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VETERINARY EPIDEMIOLOGY UNIT

TRANSMISSION OF ANTIBIOTIC RESISTANCE FROM ANIMALS TO HUMANS AND VICE VERSA, ONE HEALTH IN ACTION

Prof. Jeroen Dewulf

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SETUP

- Antimicrobial usage and resistance in animals
- Transmission of antimicrobial resistance from animals to humans and vice versa

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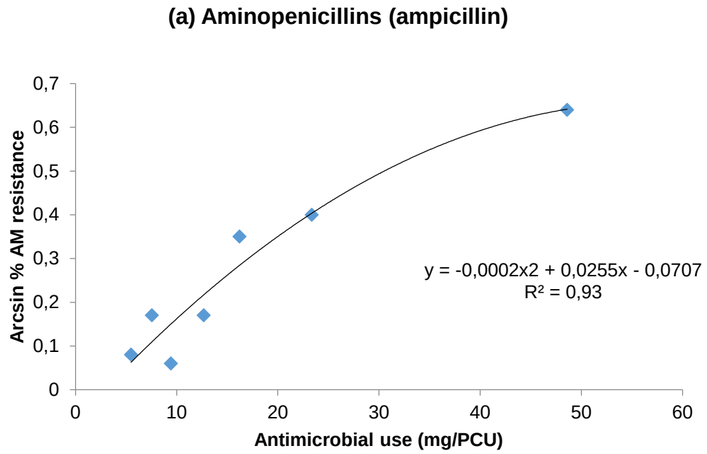
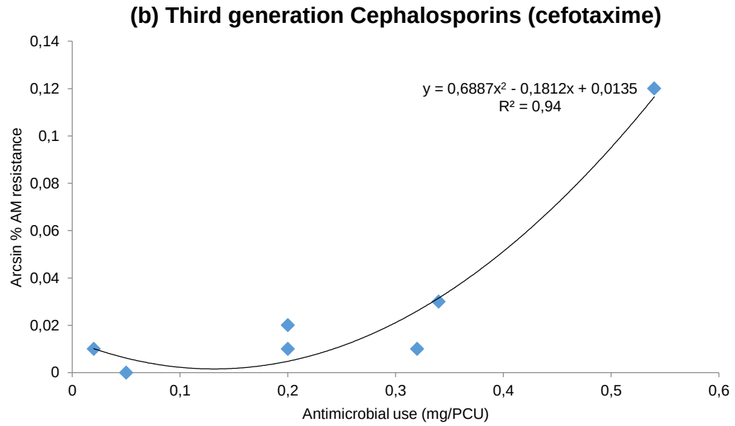
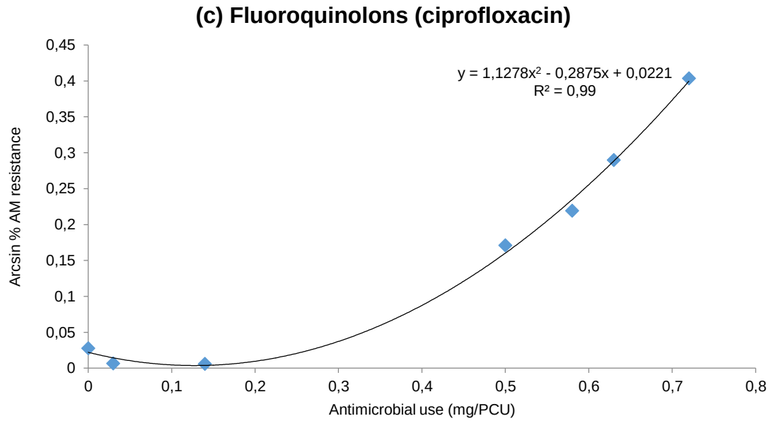
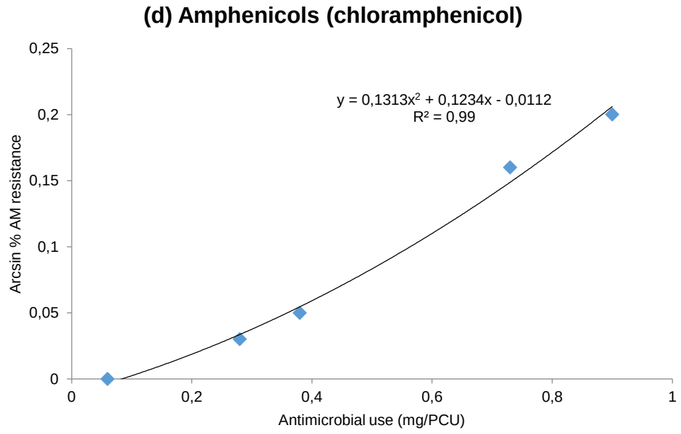
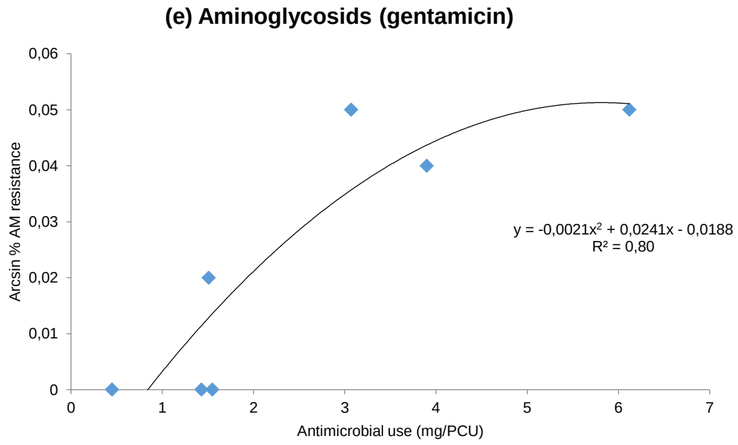
Linking antimicrobial use to antimicrobial resistance in 7 EU countries based on monitoring data

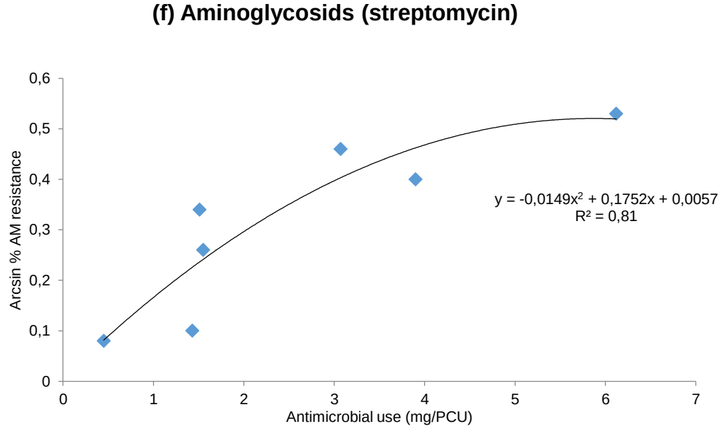












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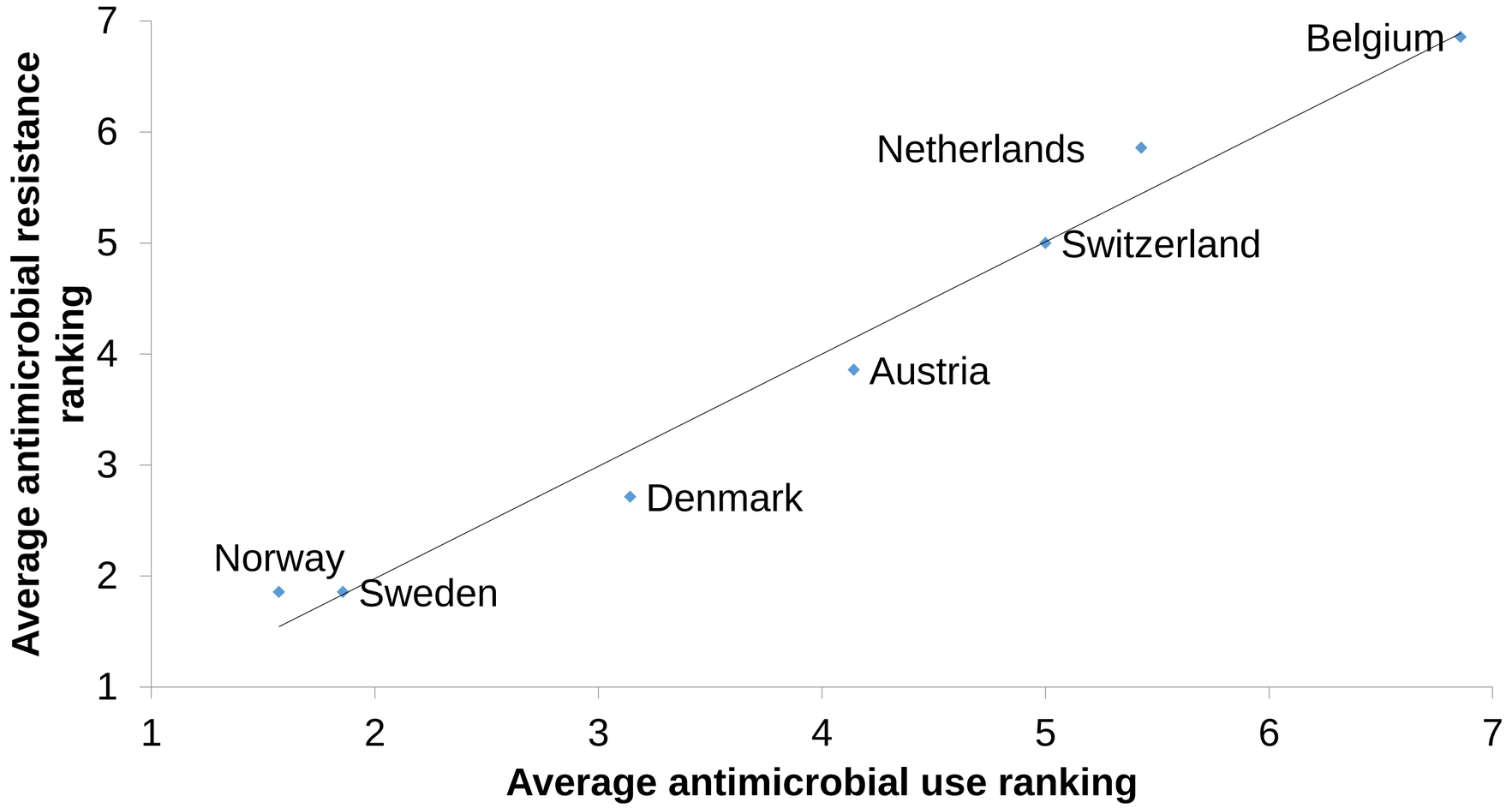
Chantziaras et al., J Antimicrob Chemother, 2014

Linking antimicrobial use to antimicrobial resistance in 7 EU countries based on monitoring data



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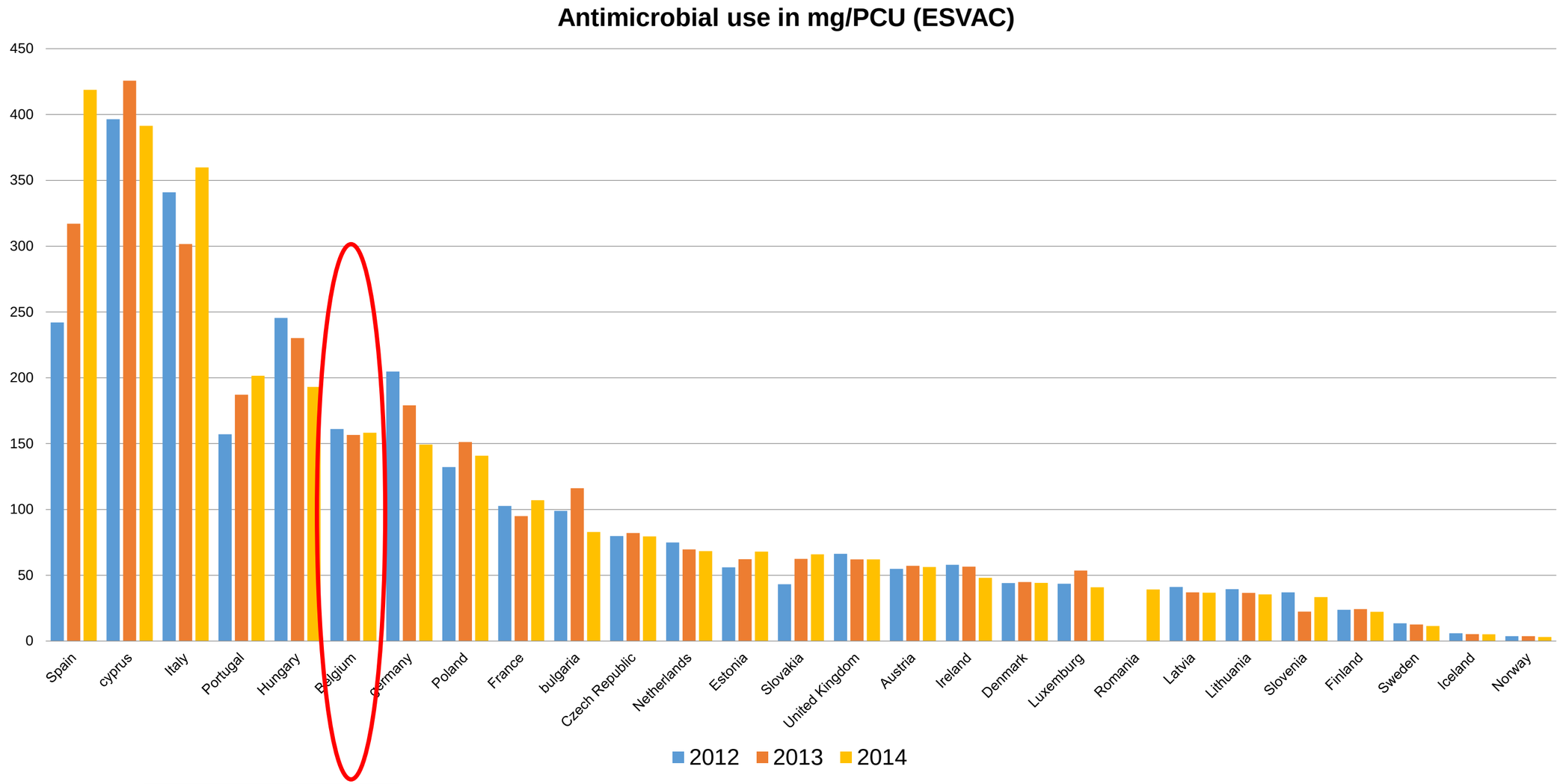
Chantziaras et al., J Antimicrob Chemother, 2014

Veterinary usage of antimicrobials in Europe: ESVAC



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Antimicrobial usage in animals in Belgium

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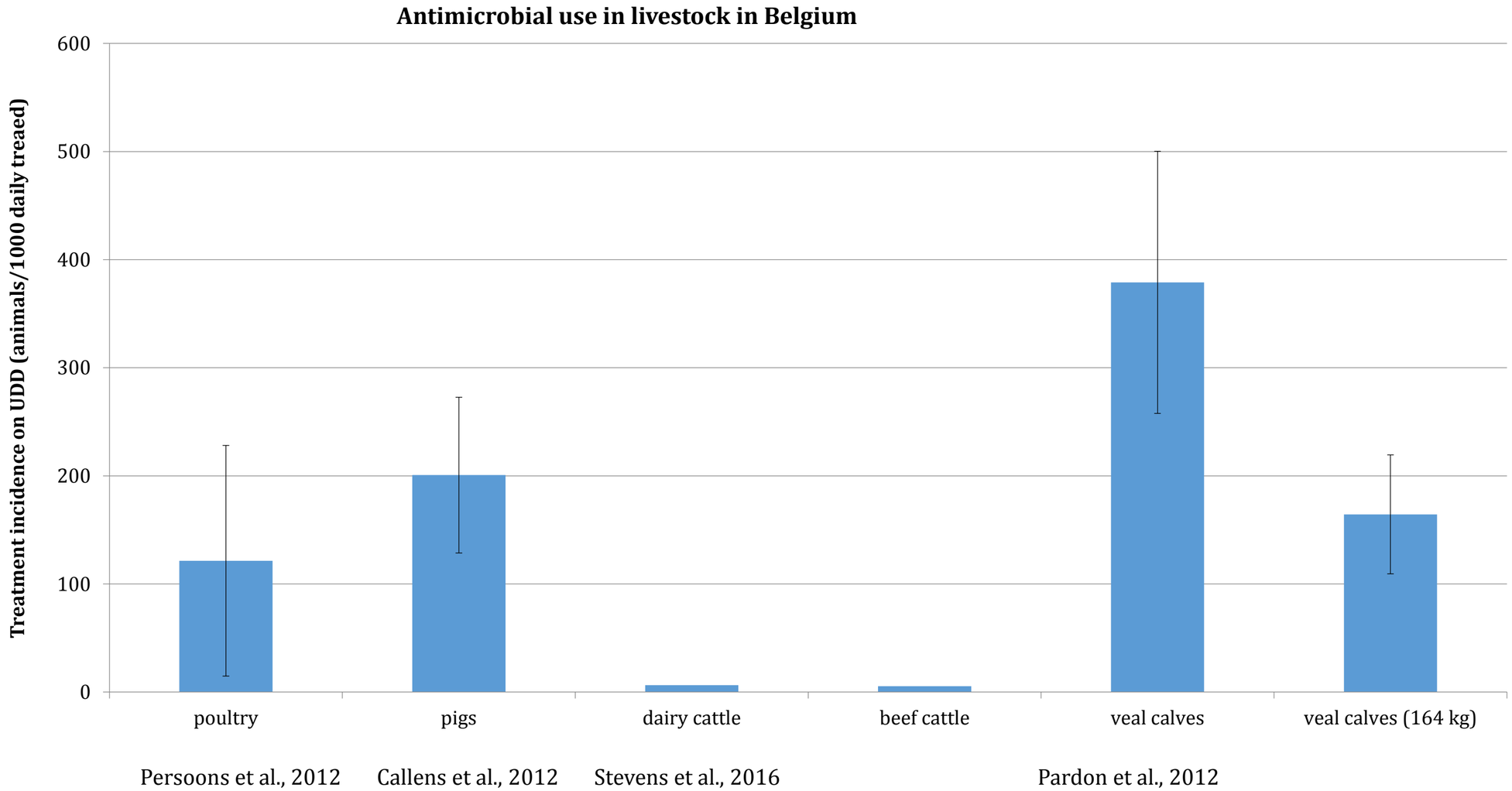
Antimicrobial usage in livestock in Belgium



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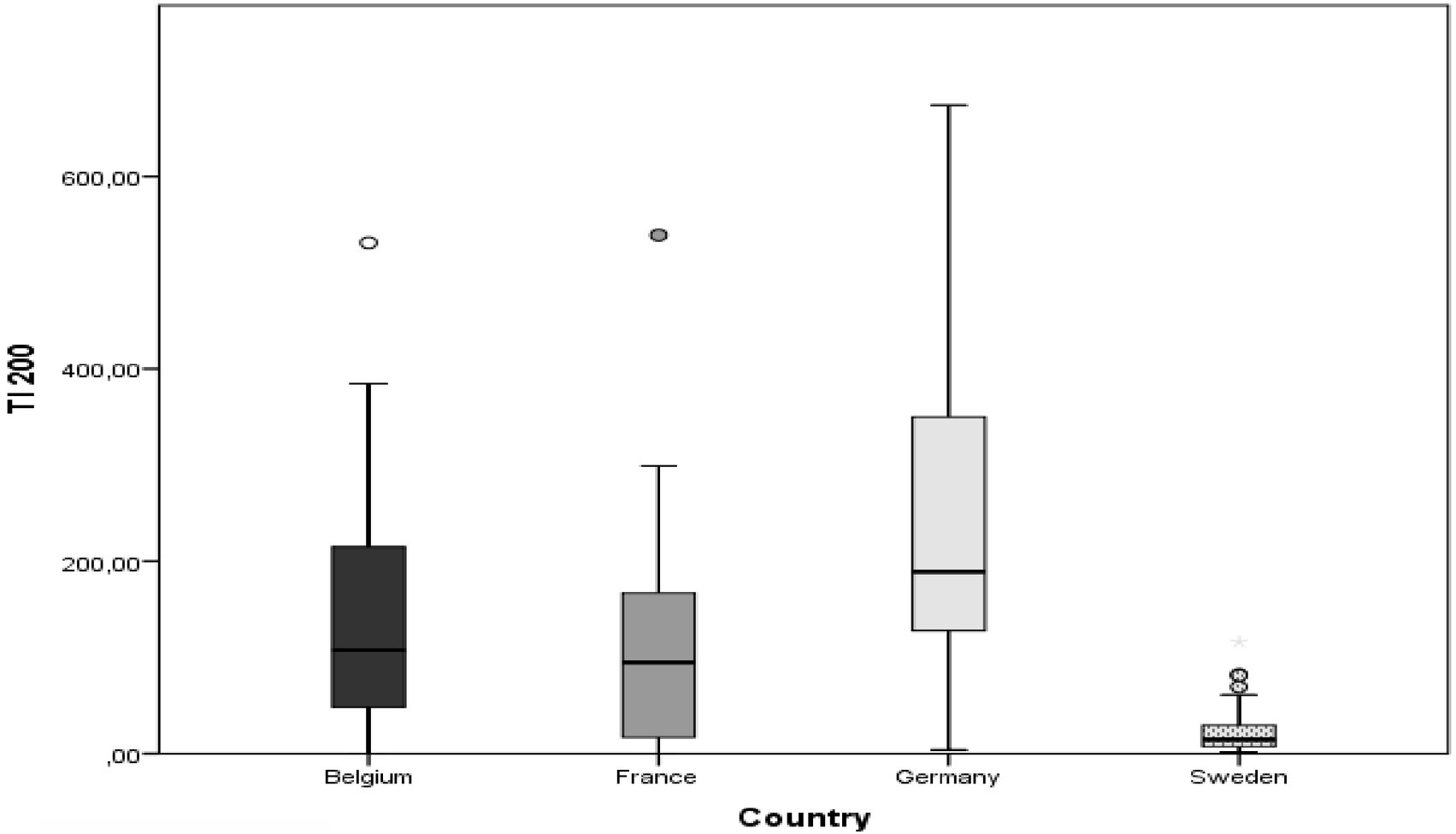
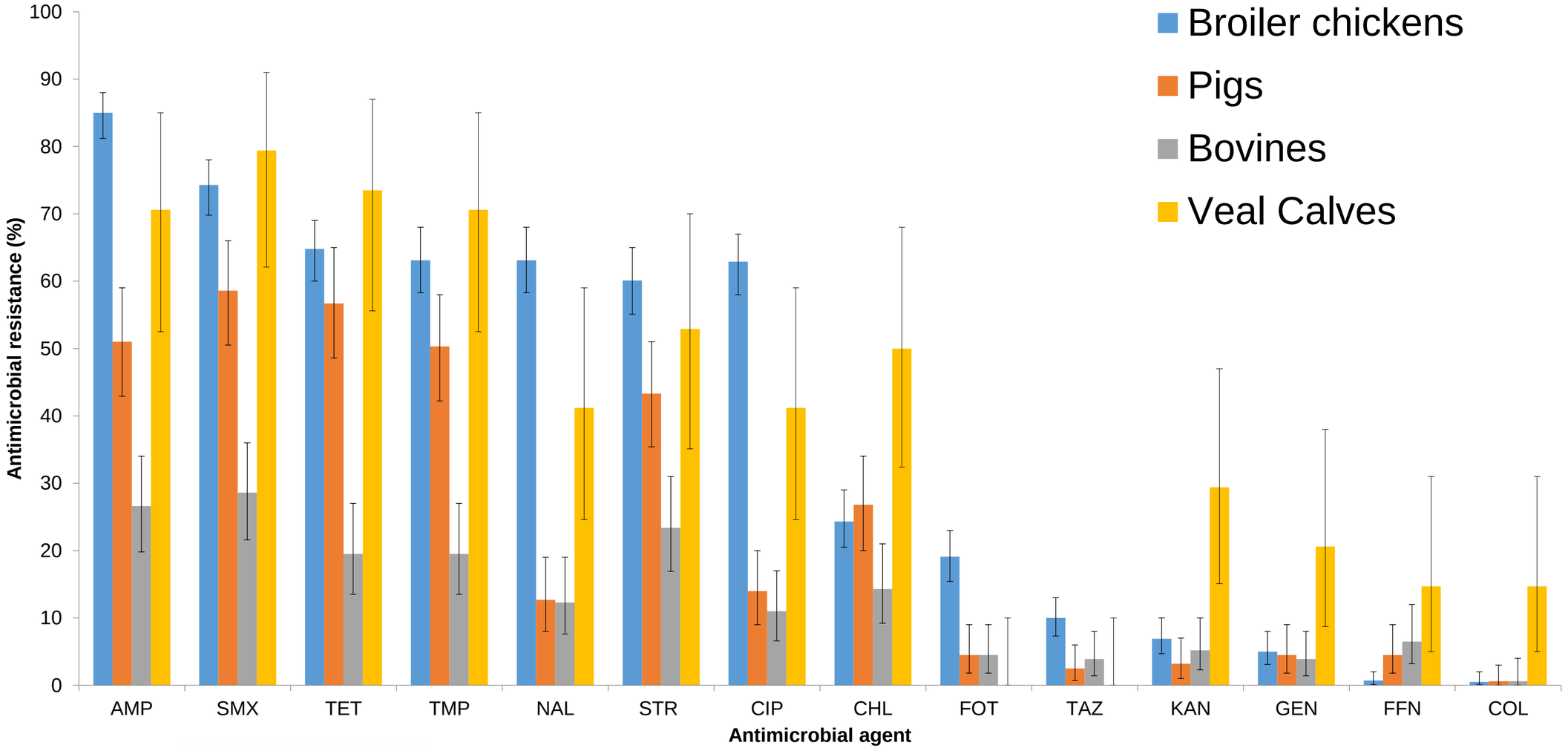
RESULTS: AMU



Sjölund et al., Prev. Vet. Med., 2016

Belgian surveillance on antimicrobial resistance 2011 (*E. coli*)



AMP: ampicillin, CHL: chloramphenicol, CIP: ciprofloxacin, COL: colistin, FFN: florfenicol, FOT: cefotaxime, GEN: gentamicin, KAN: kanamycin, NAL: nalidixic acid, SMX: sulfomethoxazole, STR: streptomycin, TAZ: ceftazidime, TET: tetracycline, TMP: trimethoprim

SETUP

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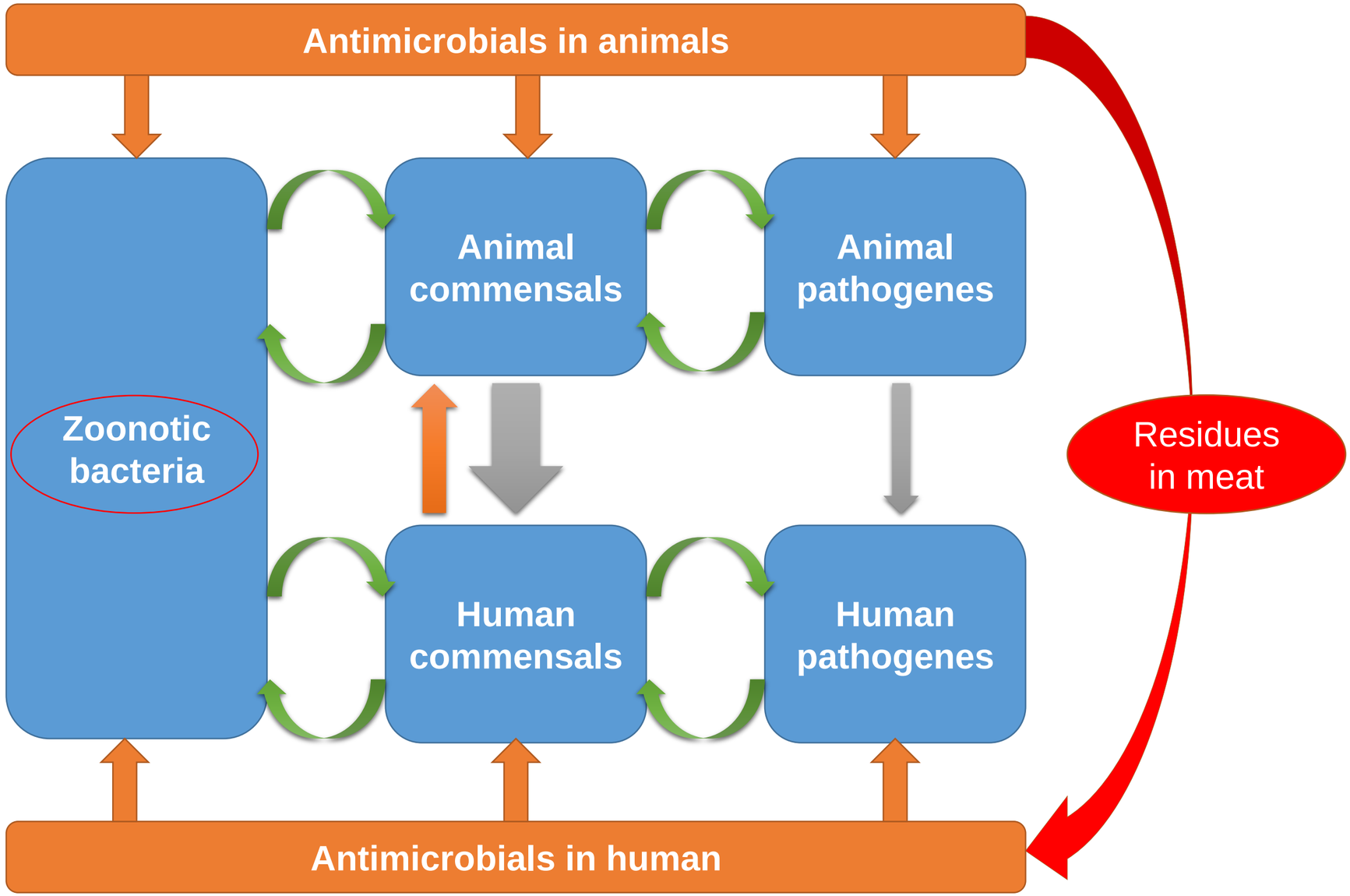

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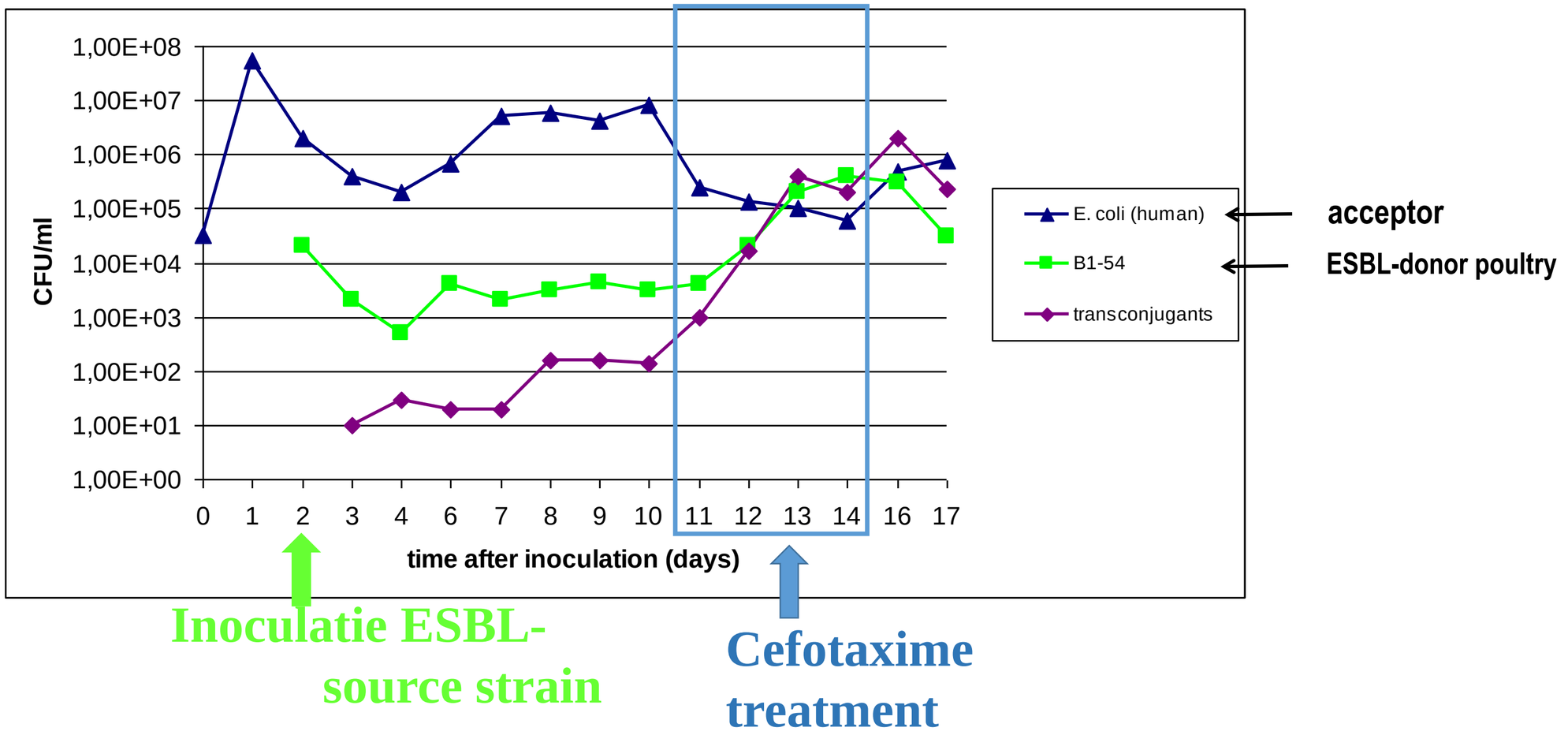
Transfer of antimicrobial resistance in the gut



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Smet et al., 2011

TRANSMISSION OF ANTIMICROBIAL RESISTANCE FROM ANIMAL-HUMAN: LITERATURE DATA

Do Human Extraintestinal *Escherichia coli* Infections Resistant to Expanded-Spectrum Cephalosporins Originate From Food-Producing Animals? A Systematic Review

Benjamin Lazarus,[1] David L. Paterson,[1] Joanne L. Mollinger,[2] and Benjamin A. Rogers[1,3]

[1]The University of Queensland, UQ Centre for Clinical Research, Royal Brisbane and Women's Hospital, Herston, [2]Biosecurity Sciences Laboratory, Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, Coopers Plains, Queensland, and [3]Monash Infectious Diseases, Monash Health, Clayton, Victoria, Australia

To find out whether food-producing animals (FPAs) are a source of extraintestinal expanded-spectrum cephalosporin-resistant *Escherichia coli* (ESCR-EC) infections in humans, Medline, Embase, and the Cochrane Database of Systematic Reviews were systematically reviewed. Thirty-four original, peer-reviewed publications were identified for inclusion. Six molecular epidemiology studies supported the transfer of resistance via whole bacterium transmission (WBT), which was best characterized among poultry in the Netherlands. Thirteen molecular epidemiology studies supported transmission of resistance via mobile genetic elements, which demonstrated greater diversity of geography and host FPA. Seventeen molecular epidemiology studies did not support WBT and two did not support mobile genetic element–mediated transmission. Four observational epidemiology studies were consistent with zoonotic transmission. Overall, there is evidence that a proportion of human extraintestinal ESCR-EC infections originate from FPAs. Poultry, in particular, is probably a source, but the quantitative and geographical extent of the problem is unclear and requires further investigation.

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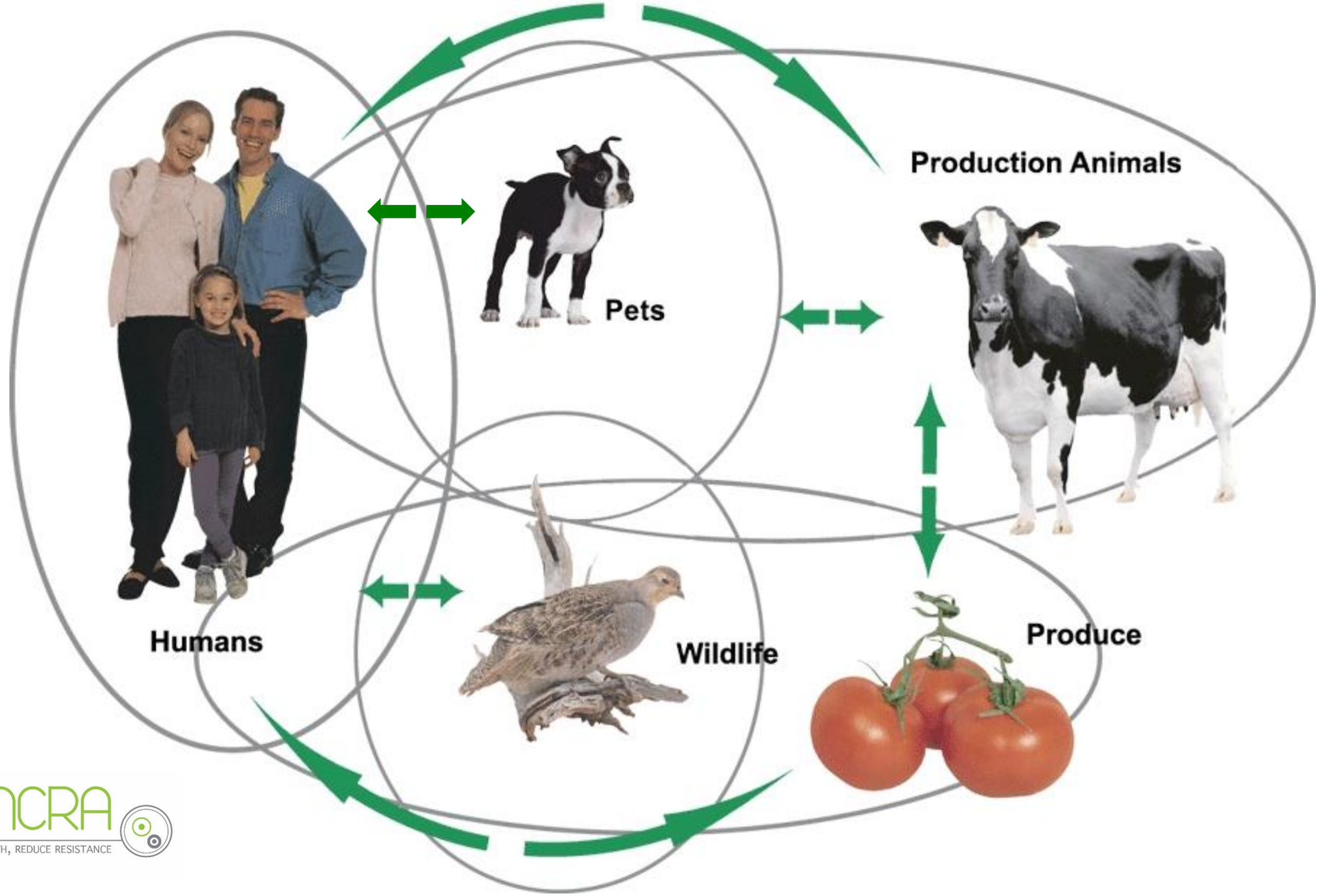
Food Safety, 2015

One health



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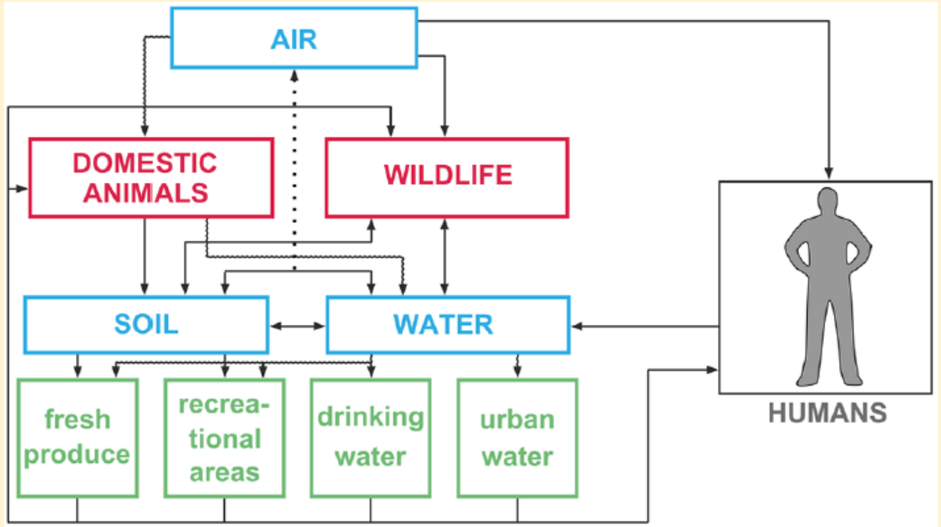
ABSTRACT: To establish a possible role for the natural environment in the transmission of clinically relevant AMR bacteria to humans, a literature review was conducted to systematically collect and categorize evidence for human exposure to extended-spectrum β-lactamase-producing Enterobacteriaceae, methicillin-resistant *Staphylococcus aureus*, and vancomycin-resistant *Enterococcus* spp. in the environment. In total, 239 datasets adhered to inclusion criteria. AMR bacteria were detected at exposure-relevant sites (35/38), including recreational areas, drinking water, ambient air, and shellfish, and in fresh produce (8/16). More datasets were available for environmental compartments (139/157), including wildlife, water, soil, and air/dust. Quantitative data from exposure-relevant sites (6/35) and environmental compartments (11/139) were scarce. AMR bacteria were detected in the contamination sources (66/66) wastewater and manure, and molecular data supporting their transmission from wastewater to the environment (1/66) were found. The abundance of AMR bacteria at exposure-relevant sites suggests risk for human exposure. Of publications pertaining to both environmental and human isolates, however, only one compared isolates from samples that had a clear spatial and temporal relationship, and no direct evidence was found for transmission to humans through the environment. To what extent the environment, compared to the clinical and veterinary domains, contributes to human exposure needs to be quantified. AMR bacteria in the environment, including sites relevant for human exposure, originate from contamination sources. Intervention strategies targeted at these sources could therefore limit emission of AMR bacteria to the environment.



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Huijbers et al., Environmental science and technology, 2015

TRANSMISSION OF ANTIMICROBIAL RESISTANCE FROM ANIMAL-HUMAN: LITERATURE DATA

Clinical Infectious Diseases

Clinical Infectious Diseases Advance

BRIEF REPORT

Evidence for Human Adaptation and Foodborne Transmission of Livestock-Associated Methicillin-Resistant *Staphylococcus aureus*

Jesper Larsen,[1] Marc Stegger,[1,5] Paal S. Andersen,[1,2] Andreas Petersen,[1] Anders R. Larsen,[1] Henrik Westh,[2,3] Yvonne Agersø,[4] Alexandra Fetsch,[7] Britta Kraushaar,[7] Annemarie Käsbohrer,[7] Andrea T. Feßler,[8] Stefan Schwarz,[8] Christiane Cuny,[9] Wolfgang Witte,[9] Patrick Butaye,[10,12] Olivier Denis,[11] Marisa Haenni,[13] Jean-Yves Madec,[13] Eric Jouy,[16] Frederic Laurent,[14,15] Antonio Battisti,[17] Alessia Franco,[17] Patricia Alba,[17] Caterina Mammina,[19] Annalisa Pantosti,[18] Monica Monaco,[18] Jaap A. Wagenaar,[20,22] Enne de Boer,[21] Engeline van Duijkeren,[23] Max Heck,[23] Lucas Domínguez,[24] Carmen Torres,[25] Myriam Zarazaga,[25] Lance B. Price,[5,6,a] and Robert L. Skov[1,a]

Fatal infections caused by methicillin-resistant *Staphylococcus aureus* of clonal complex 398: case presentations and molecular epidemiology

Christiane Berning,[1] Christian Lanckohr,[2] Helmut Baumgartner,[3] Mike Drescher,[1] Karsten Becker,[1] Georg Peters,[1] Robin Köck[4] and Barbara C. Kahl[1]

[1]Institute of Medical Microbiology, University Hospital Münster, Münster, Germany

[2]Department of Anesthesiology, Intensive Care Medicine and Pain Therapy, University Hospital Münster, Münster, Germany

[3]Division of Adult Congenital and Valvular Heart Disease, Department of Cardiovascular Medicine, University Hospital Münster, Münster, Germany

[4]Institute of Hygiene, University Hospital Münster, Münster, Germany

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VISION 2020

BOERENBOND
trouw aan land- en tuinbouw

abs
ALGEMEEN BOERENSYNDICAAT
met verstand van boeren

FWA

BEMEFA PFACA

50 % Reduction in AMU by 2020

75 % Reduction of the most critical AMU by 2020

50 % Reduction of use of AM medicated feed by 2017

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pharma.be
animal health

Vlaamse Dierenartsenvereniging
VDV

UNIVERSITEIT GENT

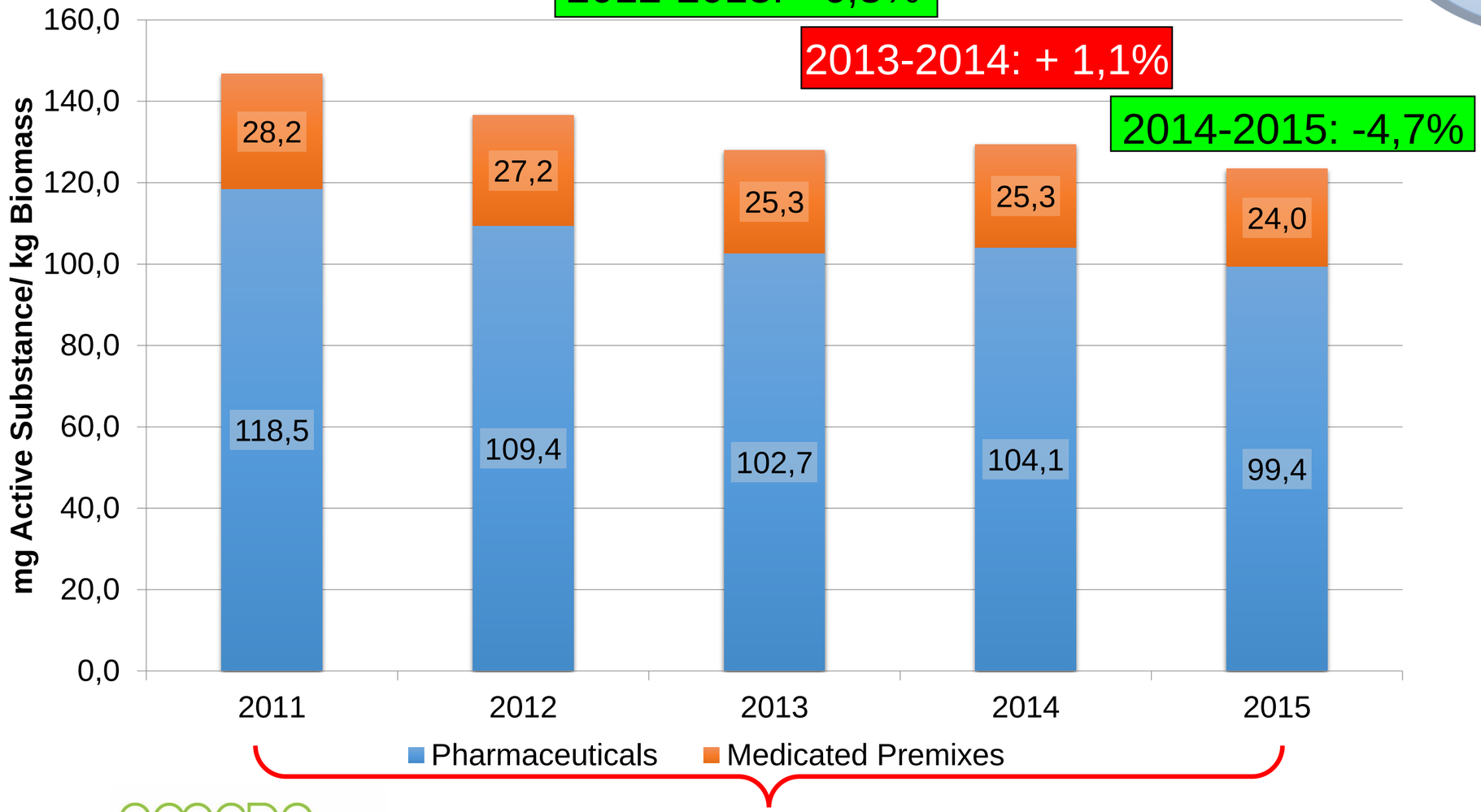
National monitoring on antimicrobial usage

2011-2012: - 6,9%

2012-2013: - 6,3%

2013-2014: + 1,1%

2014-2015: -4,7%



2011-2015: - 15,9%

VISION 2020

1. 50 % Reduction in AMU by 2020
2. 75 % Reduction of the most critical AMU by 2020
3. 50 % Reduction of use of AM medicated feed by 2017

TRENDANALYSIS ANTIMICROBIAL RESISTANCE *E. COLI* BETWEEN 2011 AND 2015

Veterinary and Agrochemical Research Centre

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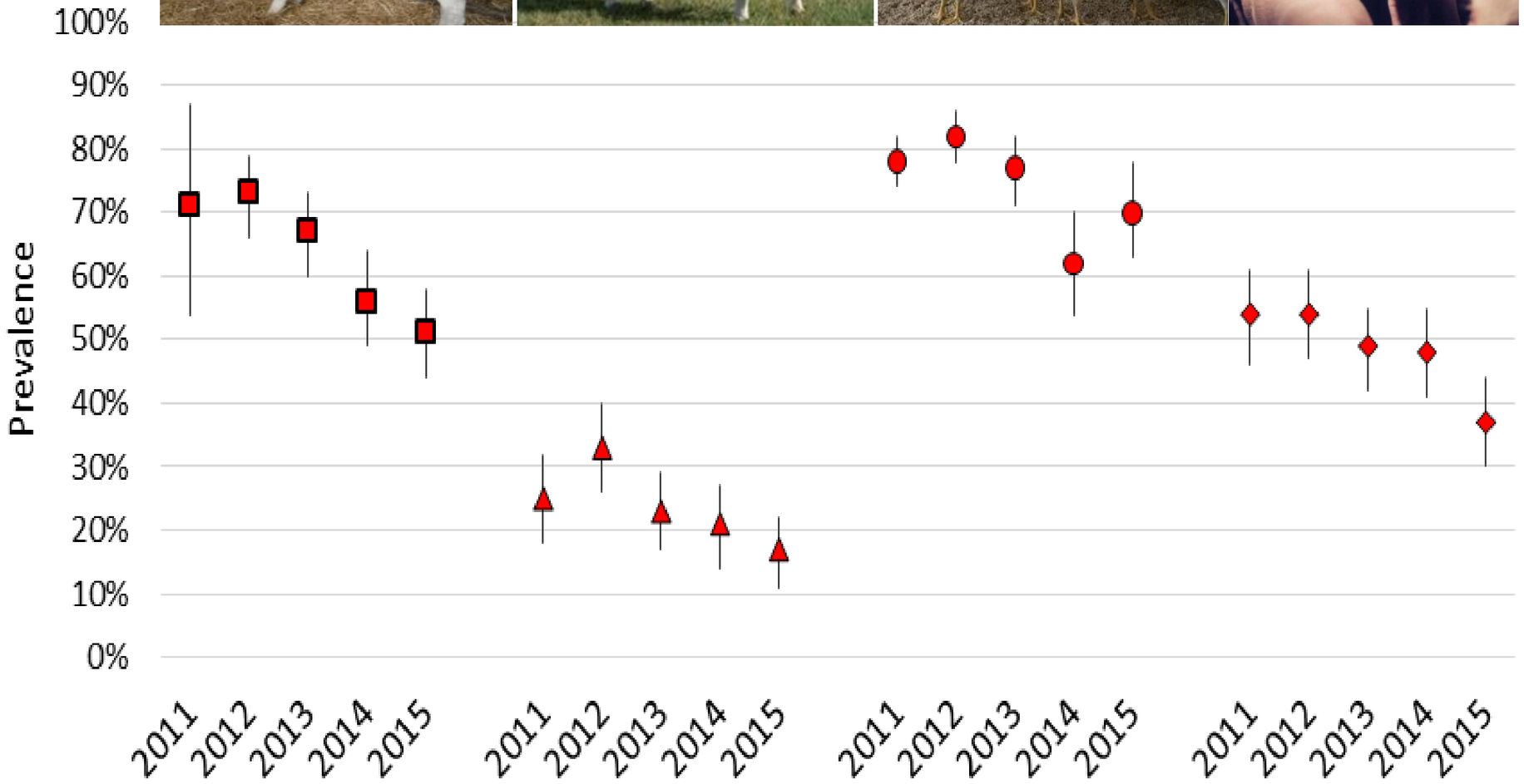
MULTI-RESISTANCE 2011-2015

Veterinary and Agrochemical Research Centre



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AMCRA - B2C

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