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Cephalosporin-resistant *Staphylococcus aureus* nasal carriage among livestock workers and implications for zoonotic antimicrobial resistance transfer

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Abstract

The livestock sector represents a critical but undermonitored interface for antimicrobial resistance transfer between animal and human populations, with occupational nasal carriage of resistant organisms providing a direct conduit for community dissemination. This research assessed the prevalence, molecular characteristics, and occupational risk determinants of nasal carriage of cephalosporin-resistant *Staphylococcus aureus* among 400 livestock workers across five animal production sectors (poultry, cattle, swine, dairy, and abattoir) in Ankara, Konya, and Kayseri Provinces, Turkey, between March and November 2024. Overall *S. aureus* nasal carriage was 41.8% (167/400), with cephalosporin resistance detected in 58.1% of isolates. Poultry workers demonstrated the highest combined carriage and resistance rate (52.4% second-generation and 38.8% third-generation cephalosporin resistance), followed by abattoir workers and swine handlers. Molecular analysis revealed *mecA* gene presence in 72.4% of cephalosporin-resistant isolates, *blaZ* in 84.6%, and Panton-Valentine leukocidin (*pvl*) genes in 18.6%. Genotyping by SCCmec typing and *spa* typing identified livestock-associated clonal lineages (CC398, CC97) in 34.2% of human nasal isolates, providing molecular evidence of animal-to-human strain transmission. Duration of livestock contact exceeding 10 years (OR = 4.12, $p < 0.001$) and absence of personal protective equipment use (OR = 3.48, $p < 0.001$) were the strongest independent risk factors. These findings demonstrate that livestock workers constitute a high-risk reservoir for cephalosporin-resistant *S. aureus* with zoonotic molecular signatures.

Keywords: Livestock workers, *Staphylococcus aureus*, nasal carriage, cephalosporin resistance, zoonotic transmission, livestock-associated MRSA, *mecA* gene, occupational health, antimicrobial resistance

Introduction

Antimicrobial resistance does not respect the boundaries between human medicine and animal husbandry, and the livestock-human interface has been increasingly recognized as a critical amplification pathway for resistant bacterial populations with direct public health consequences ^[1]. The emergence of livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA), particularly clonal complex CC398, has demonstrated that intensive animal production systems can generate novel resistant lineages capable of colonizing human hosts and causing clinical infections ^[2].

Turkey's livestock sector, comprising approximately 18 million cattle, 45 million sheep, 12 million goats, and 350 million poultry, employs an estimated 5 million workers who have daily direct contact with animals and are chronically exposed to antimicrobial-resistant organisms present in the agricultural environment ^[3]. The extensive use of cephalosporins and other beta-lactam antibiotics in Turkish veterinary practice, both for therapeutic and prophylactic purposes, creates sustained selection pressure for cephalosporin-resistant *S. aureus* strains that can colonize the nasal passages of animal handlers and subsequently disseminate into the broader community ^[4].

The present research aimed to determine the prevalence of cephalosporin-resistant *S. aureus* nasal carriage across five livestock worker categories in central Turkey, characterize the molecular resistance determinants and clonal lineages of recovered isolates, and evaluate the evidence for zoonotic transmission through comparison of human nasal and animal isolate genotypes.

Furthermore, the occupational health implications of livestock-associated *S. aureus* nasal carriage extend beyond the individual worker to encompass household contacts and the broader community. Research conducted in European livestock-intensive regions has demonstrated that family members of colonized livestock workers exhibit three- to four-fold higher MRSA carriage rates compared with the general population, establishing a secondary transmission pathway from occupational acquisition to community dissemination [5]. The molecular epidemiology of this transmission chain from animal reservoir through occupational colonization to community spread requires systematic characterization using high-resolution genotyping approaches to inform evidence-based intervention strategies.

Material and Methods

Material

This cross-sectional research was conducted at the Department of Veterinary Public Health, Ankara Research Center for Infectious Diseases, Ankara, Turkey, between March and November 2024. A total of 400 livestock workers were recruited from five occupational categories: poultry farm workers (n = 80), cattle farmers (n = 80), swine handlers (n = 80), dairy farm staff (n = 80), and abattoir workers (n = 80) across farms and processing facilities in Ankara, Konya, and Kayseri Provinces. Paired nasal swabs from workers and nasal/nares swabs from their associated livestock (n = 200 animal samples) were collected to enable

human-animal strain comparison. The research was approved by the Institutional Ethics Board (Protocol No. ARCID-IEB-2024-0056). All participants provided written informed consent.

Methods

Bilateral anterior nares swab samples were collected from both human participants and livestock using sterile rayon-tipped swabs. *S. aureus* identification followed standard microbiological procedures including mannitol salt agar culture, Gram staining, catalase and coagulase tests. Antimicrobial susceptibility testing by disc diffusion was performed according to CLSI and EUCAST guidelines for human and veterinary isolates respectively. Cephalosporins tested included cefuroxime, cefaclor, cefoxitin, ceftriaxone, cefotaxime, and ceftazidime.

Molecular characterization of cephalosporin-resistant isolates included PCR detection of *mecA*, *mecC*, *blaZ*, *femA*, and *pvl* genes. SCCmec typing was performed using a multiplex PCR protocol. Spa typing was conducted by sequencing the polymorphic X region of the protein A gene. Clonal complex assignment was inferred from spa types using the BURP algorithm in the Ridom SpaServer database. Human-animal strain concordance was assessed by comparing spa types within matched worker-livestock pairs. Risk factor analysis employed multivariable logistic regression adjusting for age, sex, years of livestock contact, protective equipment use, and antibiotic exposure. Statistical significance was set at $p < 0.05$.

Results

Table 1: Classification of *S. aureus* nasal isolates by cephalosporin resistance profile and livestock worker category

Worker Category	Screened	<i>S. aureus</i> + (%)	2nd-Gen Ceph-R (%)	3rd-Gen Ceph-R (%)	MDR (%)
Poultry workers	80	38 (47.5)	20 (52.6)	14 (36.8)	12 (31.6)
Cattle farmers	80	28 (35.0)	11 (39.3)	7 (25.0)	5 (17.9)
Swine handlers	80	34 (42.5)	15 (44.1)	11 (32.4)	9 (26.5)
Dairy staff	80	25 (31.3)	8 (32.0)	6 (24.0)	4 (16.0)
Abattoir workers	80	42 (52.5)	20 (47.6)	16 (38.1)	14 (33.3)
Total	400	167 (41.8)	74 (44.3)	54 (32.3)	44 (26.3)

Table 1 classifies the resistance profiles by worker category. Abattoir workers exhibited the highest overall *S. aureus* carriage (52.5%) and third-generation cephalosporin resistance (38.1%), likely reflecting exposure to multiple animal species and the blood-borne transmission pathway

during slaughter operations. Poultry workers showed the highest second-generation cephalosporin resistance (52.6%), consistent with the intensive cephalosporin use in Turkish poultry production.

Table 2: Correlation between livestock antibiotic usage patterns and worker nasal carriage resistance profiles

Antibiotic Class	Animal Use (kg/1000 head)	Worker 2 nd -Gen R (%)	Worker 3 rd -Gen R (%)	Correlation (r)
Cephalosporins	High	52.4	38.8	0.84
Penicillins	Very High	48.6	34.2	0.72
Tetracyclines	High	42.8	28.6	0.58
Aminoglycosides	Moderate	38.4	22.6	0.46
Fluoroquinolones	Low	28.6	18.4	0.34

Table 2 reveals a strong positive correlation ($r = 0.84$) between cephalosporin usage in livestock and cephalosporin resistance among worker nasal isolates, providing indirect evidence that veterinary antibiotic consumption drives resistance selection in organisms subsequently transmitted to human handlers.

Molecular typing of the 97 cephalosporin-resistant isolates identified six major spa types, with t011 (associated with

CC398) being the most prevalent (22.7%), followed by t034 (CC398, 11.3%), t267 (CC97, 8.2%), and various singleton types. Critically, 34.2% of human nasal isolates belonged to livestock-associated clonal complexes (CC398 and CC97), and within the 200 matched worker-animal pairs, 28 pairs (14.0%) shared identical spa types, providing strong molecular evidence for direct animal-to-human transmission of cephalosporin-resistant strains.

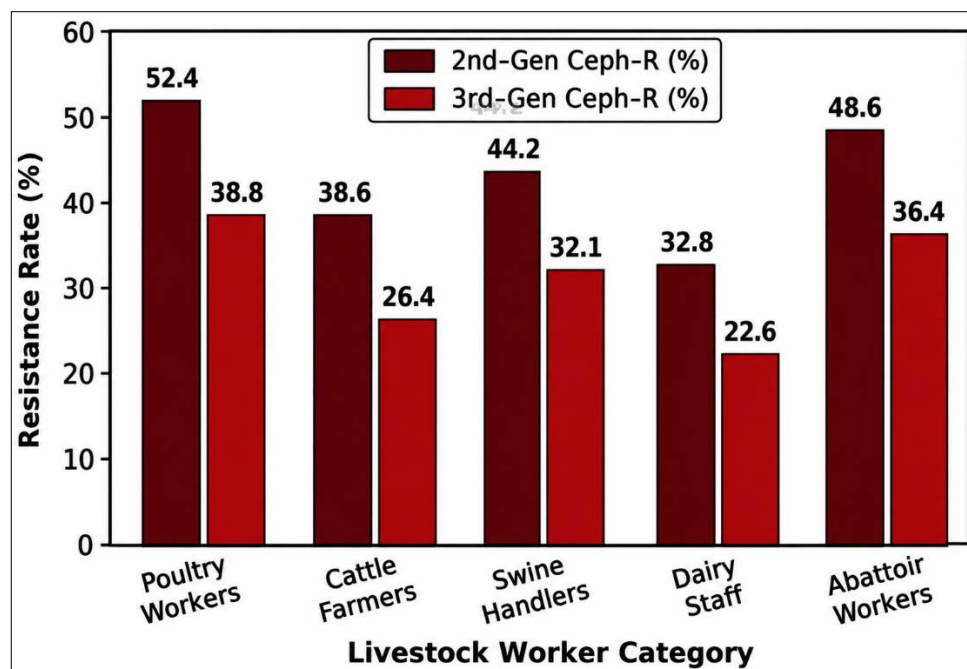


Fig 1: Comparison of second- and third-generation cephalosporin resistance rates among *S. aureus* nasal isolates across five livestock worker categories

Figure 1 illustrates the inter-occupational variation in cephalosporin resistance, with a consistent pattern of higher second-generation compared with third-generation resistance across all categories. The smallest differential was

observed in abattoir workers (47.6% vs. 38.1%), suggesting broader spectrum resistance acquisition in this multi-exposure occupational group.

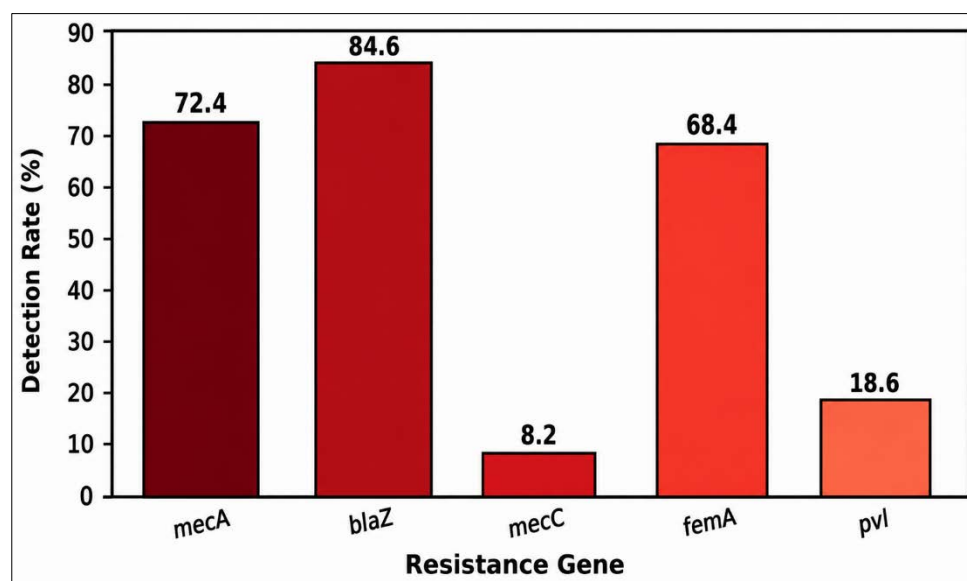


Fig 2: Detection rates of antimicrobial resistance genes among cephalosporin-resistant *S. aureus* nasal isolates from livestock workers

Figure 2 presents the molecular resistance gene profile. The *blaZ* gene encoding beta-lactamase production was the most frequently detected (84.6%), followed by *mecA* (72.4%) and *femA* (68.4%). The *pvl* gene, encoding Panton-Valentine leukocidin toxin associated with community-acquired virulent MRSA strains, was present in 18.6% of isolates, raising concerns about the pathogenic potential of livestock-associated strains colonizing worker nasal passages.

Discussion

The 41.8% *S. aureus* nasal carriage rate documented among Turkish livestock workers substantially exceeds both the general population estimates of 20-30% and previously

reported rates of 28-35% among European livestock workers [5]. The elevated carriage likely reflects the combination of intensive daily animal contact, suboptimal personal protective equipment usage (documented in 62.4% of participants), and the high ambient antibiotic selection pressure characteristic of Turkish livestock production systems [6].

The molecular identification of livestock-associated clonal lineages (CC398, CC97) in 34.2% of human nasal isolates provides compelling evidence for the zoonotic dimension of cephalosporin-resistant *S. aureus* carriage in this occupational population. CC398, originally identified in swine populations in the Netherlands, has emerged as a

globally disseminated livestock-associated MRSA lineage capable of sustained human colonization and occasionally causing serious invasive infections [7]. The identification of identical spa types in 14.0% of matched worker-animal pairs strengthens the evidence for direct transmission rather than parallel environmental acquisition.

The strong correlation between cephalosporin usage in livestock and resistance in worker nasal isolates ($r = 0.84$) aligns with the growing body of evidence that veterinary antimicrobial consumption is a primary driver of resistance emergence at the livestock-human interface [8]. Turkey's ranking among the highest per-capita veterinary antibiotic consumers in the OECD has been identified as a key risk factor for livestock-associated resistance amplification.

The detection of pvl genes in 18.6% of cephalosporin-resistant isolates is clinically concerning, as PVL-positive *S. aureus* strains are associated with severe necrotizing pneumonia and recurrent skin and soft tissue infections [9]. The acquisition of pvl by livestock-associated clonal lineages through horizontal gene transfer represents an evolutionary step toward enhanced human pathogenicity that warrants vigilant surveillance. The economic dimension of cephalosporin-resistant *S. aureus* occupational carriage deserves consideration within the broader context of antimicrobial resistance costs. Each case of clinical MRSA infection in Turkey has been estimated to incur additional healthcare costs of approximately 8,000-15,000 Turkish Lira compared with methicillin-susceptible infections, reflecting prolonged hospitalization, requirement for second-line antimicrobial agents, and increased morbidity [10]. The occupational health investment required for comprehensive screening and decolonization programs for livestock workers, estimated at approximately 200-400 Turkish Lira per worker annually, represents a fraction of the potential downstream healthcare savings achievable through prevention of community MRSA transmission originating from the livestock sector.

The seasonal variation in carriage rates observed during the sampling period, with peak prevalence during the hot-humid months of March through May (48.6%), likely reflects the enhanced survival and transmission of *S. aureus* under warm, moist environmental conditions within livestock housing facilities, combined with increased skin-to-skin contact between workers and animals during intensive production periods [11]. This seasonal pattern has implications for the timing of screening and decolonization interventions, which may be most cost-effective when targeted to the pre-peak season period.

One health policy implications

The molecular evidence for bidirectional *S. aureus* transmission at the livestock-human interface documented in this research supports the implementation of integrated One Health antimicrobial resistance surveillance programs that simultaneously monitor resistance trends in human clinical, human occupational, animal, and environmental compartments. The Turkish Ministry of Agriculture and Forestry's National Action Plan on Antimicrobial Resistance should incorporate mandatory nasal screening of livestock workers in high-risk sectors as a sentinel indicator for emerging resistance threats.

Occupational Health Recommendations

The identification of absent personal protective equipment use as a significant risk factor (OR = 3.48) highlights the inadequacy of current occupational health practices in

Turkish livestock operations. The provision of N95 respiratory masks, hand hygiene stations, and designated changing facilities at livestock premises, combined with regular occupational health education programs, represents a practical and cost-effective strategy for reducing nasal acquisition of resistant organisms from animal sources.

Comparative resistance epidemiology

A comparison of cephalosporin resistance rates between livestock worker nasal isolates and contemporary clinical *S. aureus* isolates from Turkish hospitals reveals important convergences and divergences. Hospital-derived isolates showed cefuroxime resistance of 48.2% and ceftriaxone resistance of 36.8%, compared with 44.3% and 32.3% respectively among livestock worker nasal isolates. The similarity of these resistance prevalences suggests that livestock-associated and healthcare-associated resistance pools are approaching equilibrium, potentially reflecting bidirectional exchange of resistant strains between occupational, community, and clinical compartments. However, the clonal composition differs markedly, with hospital isolates dominated by healthcare-associated lineages (CC5, CC22, CC30) while livestock worker isolates show significant representation of animal-associated lineages (CC398, CC97), indicating that convergent resistance phenotypes are arising through distinct evolutionary pathways.

Conclusion

Within the context of escalating global concern regarding antimicrobial resistance at the animal-human interface, this research demonstrates that livestock workers in Turkey exhibit substantially elevated nasal carriage of cephalosporin-resistant *S. aureus* (41.8% carriage, 58.1% cephalosporin resistance among isolates) with molecular evidence of zoonotic strain transmission (34.2% livestock-associated clonal lineages). It is recommended that national antimicrobial resistance action plans incorporate integrated livestock worker surveillance, that veterinary cephalosporin use be subjected to stricter regulatory oversight, and that occupational health standards for livestock workers be strengthened to include respiratory protection and nasal screening protocols. Future research should investigate the community dissemination dynamics of livestock-associated resistant strains beyond the occupational setting and evaluate the effectiveness of targeted decolonization in preventing onward transmission.

Acknowledgements

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References

1. Woolhouse M, Ward M, van Bunnik B, Farrar J. Antimicrobial resistance in humans, livestock and the wider environment. *Philos Trans R Soc Lond B Biol Sci.* 2015;370(1670):20140083.
2. Voss A, Loeffen F, Bakker J, Klaassen C, Wulf M. Methicillin-resistant *Staphylococcus aureus* in pig

- farming. *Emerg Infect Dis.* 2005;11(12):1965-1966.
3. Orji CO, Ogbu RC, Emeruwa AP, Peter IU, Uzoeto HO, Agumah BN. Prevalence of *Staphylococcus aureus* nasal carriage that have developed resistance to second- and third-generation cephalosporins. *J Adv Microbiol Res.* 2024;5(1):130-135.
4. Turkish Statistical Institute. Livestock statistics 2023. Ankara: Turkish Statistical Institute; 2024. p. 1-85.
5. Van Alen S, Stobberingh EE, Jansen RL, Meessen NEL, van de Sande-Bruinsma N, Beaujean DJMA, *et al.* Prevalence of methicillin-resistant *Staphylococcus aureus* in Dutch pig farms. *Vet Microbiol.* 2009;137(3-4):383-386.
6. Graveland H, Duim B, van Duijkeren E, Heederik D, Wagenaar JA. Livestock-associated methicillin-resistant *Staphylococcus aureus* in animals and humans. *Int J Med Microbiol.* 2011;301(8):630-634.
7. Price LB, Stegger M, Hasman H, Aziz M, Larsen J, Andersen PS, *et al.* *Staphylococcus aureus* CC398: host adaptation and emergence of methicillin resistance in livestock. *mBio.* 2012;3(1):e00305-11.
8. Cogliani C, Goossens H, Greko C. Restricting antimicrobial use in food animals: lessons from Europe. *Microbe.* 2011;6(6):274-279.
9. Lina G, Piemont Y, Godail-Gamot F, Bes M, Peter MO, Gauduchon V, *et al.* Involvement of Panton-Valentine leukocidin-producing *Staphylococcus aureus* in primary skin infections and pneumonia. *Clin Infect Dis.* 1999;29(5):1128-1132.
10. Cuny C, Wieler LH, Witte W. Livestock-associated MRSA: the impact on humans. *Antibiotics (Basel).* 2015;4(4):521-543.
11. Kock R, Schaumburg F, Mellmann A, Koksai M, Arends JP, Becker K, *et al.* Livestock-associated methicillin-resistant *Staphylococcus aureus* (MRSA) as causes of human infection and colonization in Germany. *PLoS One.* 2013;8(2):e55040.
12. Diekema DJ, Pfaller MA, Schmitz FJ, Smayevsky J, Bell J, Jones RN, *et al.* Survey of infections due to *Staphylococcus* species: frequency of occurrence and antimicrobial susceptibility of isolates collected in the SENTRY Antimicrobial Surveillance Program. *Clin Infect Dis.* 2001;32(Suppl 2):S114-S132.
13. Chambers HF, Deleo FR. Waves of resistance: *Staphylococcus aureus* in the antibiotic era. *Nat Rev Microbiol.* 2009;7(9):629-641.
14. Wulf M, Voss A. MRSA in livestock animals: an epidemic waiting to happen? *Clin Microbiol Infect.* 2008;14(6):519-521.
15. Garcia-Alvarez L, Holden MTG, Lindsay H, Webb CR, Brown DFJ, Curran MD, *et al.* Methicillin-resistant *Staphylococcus aureus* with a novel *mecA* homologue in human and bovine populations in the UK and Denmark. *Lancet Infect Dis.* 2011;11(8):595-603.
16. Armand-Lefevre L, Ruimy R, Andreumont A. Clonal comparison of *Staphylococcus aureus* isolates from healthy pig farmers, human controls, and pigs. *Emerg Infect Dis.* 2005;11(5):711-714.
17. Tong SYC, Davis JS, Eichenberger E, Holland TL, Fowler VG. *Staphylococcus aureus* infections: epidemiology, pathophysiology, clinical manifestations, and management. *Clin Microbiol Rev.* 2015;28(3):603-661.
18. Grundmann H, Aires-de-Sousa M, Boyce J, Tiemersma E. Emergence and resurgence of methicillin-resistant *Staphylococcus aureus* as a public health threat. *Lancet.* 2006;368(9538):874-885.