ECM 2023
The 2nd International Electronic Conference on Microbiology
01–15 December 2023 | Online

Antimicrobial resistance of foodborne pathogens in pork sausages – A review

Conceição S.[1,*], Queiroga, C.[1,2] and Laranjo, M.[1,2]

[1] MED - Mediterranean Institute for Agriculture, Environment and Development & CHANGE – Global Change and Sustainability Institute, Institute for Advanced Studies and Research, Universidade de Évora, Évora, Portugal.

[2] Departamento de Medicina Veterinária, Escola de Ciências e Tecnologia, Universidade de Évora, Évora, Portugal.

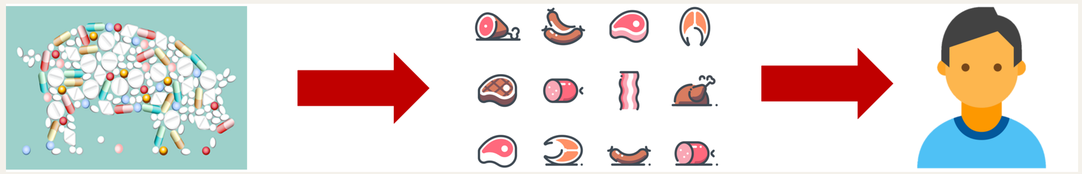
*email: smpc@uevora.pt

INTRODUCTION

- Pork sausages are highly appreciated in Mediterranean countries
- Antimicrobial resistance (AMR) in foodborne bacteria represents a major challenge for public health
- The Antimicrobial Stewardship strategy aims to optimize treatment outcomes for bacterial infections[1]
- AMR within the food industry primarily origins from the use of multiple antimicrobials in food-producing animals
- Three pathogenic microbial groups of major concern: methicillin-resistant *Staphylococcus aureus* (MRSA), extended-spectrum beta-lactamase (ESBL) producing *Enterobacteriaceae*, and vancomycin-resistant *Enterococcus* (VRE)

PORK & FARM-TO-FORK TRANSMISSION

- Pork meat is a significant reservoir of AMR
- Pig slaughterhouses have two main contamination challenges: microorganisms present on the pig's skin, and those introduced by the evisceration step
- The transmission of AMR via the food chain contributes to the proliferation of drug-resistant pathogens



- Antimicrobials administered to food-producing animals
- Increased selective pressure resulting in increasing AMR

Consumption of contaminated meat and meat products may transmit multi-drug resistant bacteria to humans

METHICILLIN-RESISTANT *Staphylococcus aureus* (MRSA)

- Opportunistic pathogens[2]
- Resistant to nearly all β-lactams, vancomycin, and fluoroquinolones[3,4]
- Staphylococcal cassette chromosome (sccmec) → *mec*A, *mec*B, and *mec*C genes[5,6,7]

VANCOMYCIN-RESISTANT Enterococcus spp. (VRE)

- Classified as high-priority pathogens by the WHO[8]
- Resistant to vancomycin, penicillin, aminoglycosides and macrolides[5]
- Aqquisition of *van*, *cfr*, *cfr*(B), *cfr*(C), and *optr*A genes, mutations in the 23S rRNA and ribosomal proteins L3 and L4 genes[9-12]

ESBL-PRODUCING *Enterobacteriaceae*

- Categorized as critical priorities by the WHO[8]
- Resistant to a broad spectrum of β-lactam, and colistin (last-resort antimicrobial)[13]
- *Escherichia coli* and *Klebsiella pneumoniae*: primary species associated with nosocomial infections[14-17]

References

1. Dellit, et al. (2007) Clinical Infectious Diseases 44
2. Li, et al. (2019) Frontiers in Microbiology 10
5. Wen, et al. (2020) Frontiers in Microbiology 11
3. Barros et al. (2019) Antimicrobial Agents and Chemotherapy 63
4. Correia, et al. (2019) Frontiers in Microbiology 10
6. Hau, et al. (2018) Frontiers in Microbiology 9
7. Neyaz, et al. (2020) Frontiers in Microbiology 11
8. https://www.who.int/news/item/27-02-2017-who-publishes-list-of-bacteria-for-which-new-antibiotics-are-urgently-needed.
9. Abbo et al. (2019) Clinical Infectious Diseases 69
10. Farman et al. (2019) Antimicrobial Resistance and Infection Control 8
11. Deshpande, et al. (2018) Journal of Antimicrobial Chemotherapy 73
12. Sacramento, et al. (2022) Preventive Veterinary Medicine 202
13. Richter, et al. (2019) Frontiers in Microbiology 11
14. Collis, et al. (2019) Foodborne Pathogens and Disease 16
15. Moosavian, et al. (2019) Infection and Drug Resistance 12
16. Castanheira, et al. (2019) Open Forum Infectious Diseases 6
17. Song, et al. (2020) Frontiers in Microbiology 11

Funding

This work was funded by National Funds through FCT - Foundation for Science and Technology under Project UIDB/05183/2020.
FCT PhD fellowship with reference UI/BD/153510/2022