PhD School in Veterinary Sciences – XXXII Cycle
Curriculum: Animal Production and Food Safety

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# Evaluation of antimicrobial resistance patterns in commensal *Escherichia coli* isolated from food and animal sources.

## INTRODUCTION

Antimicrobial resistance is an emerging global problem, affecting humans and animals infection treatments and prognosis. There are many reasons for the quick diffusion of antimicrobial resistance, among all, an excessive usage of antimicrobials for animal and human disease treatments in combination with an efficient and quick transfer (vertically and horizontally) of resistance genes between bacteria. Particulars, the presence of self transmissible and mobilizable plasmids and integrons enable the diffusion and the acquisition of antimicrobial resistance genes between different microbial population, making antimicrobial resistance a constantly evolving phenomenon with different possible sources. Antimicrobial resistance genes and bacteria are also present in many environments, all of them interconnected by different paths, and can be transmitted to human by different means.
Commensal *Escherichia coli,* normally present in intestine of food-producing/companion animals and in different environments, constitute a reservoir of resistance genes transmitted horizontally through zoonotic and other bacteria present in the same context. For this reason, *E. coli* are typically chosen as the representative indicator of antimicrobial resistance in Gram-negative bacteria, revealing emergence and changes in antimicrobial resistance pattern of bacteria population.

## AIM OF THE STUDY

The aim of the study is the evaluation of antimicrobial resistance pattern in commensal *Escherichia coli* indicator isolated from food and food producing/companion animals in order to obtain valuable data on antimicrobial resistance occurring in microbial population and to investigate the different sources as possible vehicle of antimicrobial resistance genes and bacteria for human, focusing on the epidemiology traits involved in antimicrobial resistance diffusion.

## MATHERIALS & METHODS

A total of 25 strains of commensal *Escherichia coli* were collected from 10 different food and animal sources (beef, dairy, swine, boar, poultry, fish, cat and dog, rabbit, vegetable, mollusc) during the period november 2016 - january 2018.
10 μl of overnight culture in EC-Broth were streaked onto MacConkey's and Levine's agar plates and incubated for 24h at 37°C. Colonies with *E. coli* morphology were selected and identified by biochemical (indole probe) and molecular tests (Horakowa *et al.*, 2008).
Susceptibility to 12 antimicrobial agents (ampicillin; nalidixic acid; ceftiofur; ceftazidime; chloramphenicol; enrofloxacin; gentamicin; meropenem; streptomycin; sulfisoxazole; tetracycline; trimethoprim/sulfamethoxazole) was carried out by disk agar diffusion method. The results were interpreted following performance standards publisched by European Committee on Antimicrobial Susceptibility Testing (EUCAST) and, when not present, these published by Clinical and Laboratory Standards Institute (CLSI).
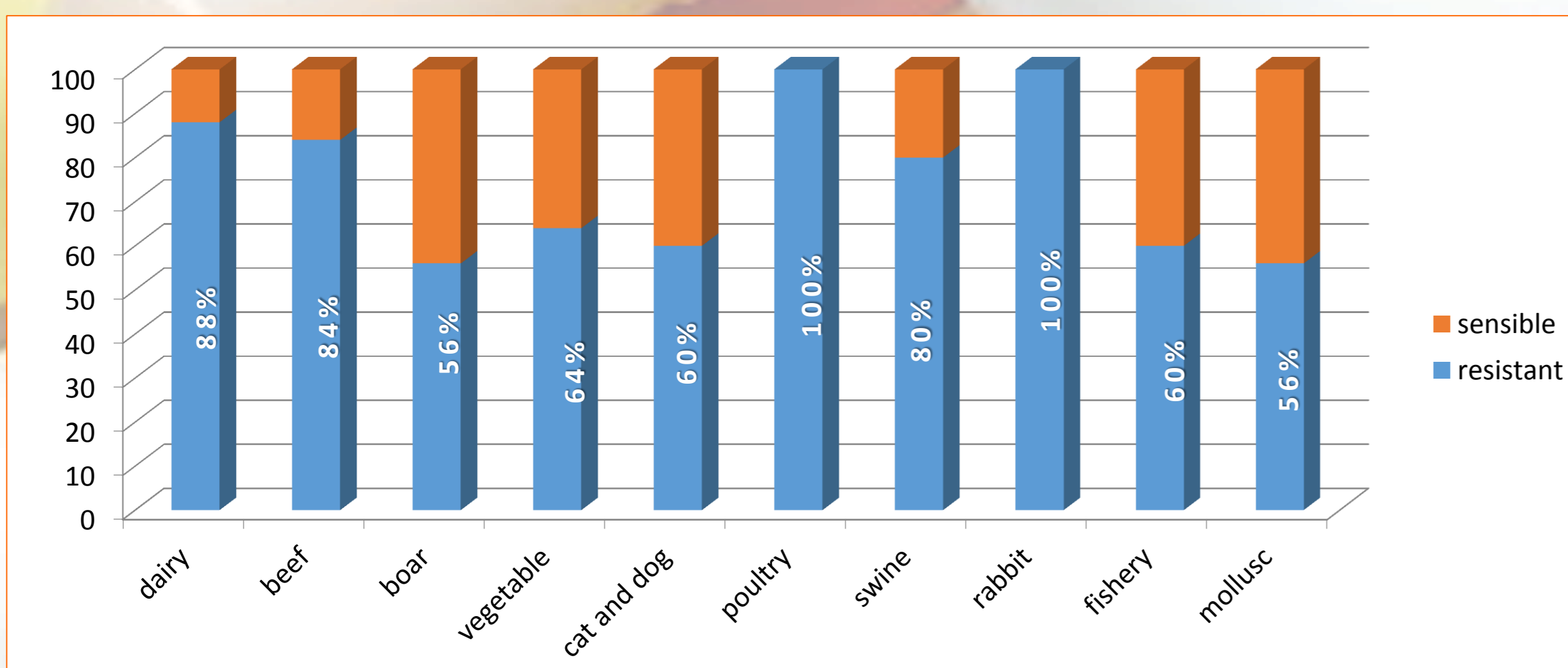
## RESULTS & DISCUSSION



Figure 1: Percentages of strains showing resistance to almost one of the twelve antimicrobial tested in all the sources considered in the study.
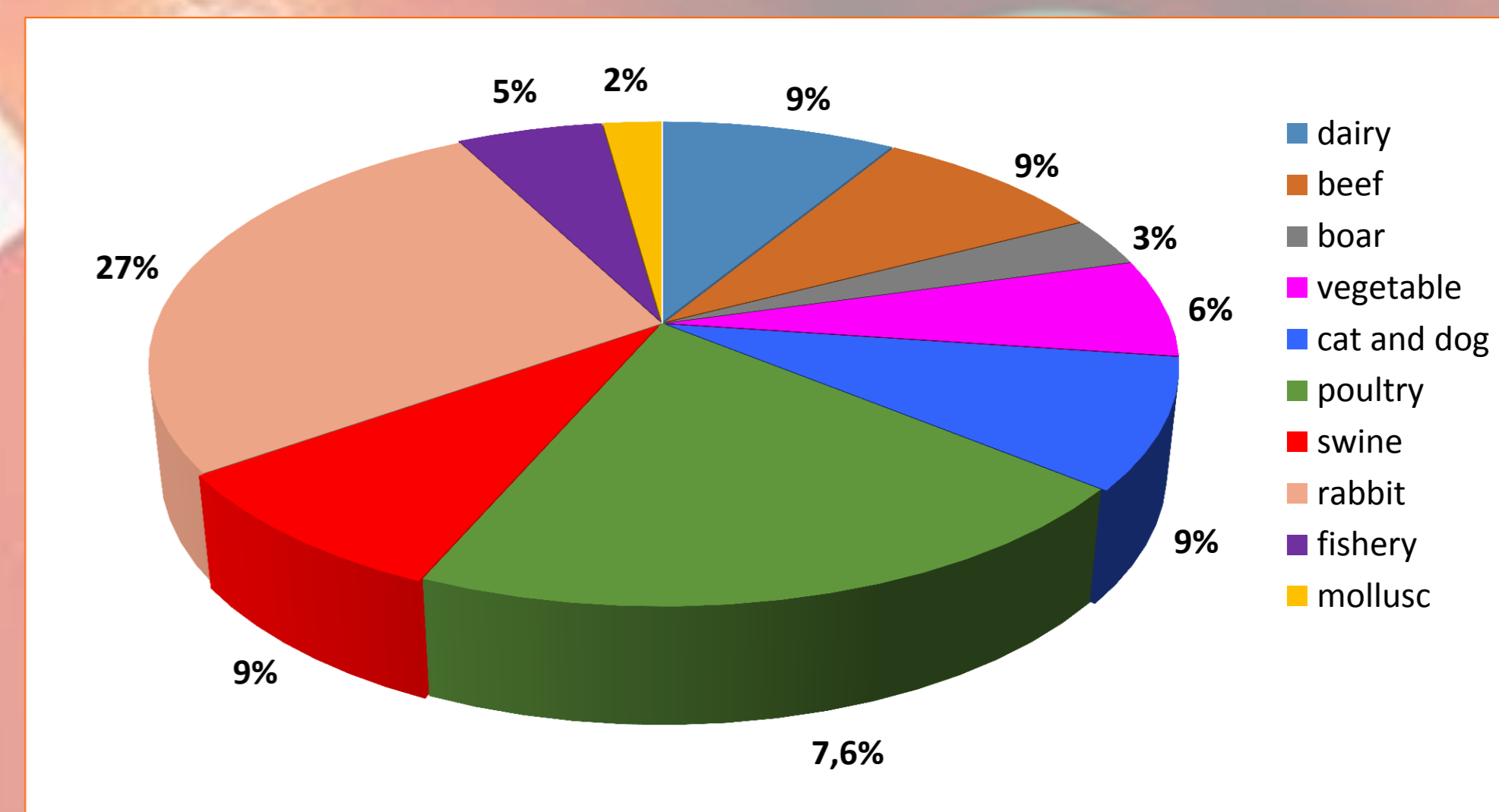


Figure 2: Percentages of strains showing multidrug –resistance pattern (resistance to al least three antimicrobial of different classes) in all the sources considered in the study.
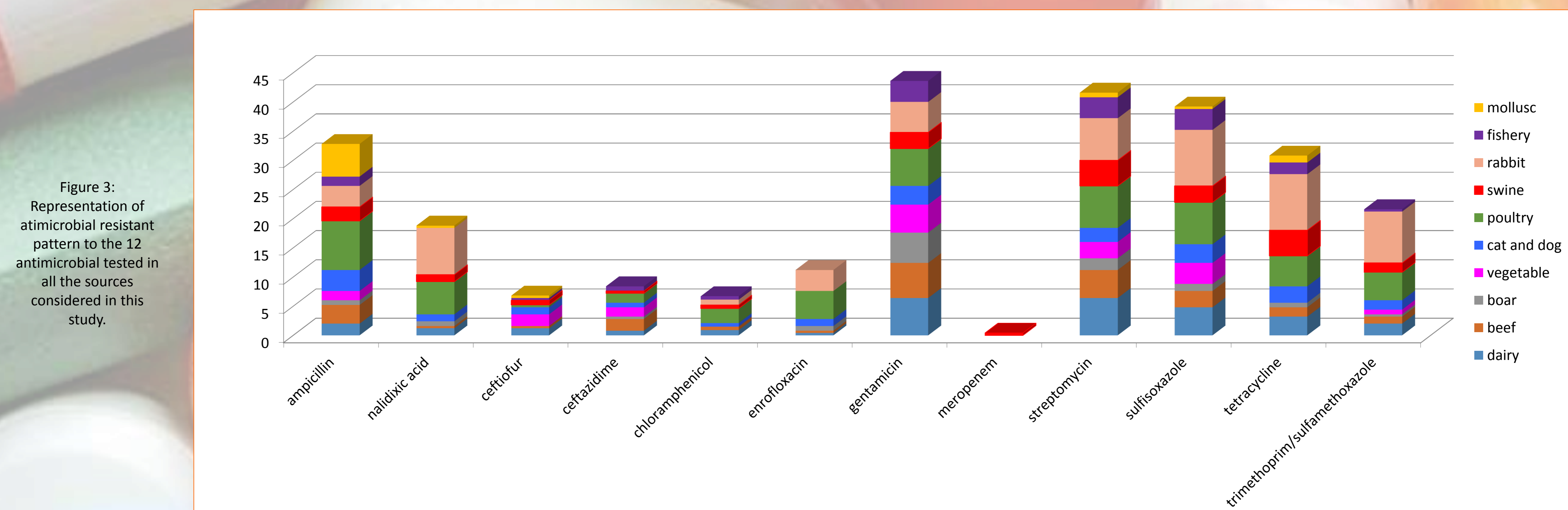
Figure 3: Representation of atimicrobial resistant pattern to the 12 antimicrobial tested in all the sources considered in this study.



## IN THE FUTURE...

In the future we would collect 25 commensal *E. coli* from human origin evaluating antimicrobial pattern for the same antimicrobials tested in the other sources. Moreover we would performed molecular evaluation of all the isolates focusing on the identification of antimicrobial resistance genes, plasmids and integrons involved in antimicrobial resistance transmission, with particular interest on antimicrobial resistance to Human Critically Important Antibiotics (CIA). In addition, we would evaluate the co-transmission of antimicrobial resistance genes, virulence genes and disinfectant resistance genes (especially these leading quaternary ammonium compound resistance) by plasmids and integrons.

References: Horakova K, Mlejnkova H, Mlejnek P, 2008. Specific detection of Escherichia coli isolated from water samples using polymerase chain reaction targeting four genes: cytochrome bd complex, lactose permease, β-d-glucuronidase, and β-d-galactosidase. J Appl Microbiol, 105: 970-976.