUMMARY

This study aimed to collect data on the occurrence and antibiogram of the *Staphylococcus* genus members in a natural habitat shared with different game species. The investigation was carried out on red deer (n=19) and wild boars (n=19) hunted in natural habitat located in southwestern Hungary. A total of 42 strains of *Staphylococcus* strain were isolated, of which 18 were red deer origin, and 23 were wild boar origin. The number of species found in both host species was four (*S. equorum*, *S. hyicus*, *S. sciuri*, and *S. xylosus*). In addition, two more species were isolated exclusively from red deer (*S. aureus*, *S. lentus*) and six more from wild boar (*S. carnosus* ssp. *carnosus*, *S. chromogenes*, *S. gallinarum*, *S. homisi* ssp. *hominis*, *S. saprophyticus*, *S. simulans*). The most prevalent germs were *Staphylococcus aureus* (52.63%) in red deer and *S. scuri* (21.74%) in wild boar.

All but one isolate could be subjected to antibiograms. The analysis revealed that 16 isolates showed penicillin resistance (39.02%). One isolate from both wild boar and red deer was also found to be methicillin resistant.

Based on the Sørensen-Dice similarity index, the staphylococci of the two studied host species showed a moderate overlap (SDI=0.471). Regarding antibiotic resistance, staphylococci isolated from the two species showed a strong closeness (SDI=0.833). Based on the localisation of the animals carried penicillin-resistant strain, it was concluded that the human presence (settlement, tourist attraction, hotel) or significant livestock activity occurs in all concerned localities, which may have contributed to the spread of penicillin resistance in the environment. The difference in the proportion of resistant isolates between red deer and wild boar may be explained by two reasons. The first is the species' different nutrition. Red deer typically consume only plant material. Consequently, the uptake of resistant bacteria is conceivable on pastures and artificial feeders for wildlife that are also intensively used by other species (e.g., sheep, beef cattle, wild boar). The wild boar is an omnivore species with a high rooting and scavenging activity; therefore, this host may accumulate resistant bacteria from the food chain or the soil. Secondly, the two species are characteristically different in their tolerance to humans. Red deer avoid areas where human presence is high. It responds to continuous interference by avoiding in space or time. Consequently, the risk of direct infection with resistant bacteria associated with human presence is low. Wild boar, on the contrary, tolerates better the presence of human. Thus, direct uptake of resistant pathogens transmitted by human waste may occur more often.

Based on the results, we concluded that resistance to antibiotics is present even in natural habitats. Its spread between the three domains of health, environment, animals, and humans, poses significant health and economic risks. Therefore, it is advisable to develop surveillance programmes within which different habitats should be continuously monitored. Only with such comprehensive studies control strategies can be developed to slow the spread of resistant bacteria.