***UNIVERSITY OF AGRICULTURAL SCIENCES AND VETERINARY MEDICINE CLUJ-NAPOCA***

***DOCTORAL SCHOOL OF VETERINARY MEDICAL SCIENCES***

**HABILITATION THESIS ABSTRACT**

**The Food Chain as a Reservoir of Resistant Pathogens:**

**Insights into Prevalence and Risk Assessment Needs**

Domain: **VETERINARY MEDICINE**

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Cluj-Napoca

2025

**ABSTRACT**

*Chapter 1 – Introduction, Scientific Visibility, Aim of Research and Prestige*

This thesis explores a deeply important and timely issue: the food chain as a vehicle for antimicrobial-resistant pathogens. Dr. Alexandra Tăbăran, an associate professor and a researcher with an established international profile, addresses the critical problem of resistant foodborne bacteria and their impact on public health.

Her research has focused over the past decade on *Escherichia coli*, *Salmonella* spp., *Listeria monocytogenes*, and *Clostridium perfringens*, with a particular emphasis on their virulence and antimicrobial resistance. The scope of her work aligns with One Health principles and is especially relevant for countries like Romania, where standardized AMR surveillance is still developing.

Dr. Tăbăran has made substantial contributions through high-impact publications, leadership in national projects, and extensive citation metrics. She has taught and published in three languages, reviewed for top journals, and developed course materials for food safety and inspection. The thesis is both a synthesis of her achievements and a structured analysis of the food chain as a microbial reservoir.

*Chapter 2 – Assessment of Microbiological Contamination and Prevalence of Pathogenic Strains in Carcasses from Various Species*

This central chapter is divided into sub-studies on cattle, swine, and poultry carcasses, offering a comprehensive evaluation of contamination risks at slaughterhouse level.

**Bovine Carcasses**

The study focused on two Romanian slaughterhouses and sampled bovine carcasses at two critical stages: after evisceration and after cooling. Using classical microbiology and PCR-based identification, results showed a significant reduction in microbial loads post-cooling. Yet, 14% of fecal samples were positive for pathogenic *E. coli*, including serogroups like O101 and O26.

Approximately 5% of carcass samples carried *E. coli* strains with virulence genes, some of which matched fecal isolates, indicating contamination likely occurred during evisceration. No *Salmonella* or *Listeria* were found on carcasses, but *Salmonella* was detected in 28% of fecal samples (mainly *S. Typhimurium*). The study emphasized the crucial need for effective hygiene during slaughter, especially considering that *E. coli* and *Salmonella* may not be visually detected yet pose significant risk.

**Swine Carcasses**

In swine, samples collected between 2013 and 2018 revealed varying degrees of surface contamination. A notable seasonal effect was observed: higher microbial loads were recorded during warmer months, likely due to inadequate temperature control and lapses in hygiene.

In total, *E. coli* was detected in 14.28% of samples and *Salmonella Typhimurium* in 7.14%. Contamination of internal muscle tissues appeared to result from tools or ruptured intestines during processing. Following early results, the slaughterhouse implemented corrective actions, and by 2018, no pathogens were detected—an encouraging sign that hygiene interventions were effective. The study also showed lower contamination rates compared to similar research in Southeast Asia, but still highlighted concerns around warm-season processing.

 **Poultry Carcasses**

Samples collected from poultry production and retail environments showed *Salmonella* spp. contamination in 22.92% of tested meats. Thirteen serovars were identified, including *S. Infantis*, *S. Typhimurium*, and *S. Derby*—all of which are frequently implicated in human salmonellosis.

Molecular confirmation and serotyping were conducted via PCR, and antibiotic susceptibility was tested using disk diffusion. Results showed that more than 80% of isolates were resistant to three or more antimicrobials. The most common resistance patterns included resistance to tetracycline, streptomycin, and sulfamethoxazole. Some strains showed resistance to fluoroquinolones such as ciprofloxacin, a critical concern given its use in human medicine.

*Chapter 3 – Antibiotic Resistance Profiles of the Bacteria Isolated Within the Food Chain*

This chapter dives deeper into the antimicrobial susceptibility profiles of bacterial isolates gathered in the earlier studies. Testing was conducted on strains of *E. coli*, *Salmonella*, and *Listeria monocytogenes*, using both phenotypic methods (disk diffusion, MIC) and genotypic tools (PCR detection of resistance genes).

The most prevalent resistance genes detected included *tetA* (tetracycline resistance), *sul1* (sulfonamide resistance), *aadA* (aminoglycosides), and *blaTEM* (beta-lactams). Integrons were also found in multiple isolates, suggesting a genetic mechanism for multi-resistance and gene transfer.

The resistance trends identified were consistent across animal species and product types, underlining a systematic issue in antimicrobial use and residue management in Romanian food production systems.

*Chapter 4 – Virulence and Antimicrobial Resistance of Bacteria Isolated from Food Products*

**Meat Products**

Studies on processed meat products, including sausages, pork ham, and fillets, showed contamination with both Gram-negative (e.g., *Pseudomonas*, *Acinetobacter*) and Gram-positive bacteria (e.g., Staphylococcus, Streptococcus). Psychrotrophic bacteria were dominant, especially in products stored or sold during warmer months.

*Salmonella* was detected in pork and chicken meat. The majority of *Salmonella* isolates were MDR and carried resistance genes. In Listeria monocytogenes, virulence genes such as inlA, *prfA*, and *actA* were detected, as well as moderate resistance to tetracycline and erythromycin. These strains were mostly isolated from ready-to-eat products—raising important concerns about consumer safety.

**Dairy Products**

In dairy products, *E. coli* isolates showed moderate resistance but did not carry shiga toxin genes (*stx1*/*stx2*), suggesting they were non-toxigenic. Still, resistance profiles similar to meat-borne isolates were present, with *tetA* and *blaTEM* being the most commonly found genes. The findings suggest the dairy sector has better control systems, but low-level resistance remains a concern.

*Chapter 5 – Overall Conclusions and Further Recommendations*

This chapter synthesizes the findings into a unified risk picture. The studies revealed that antimicrobial-resistant pathogens are present in all segments of the Romanian food chain—from primary production to processing and distribution.

Key conclusions include:

The prevalence of MDR *Salmonella*, especially in poultry and pork, is alarming.

E. coli strains carrying virulence and resistance genes are more common than expected, including non-O157 serogroups like O101 and O26.

Seasonal variation significantly affects contamination risks.

Effective hygiene controls at slaughterhouses can drastically reduce pathogen prevalence, as seen in swine post-2013.

Resistance gene profiles suggest an urgent need to regulate and monitor antimicrobial usage in veterinary practice.

Dr. Tăbăran calls for the implementation of a more comprehensive AMR surveillance program in Romania, aligned with EU standards. She emphasizes the importance of using molecular methods routinely in food inspection, enforcing cold-chain integrity, and applying a One Health approach in policy development.

Through detailed microbiological, molecular, and epidemiological research, this thesis makes a strong case for re-evaluating food safety strategies in Romania and similar Eastern European countries. Dr. Tăbăran's work builds a solid bridge between science and policy, providing actionable insights that can improve both public health and the integrity of the food supply chain.