



The occurrence of staphylococci on dairy farms and the spread of their resistance within the framework of the concept “One health”

Zigo, F.¹, Regecová, I.², Výrostková, J.², Łozicki, A.³, Pavlík, A.⁴, Ozbey, G.⁵

¹University of Veterinary Medicine and Pharmacy, Košice, Department of Animal Nutrition and Husbandry, Slovakia

²University of Veterinary Medicine and Pharmacy, Košice, Department of Hygiene, Technology and Food Safety, Slovakia

³Warsaw University of Life Sciences, Division of Animal Nutrition, Institute of Animal Sciences, Poland

⁴Mendel University in Brno, Faculty of AgriSciences, Department of Animal Morphology, Physiology and Genetics, Czech Republic

⁵Firat University, Department of Medical Services and Techniques, Vocational School of Health Services, Turkey

Introduction: Animal breeders often face an increased risk of pathogen transmission from primary production into the food chain. In this context, the rise in diseases affecting both human and animal health presents a significant challenge for the scientific community and industry. The "One Health" concept, which acknowledges the interconnectedness of human, animal, and environmental health, therefore holds an important and indispensable role.

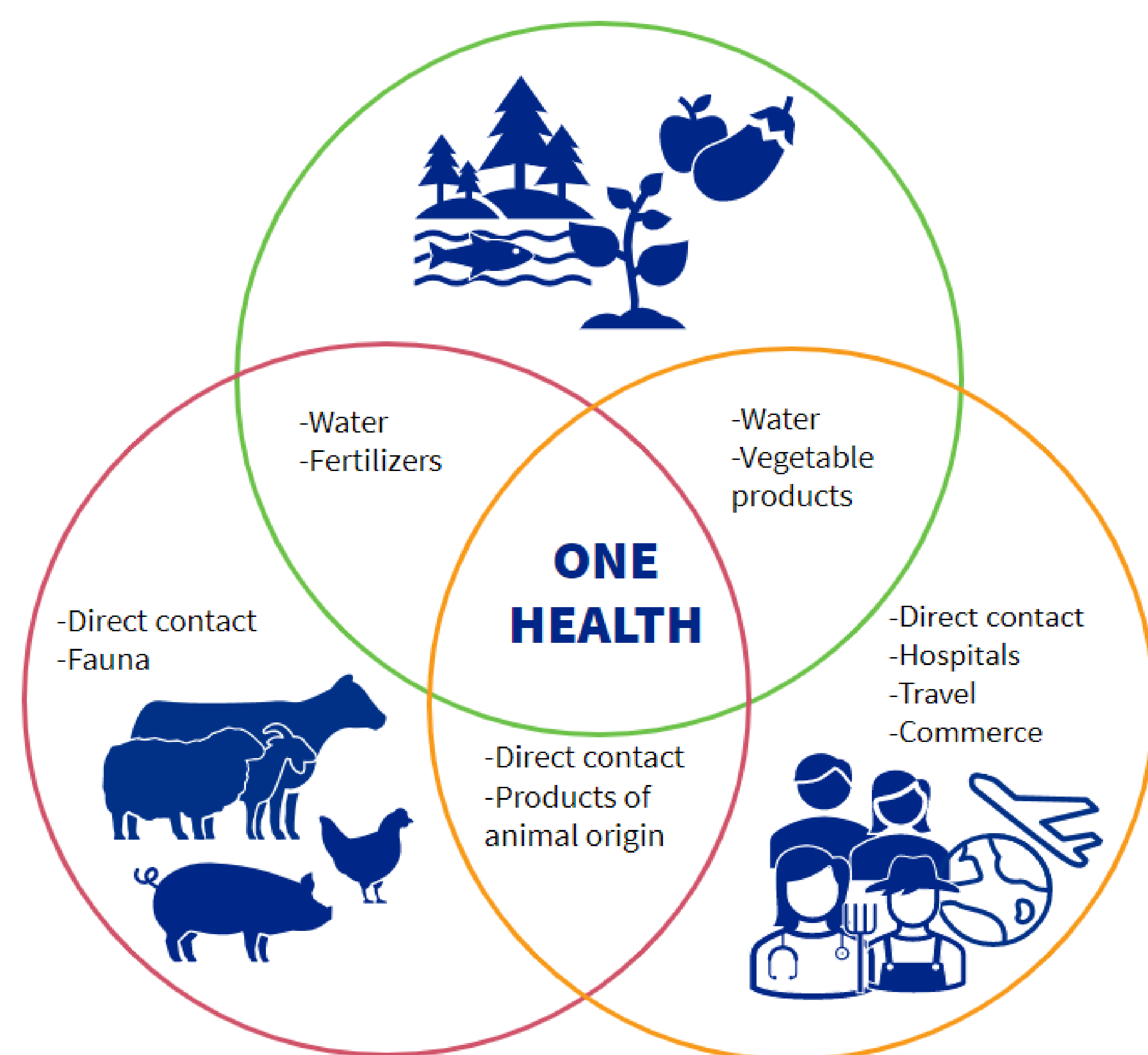


Figure 1. Processes of bacterial spread between humans-animals-environment

Staphylococcus spp.	Category n	Hemolysis n (%)	Biofilm n (%)	Resistance			mecA gene
				R1 n (%)	R2 n (%)	MDR n (%)	
<i>S. aureus</i> (n=67)	Cows (48)	25 (52.1)	22 (45.8)	25 (52.1)	9 (18.8)	4 (8.3)	2 (4.1)
	Milk Automat (5)	3 (60)	4 (80)	1 (20)	2 (40)	1 (20)	0
	Milk Parlour (14)	6 (42.8)	2 (14.3)	5 (35.7)	3 (21.4)	2 (14.3)	0
CoNS (n=151)	Cows (131)	27 (20.6)	51 (38.9)	23 (17.6)	14 (10.7)	5 (3.8)	2 (1.5)
	Milk Automat (9)	2 (22.2)	3 (33.3)	2 (22.2)	3 (33.3)	0	0
	Milk Parlour (11)	4 (36.4)	4 (36.4)	5 (45.5)	4 (36.4)	0	0

Table 1. Evaluation of the basic indicators of ewe's milk, depending on the month of milking

Note: CoNS – coagulase-negative staphylococci (*S. chromogenes*, *S. xylosus*, *S. simulans*, *S. warneri*, *S. haemolyticus* and *S. epidermidis*)

Conclusion: Antibiotic susceptibility testing revealed that *S. aureus* isolates from mastitic cow milk samples were resistant to β -lactam antibiotics. The results of this study showed that the *mecA* gene was detected in 4 isolates out of all tested staphylococci (1.8%, 4/217), including two isolates of *S. aureus* and two isolates of *S. chromogenes* from milk samples of cows with mastitis.. These results lead to serious complications in the treatment of dairy cows and pose a significant health risk to milk consumers.

Funding: This work was supported by Visegrad Grant No. 22430046: Control of antimicrobial resistance by the Integrated Farm System within "Farm to Fork" strategy. The project is co-financed by the Governments of the Czechia, Hungary, Poland and Slovakia through Visegrad Grants from International Visegrad Fund. The mission of the fund is to advance ideas for sustainable regional cooperation in Central Europe. This work was also supported by the Slovak Research and Development Agency under the Contract no. APVV-22-0457 and project VEGA no. 1-0162-23: Reduction in antibiotic use in dairy mastitis control programs.

Aim of the work: The study determines the prevalence of bacterial pathogens in animal and environmental sources, as well as the antimicrobial resistance levels of staphylococci, within the framework of the One Health approach in the region of eastern Slovakia, with a focus on dairy cattle breeding.

Material and methods: The current study was conducted using quarter milk samples (n = 3600) from 900 dairy cows from six different dairy herds located in eastern Slovakia, 140 raw milk samples consumed by the public, and 81 swabs from the surfaces of the floor, teat cups, and cow restraints. Confirmed staphylococci based on cultivation and biochemical identification were tested for biofilm formation, hemolysin production, and susceptibility to 14 antimicrobial agents using the disk diffusion method. Phenotypically positive CoNS and *S. aureus*, based on their antimicrobial resistance to β -lactam antibiotics, were subjected to PCR for the presence of the methicillin resistance gene (*mecA*).

Results: Of the 900 dairy cows tested, 252 (28%, 252/900) were found to be CMT positive. In this study, bacterial growth was observed in 87% (219/252), with coagulase-negative staphylococci (CoNS) (52.1%, 131/252) being the most frequently isolated organisms, followed by *S. aureus* (19.1%, 48/252), *E. coli* (9.1%, 23/252) and streptococci (5.9%, 15/252). Of the 140 unpasteurised cow's milk samples, the most common organisms were CoNS (6.4%, 9/140), *S. aureus* (3.5%, 5/140) and *Bacillus subtilis* (2.8%, 4/140). From the 81 swab samples, the most isolated bacteria were *E. coli* with 38.3% (31/81), followed by *S. aureus* with 16% (13/81), and *Enterococcus faecalis* with 11.3% (14/81). While virulence factors and resistance to 14 antimicrobial agents of *S. aureus* and CoNS were determined by disc diffusion, the methicillin resistance gene (*mecA*) was detected by PCR. Staphylococci with resistance to one or more antimicrobial classes were found in 52 and 56 isolates of *S. aureus* and CoNS, respectively. In addition, the results of the present study showed that *mecA* was confirmed in four isolates (1.8% 4/218) of resistant staphylococci to β -lactam antimicrobials, including two isolates of *S. aureus* and two isolates of *S. chromogenes* from the milk of mastitic cows.

