

L'approccio "One Health" in Italia: fact checking

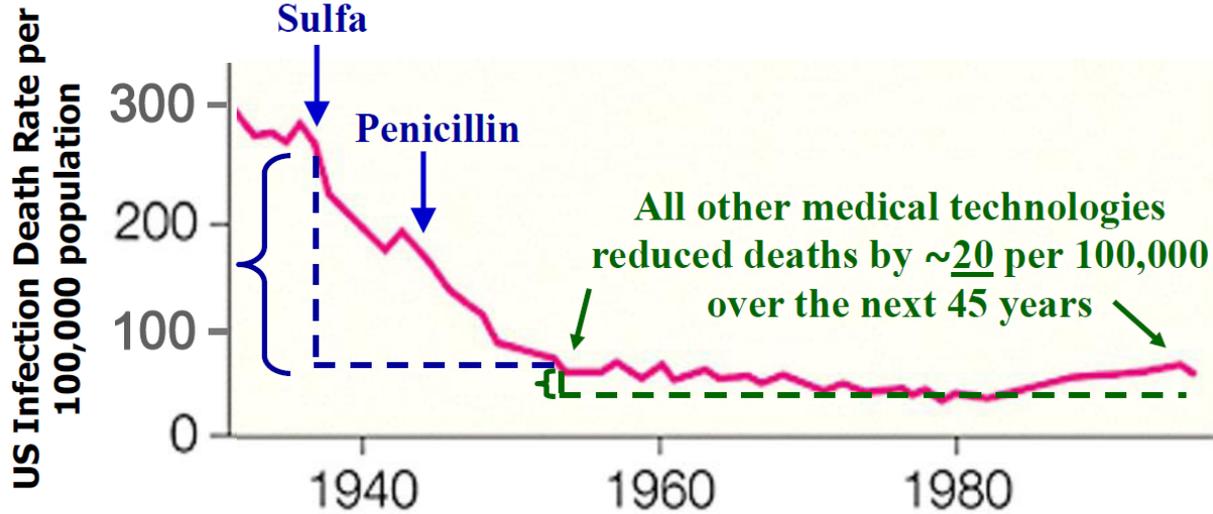
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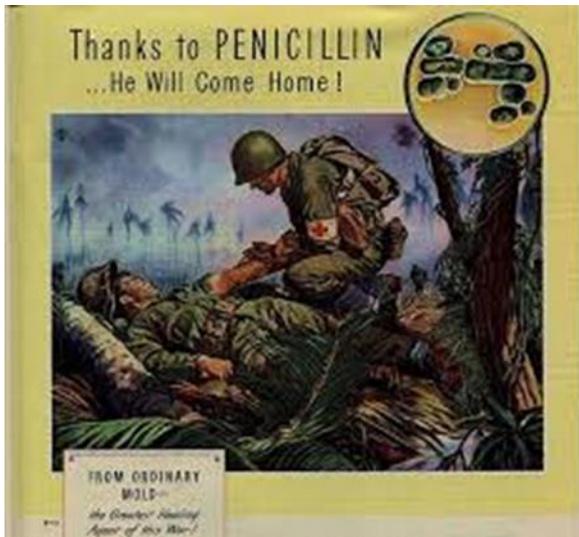
Executive Board of "Global Alliance for Infections in Surgery"

Padua, May 25, 2022

Antibiotics caused US deaths to decline by ~220 per 100,000 in 15 years

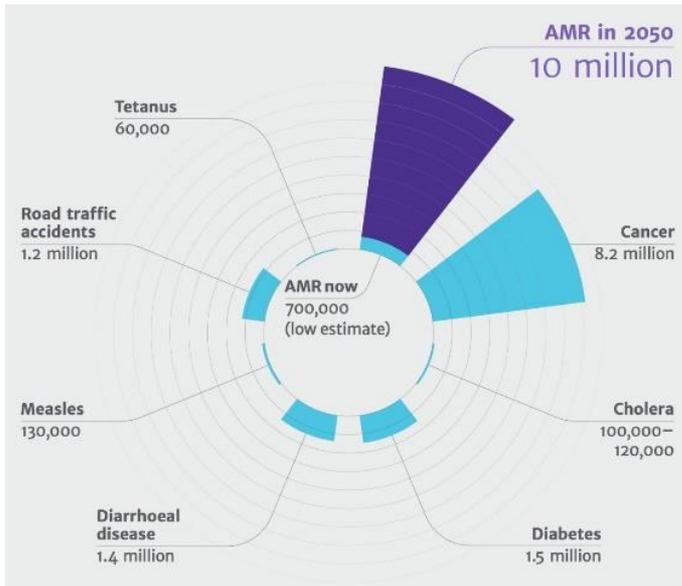
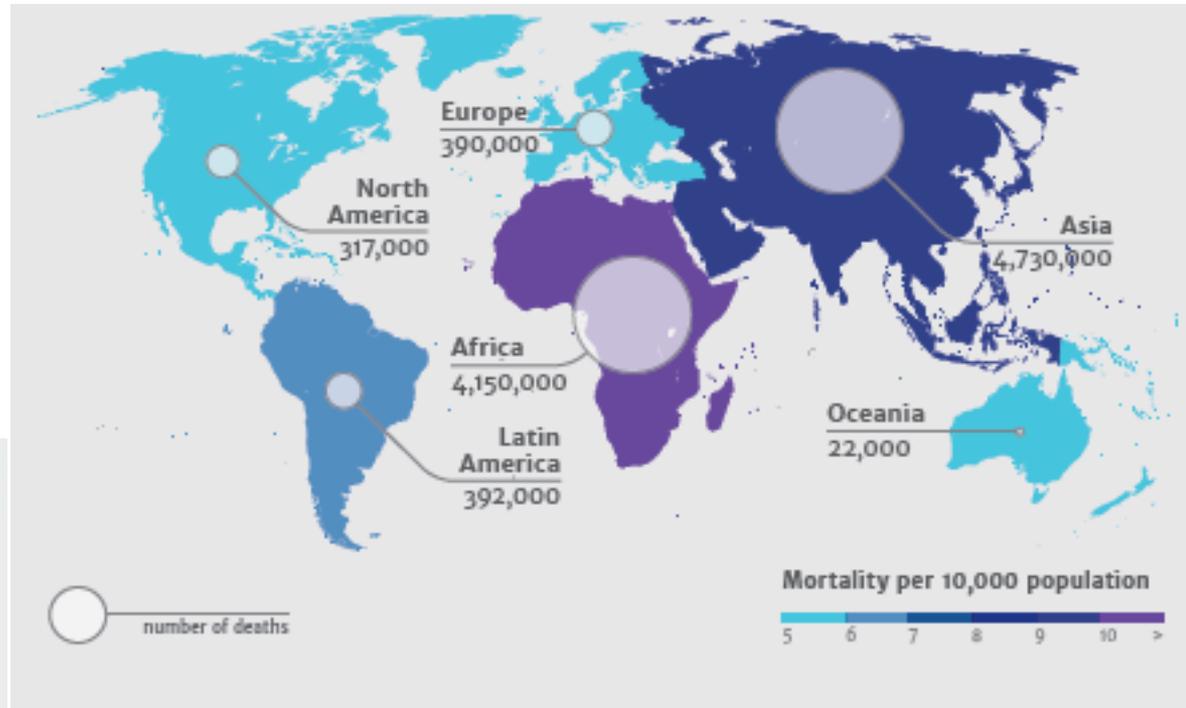


Armstrong, G. L. et al. JAMA 1999;281:61-66.



The perfect storm is approaching..

Deaths attributable to AMR every year by 2050



...and this scenario did not even take into account the upcoming pandemic “era” ...

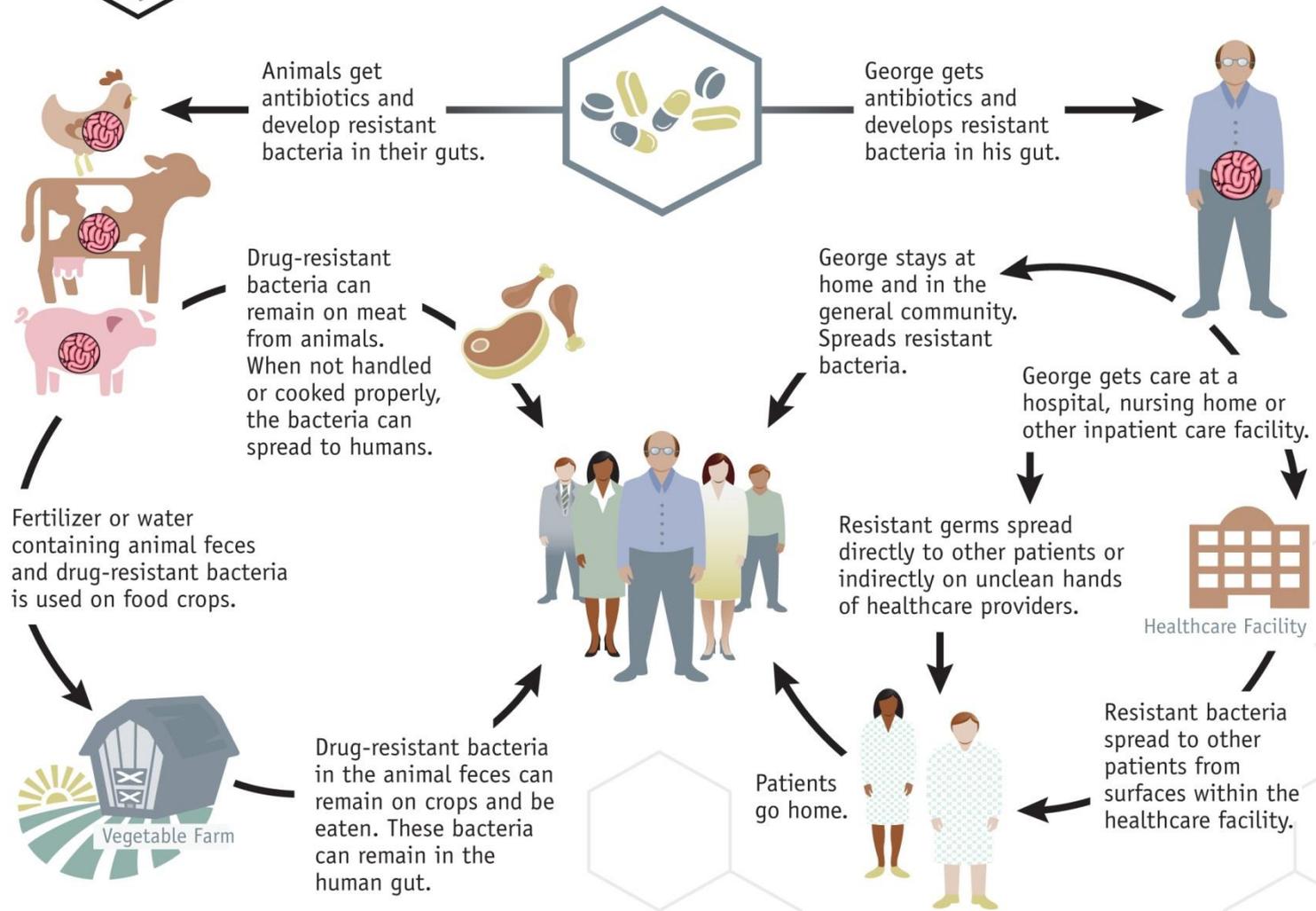
Consequences of resistance

- Even simple infections will become impossible to treat
- Many medical achievements are only possible with effective antimicrobials





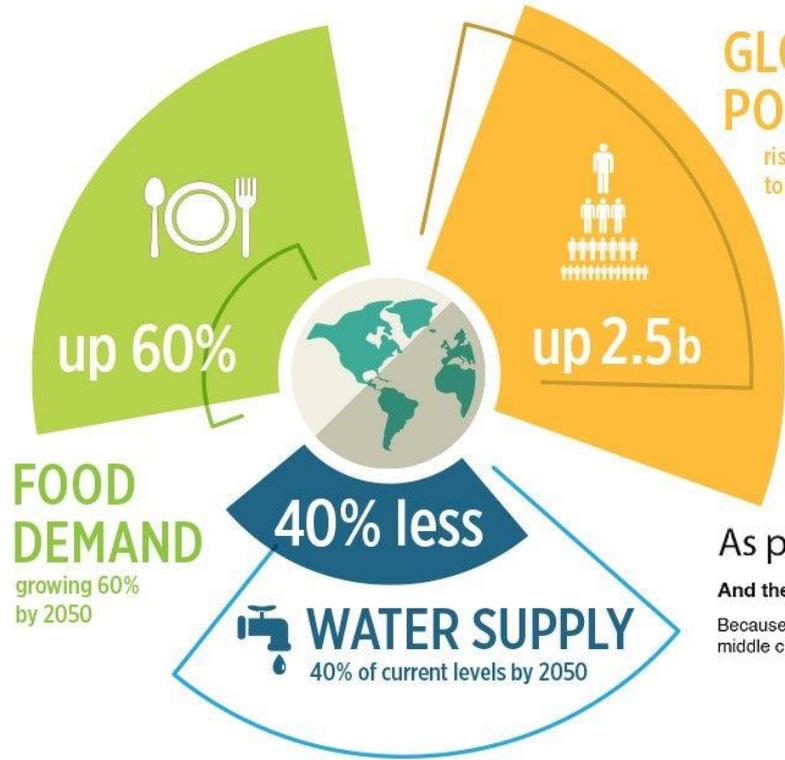
Examples of How Antibiotic Resistance Spreads



Simply using antibiotics creates resistance. These drugs should only be used to treat infections.

GLOBAL POPULATION

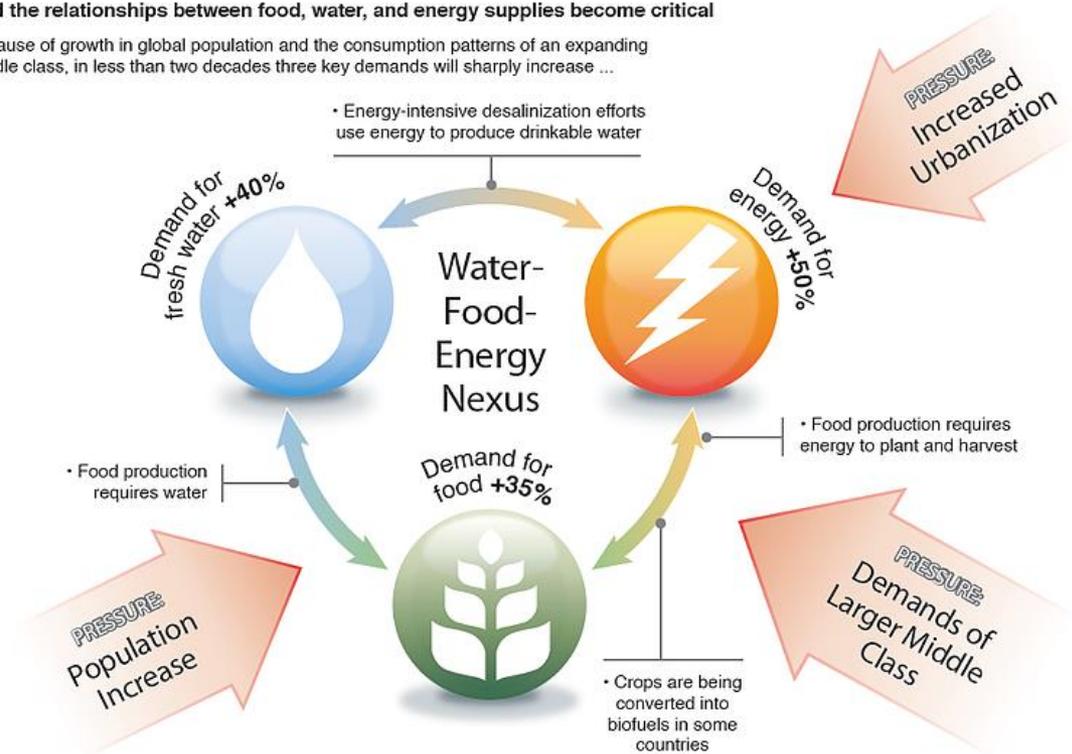
rising from 7.2 billion to 9.7 billion by 2050



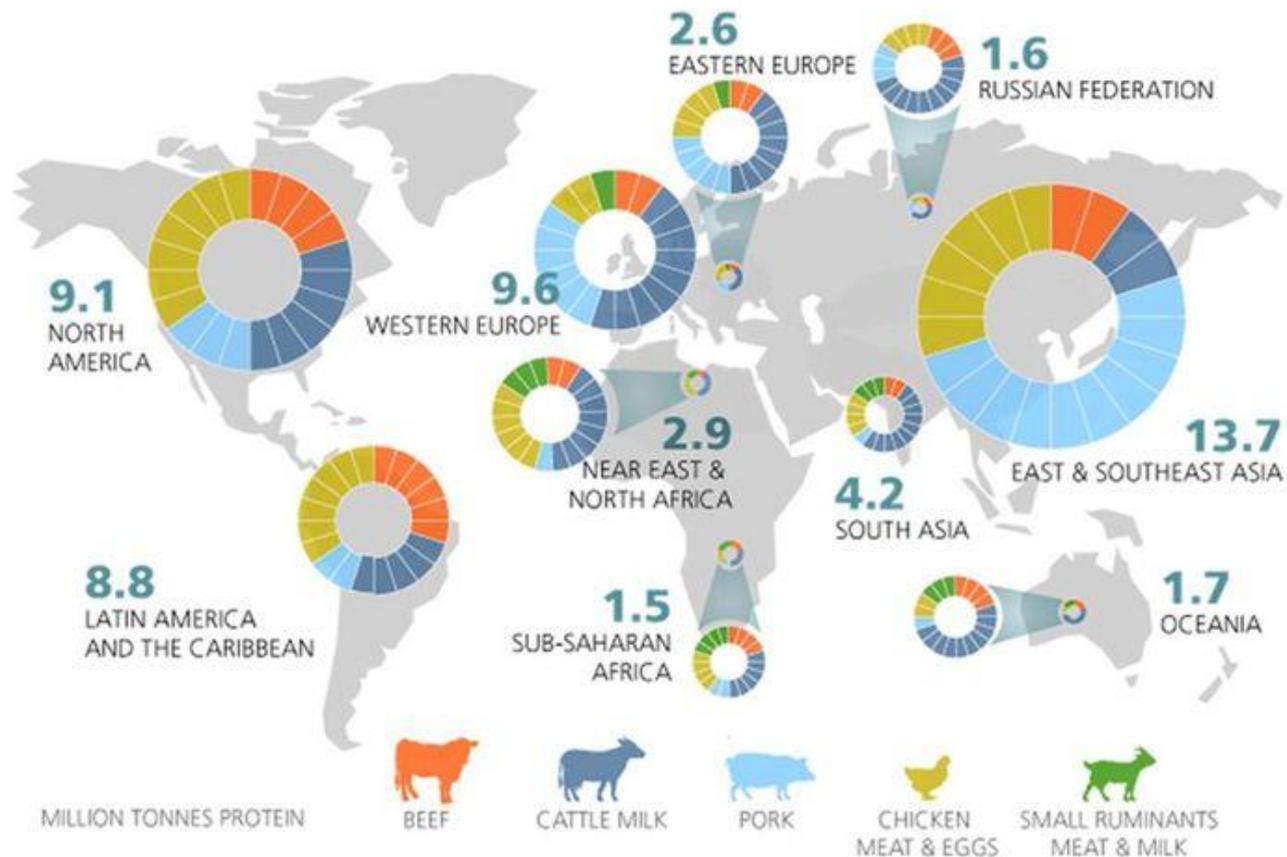
As population grows, pressures mount

And the relationships between food, water, and energy supplies become critical

Because of growth in global population and the consumption patterns of an expanding middle class, in less than two decades three key demands will sharply increase ...



LIVESTOCK PRODUCTION



Regional production. Regional total production and their profile by commodity are shown. Meat production in protein basis was calculated by using data on dressing percentages, carcass to bone-free meat and average bone-free meat protein content. Milk from all species was converted into fat and protein corrected milk. Eggs production is also expressed in protein terms.

Intensive (factory) farming: emergence and spread of AMR

- Failure of Infection Control

- Crowding
- Lack of hygiene



- Exposure to Antibiotics

- Widespread
- Prolonged
- Sub-lethal doses



- Stress reaction

- Increased shedding





SHORT COMMUNICATION

OPEN ACCESS

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Excessive use of medically important antimicrobials in food animals in Pakistan: a five-year surveillance survey

Mashkoo Mohsin ^a, Thomas P. Van Boeckel ^{b,c}, Muhammad Kashif Saleemi ^d, Muhammad Umair ^a, Muhammad Noman Naseem ^d, Cheng He ^e, Ahrar Khan ^f and Ramanan Laxminarayan ^{c,g}

^aInstitute of Microbiology, University of Agriculture, Faisalabad, Pakistan; ^bInstitute for Environmental Decisions, ETH Zurich, Zurich, Switzerland; ^cCenter for Disease Dynamics, Economics & Policy, Washington, DC, USA; ^dDepartment of Pathology, University of Agriculture, Faisalabad, Pakistan; ^eCollege of Veterinary Medicine, China Agricultural University, Beijing, China; ^fShandong Vocational Animal Science and Veterinary College, Weifang, China; ^gPrinceton Environment Institute, Princeton, NJ, USA

ABSTRACT

Demand for poultry meat is rising in low- and middle-countries, driving the expansion of large commercial farms where antimicrobials are used as surrogates for hygiene, good nutrition. This routine use of antimicrobials in animal production facilitates the emergence and spread of antibiotic-resistant pathogens. Despite potentially serious consequences for the animal industry, few studies have documented trends in antimicrobial use (AMU) at the farm level in low- and middle-income countries. The objective of this study was to estimate

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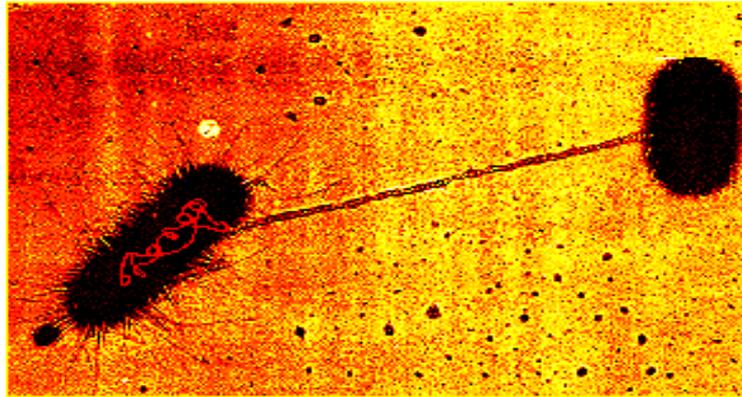
(41.71 mg/fPU), doxycycline (81.81 mg/fPU), and enrofloxacin (26.19 mg/fPU) were the most frequently used antimicrobials for prophylactic or therapeutic use. Lincomycin was the most frequently used antimicrobial used in-feed (29.09 mg/fPU). Our findings suggest that the annual consumption of antimicrobials in the broiler sector in Pakistan could be as high as 568 tons. This alarmingly high consumption estimate is the first baseline study on antimicrobial use in animals in Pakistan. Our findings call for immediate actions to reduce antimicrobial use in Pakistan, and countries with comparable farming practices.

Transfer of resistance

- Bacteria (with resistance) may transfer between animals and to humans

- Pathogens:

- *Salmonella*
- *Listeria*
- *Campylobacter*



Plasmids encoding resistance to several antibiotic classes

- Commensals (gut-flora = reservoir of resistance genes)

- *E. coli* (ESBL in chickens)



RESEARCH

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Antibiotic use on crops in low and middle-income countries based on recommendations made by agricultural advisors

Philip Taylor*  and Robert Reeder



Table 6 Ten crops on which antibiotics were most frequently recommended

Crop	Cases in which antibiotic was included on that crop
Rice	974
Tomato	143
Citrus	117
Paprika	61
Potato	36
Cabbage	35
Eggplants	25
Pumpkin	23
Onions	15
Maize	14

Crop names were grouped and harmonised to allow analysis e.g. "Citrus" is an amalgamation of all named citrus crops





Fungicide for spoilage control of citrus fruit; for treatment of dutch elm disease in trees; for control of fungal diseases of seed potatoes... to warrant **“shelf-life”**

Budavari, S. (ed.). The Merck Index - An Encyclopedia of Chemicals, Drugs, and Biologicals. Whitehouse Station, NJ: Merck and Co., Inc., 1996., p. 1585

Thiabendazole is a fungicide and parasiticide.

Thiabendazole is also a chelating agent, which means that it is used medicinally to bind metals in cases of metal poisoning, such as lead poisoning, [mercury](#) poisoning or [antimony](#) poisoning.

Thiabendazole is vermifugal and/or vermifugal against *Ascaris lumbricoides* ("common roundworm"), *Strongyloides stercoralis* (threadworm), *Necator americanus*, *Ancylostoma duodenale* (hookworm), *Trichuris trichiura* (whipworm), *Ancylostoma braziliense* (dog and cat hookworm), *Toxocara canis*, *Toxocara cati* (ascarids), and *Enterobius vermicularis* (pinworm).

Thiabendazole also suppresses egg and/or larval production and may inhibit the subsequent development of those eggs or larvae which are passed in the feces.





Sanitation and AMR

WASH

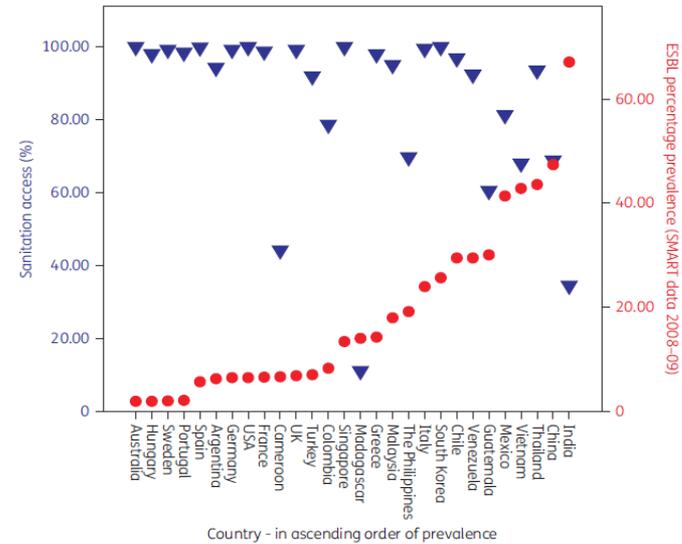


Figure 2. Sanitation access and ESBL prevalence. Sanitation access is access to improved sanitation facilities, 2008–09, as defined by WHO/UNICEF (data.worldbank.org/indicator/SH.STA.ACSN). ESBL prevalence is for 2008–09 and is derived from SMART study data.^{111,147,148} This figure appears in colour in the online version of JAC and in black and white in the print version of JAC.





Occurrence of Extended Spectrum β -Lactamases, KPC-Type, and MCR-1.2-Producing *Enterobacteriaceae* from Wells, River Water, and Wastewater Treatment Plants in Oltrepò Pavese Area, Northern Italy

Mariasofia Caltagirone¹, Elisabetta Nucleo¹, Melissa Spalla¹, Francesca Zara¹, Federica Novazzi¹, Vittoria M. Marchetti¹, Aurora Piazza^{1,2}, Ibrahim Bitar^{1,3}, Marica De Cicco¹, Stefania Paolucci⁴, Giorgio Pilla⁵, Roberta Migliavacca^{1*} and Laura Pagani¹

TABLE 5 | Phenotypical and molecular characteristics of 3GCs-resistant transconjugants; comparison with *E. coli* and *Klebsiella* spp. donors resistance and β -lactamases.

Isolates	Resistance ^a	Enzyme	Inc (Replicon) ^b
1T <i>E. coli</i>	<u>AMP</u> , <u>CAZ</u> , <u>CTX</u> , <u>FEP</u> , <u>CIP</u> , <u>PIP</u> , <u>LEV</u> , <u>MOXI</u> , <u>NOR</u> , TOB, <u>TMS</u> .	<u>CTX-M-1</u>	IncF (FIB)
3T <i>E. coli</i>	AMC, <u>AMP</u> , <u>CAZ</u> , <u>CTX</u> , <u>FEP</u> , <u>PIP</u> , ERT, MEM, TZP, <u>CIP</u> , <u>CL</u> , <u>MOXI</u> , <u>NOR</u> .	<u>CTX-M-28</u> , <u>TEM-1</u>	IncP (P), IncF(FIB)
7T <i>E. coli</i>	AMC, AMP, CAZ, PIP, TMS, <u>CO</u> .	CTX-M-1, <u>MCR-1.2</u> , SHV-12	IncX4 (X4)
11T <i>E. coli</i>	<u>AMC</u> , AMP, CAZ, <u>CTX</u> , FEP, <u>PIP</u> , TZP.	<u>SHV-12</u>	IncF (FIB)
1TP <i>E. coli</i> Broni	AMC, <u>AMP</u> , <u>CTX</u> , CAZ, <u>FEP</u> , <u>PIP</u> , <u>CIP</u> , <u>LEV</u> , <u>MOXI</u> , <u>NOR</u> , TOB, <u>CL</u> , FOS.	<u>CTX-M-28</u>	IncHI2 (HI2), IncF (FIA, FIB)
2TP <i>E. coli</i> Broni	<u>AMP</u> , CAZ, <u>CTX</u> , <u>FEP</u> , <u>PIP</u> , CIP, <u>LEV</u> , MOXI, NOR, CL.	<u>CTX-M-14</u>	IncX1(X1)
1TP <i>E. coli</i> Varzi	<u>AMP</u> , <u>CTX</u> , <u>FEP</u> , <u>PIP</u> , TMS.	<u>CTX-M-15</u>	IncT (T)
2TP <i>E. coli</i> Varzi	<u>AMP</u> , <u>CTX</u> , <u>CIP</u> , <u>LEV</u> , <u>MOXI</u> , <u>NOR</u> , PI, TMS.	<u>CTX-M-15</u>	IncF (FIA)
3TP <i>E. coli</i> Varzi	<u>AMP</u> , <u>CTX</u> , CAZ, FEP, PIP.	<u>CTX-M-15</u> , TEM-1	IncF (FIA, FIB)
6TP <i>E. coli</i> Varzi	<u>AMP</u> , <u>CTX</u> , <u>CAZ</u> , <u>PIP</u> , <u>CIP</u> , <u>LEV</u> , <u>MOXI</u> , <u>NOR</u> , <u>TOB</u> , <u>TMS</u> .	<u>CTX-M-1</u> , <u>SHV-5</u>	IncF (FIA, FIB)
1TP <i>E. coli</i> Stradella	<u>AMP</u> , <u>CTX</u> , <u>FEP</u> , CIP, CO,GM, MOXI, NOR, LEV, <u>TMS</u> , TOB.	<u>CTX-M-1</u>	IncF (FIA, FIB)
1TP <i>K. pneumoniae</i> Varzi	<u>AMP</u> , <u>CTX</u> , <u>FEP</u> , <u>PIP</u> .	<u>CTX-M-15</u>	IncF (FIA)
3TP <i>K. pneumoniae</i> Varzi	<u>AMP</u> , CAZ, <u>CTX</u> , FEP, PIP, TMS.	<u>CTX-M-28</u>	IncN (N)
5TP <i>K. pneumoniae</i> Varzi	<u>AMC</u> , <u>AMP</u> , <u>CTX</u> , CAZ, FEP, MEM, <u>ERT</u> , <u>TZP</u> , CIP, NOR, MOXI, FOS, CL, GM, TMS.	<u>TEM-1</u> , <u>KPC-2</u>	IncFIIk (FIIk, FIBKQ)
9T <i>K. oxytoca</i>	<u>AMP</u> , <u>CTX</u> , <u>FEP</u> , FOS, <u>PIP</u> .	<u>CTX-M-1</u>	IncN (N), R (NA ^c)

^aAMC, amoxicillin/clavulanic acid; AMP, ampicillin; CAZ, ceftazidime; CIP, ciprofloxacin; CL, chloramphenicol; CO, colistin; CTX, cefotaxime; ERT, ertapenem; FEP, cefepime; FOS, fosfomicin; GM, gentamicin; LEV, levofloxacin; MEM, meropenem; MOXI, moxifloxacin; NOR, norfloxacin; PIP, piperacillin; TZP, piperacillin-tazobactam; TOB, tobramycin; TMS, trimetoprim/sulfamethoxazol; ^bInc, incompatibility group; ^cNA, not assigned.

The antibiotic resistance and the determinants transferred in the transconjugants are underlined and provided in bold.



and Multi-Locus-Sequence-Typing. During one-year study and taking in account the whole Gram-negative bacterial population, an average percentage of cefotaxime resistance of 69, 32, and 10.3% has been obtained for the wastewater treatment plants, streams, and wells, respectively. These results, of concern for public health, highlight the need to improve hygienic measures to reduce the load of discharged bacteria with emerging resistance mechanisms.

Keywords: water ecosystems, Gram-negative bacteria, carbapenemases, colistin resistance, molecular characterization

MDR bacteria do not need passport to cross country borders

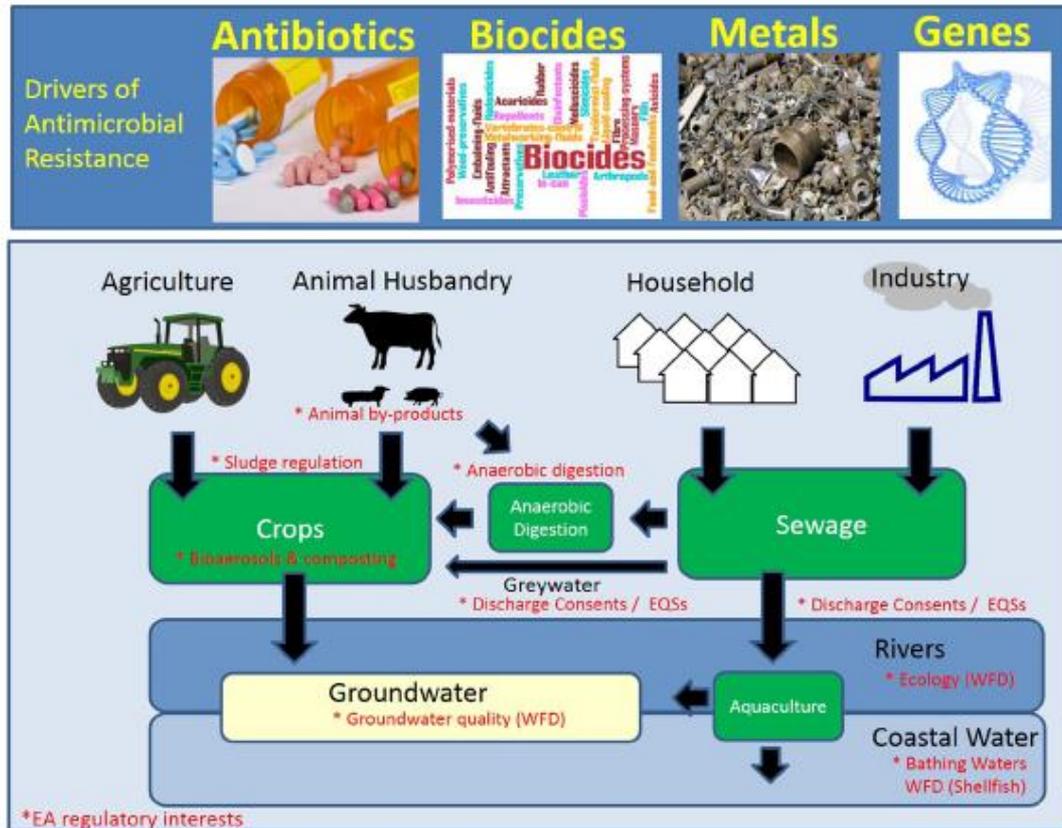
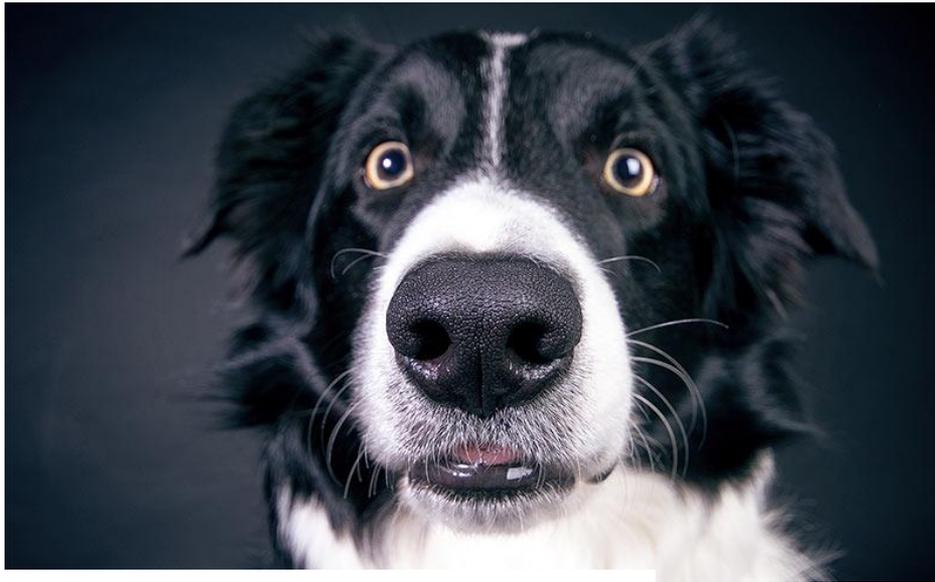


FIGURE 1 | Schematic of the hot-spots and drivers of antimicrobial resistance (AMR). The environmental compartments that are currently monitored or regulated by the Environment Agency (EA; England) are denoted by an asterisk in red. WFD, Water Framework Directive.



ORIGINAL RESEARCH
published: 16 November 2016
doi: 10.3389/fmicb.2016.01843



New Delhi Metallo- β -Lactamase-5-Producing *Escherichia coli* in Companion Animals, United States

Stephen D. Cole, Laura Peak, Gregory H. Tyson, Renate Reimschuessel, Olgica Ceric, Shelley C. Rankin

Author affiliations: University of Pennsylvania School of Veterinary Medicine, Philadelphia, Pennsylvania, USA (S.D. Cole, S.C. Rankin); Louisiana State University, Baton Rouge, Louisiana, USA (L. Peak); US Food and Drug Administration, Silver Spring, Maryland, USA (G.H. Tyson, R. Reimschuessel, O. Ceric)

DOI: <https://doi.org/10.3201/eid2602.191221>

We report isolation of a New Delhi metallo- β -lactamase-5-producing carbapenem-resistant *Escherichia coli* sequence type 167 from companion animals in the United States. Reports of carbapenem-resistant *Enterobacteriaceae* in companion animals are rare. We describe a unique cluster of *bla*_{NDM-5}-producing *E. coli* in a veterinary hospital.

High Prevalence of β -lactamase and Plasmid-Mediated Quinolone Resistance Genes in Extended-Spectrum Cephalosporin-Resistant *Escherichia coli* from Dogs in Shaanxi, China

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¹ Department of Basic Veterinary Medicine, College of Veterinary Medicine, Northwest A&F University, Yangling, China,

² Department of Aquaculture, College of Animal Science and Technology, Northwest A&F University, Yangling, China

Objective: The aim of this study was to investigate the occurrence and molecular characterization of extended-spectrum β -lactamases (ESBL), plasmid-mediated AmpC β -lactamase (pAmpC) and carbapenemases as well as plasmid-mediated quinolone-resistant (PMQR) among extended-spectrum cephalosporin-resistant (ESC-R) *Escherichia coli* from dogs in Shaanxi province in China.



Wildlife Is Overlooked in the Epidemiology of Medically Important Antibiotic-Resistant Bacteria

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ABSTRACT Wild animals foraging in the human-influenced environment are colonized by bacteria with clinically important antibiotic resistance. The occurrence of such bacteria in wildlife is influenced by various biological, ecological, and geographical factors which have not yet been fully understood. More research focusing on the human-animal-environmental interface and using novel approaches is required to understand the role of wild animals in the transmission of antibiotic resistance and to assess potential risks for the public health.

KEYWORDS antibiotics, carbapenemase, environment, landfill, transmission, wild animal

In this issue of *Antimicrob Agents Chemother*, Ahlstrom et al. (3) provide data on the first detection of CPE isolates in wildlife in the United States. By examining feces of almost 1,000 gulls from seven locations near solid waste sites in Alaska for CPE using antibiotic-supplemented medium, they obtained 7 *Escherichia coli* isolates positive for the carbapenemase genes *bla*_{KPC-2} or *bla*_{OXA-48}. Although the overall prevalence of CPE found in wild birds in this study was quite low (<1%), this observation is surprising since the surveillance of carbapenem resistance in Alaska initiated in 2013 has so far revealed only four imported cases of human infections by CPE. Three *bla*_{KPC-2}-positive *E. coli* isolates from gulls were assigned to sequence type 410 (ST410), a successful clone with reported interspecies transmission between wildlife, humans, and companion animals (4). Four highly related (only two single nucleotide polymorphisms [SNPs]) sequence type 38 (ST38) *E. coli* isolates with chromosomally integrated *bla*_{OXA-48} were found in the gulls as well. Of note, ST38 is considered a globally dispersed multidrug-

Citation Dolejska M, Literak I. 2019. Wildlife is overlooked in the epidemiology of medically important antibiotic-resistant bacteria. *Antimicrob Agents Chemother* 63:e01167-19. <https://doi.org/10.1128/AAC.01167-19>.

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The views expressed in this article do not necessarily reflect the views of the journal or of ASM.

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Review

Country Income Is Only One of the Tiles: The Global Journey of Antimicrobial Resistance among Humans, Animals, and Environment

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Sewage from Airplanes Exhibits High Abundance and Diversity of Antibiotic Resistance Genes

Stefanie Heß*, David Kneis, Tobias Österlund, Bing Li, Erik Kristiansson, and Thomas U. Berendonk

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Abstract



Environmental Science & Technology

MDR bacteria do not need passport to cross country borders



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Sewage from Airplanes Exhibits High Abundance and Diversity of Antibiotic Resistance Genes

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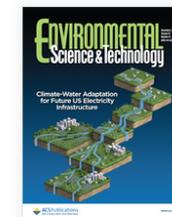
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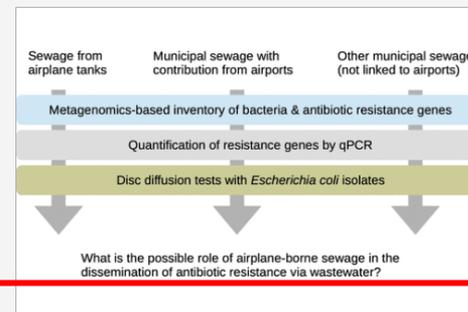
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Abstract

Abstract

Airplane sanitary facilities are shared by an international audience. We hypothesized the corresponding sewage to be an extraordinary source of antibiotic-resistant bacteria (ARB) and resistance genes (ARG) in terms of diversity and quantity. Accordingly, we analyzed ARG and ARB in airplane-borne sewage using complementary approaches: metagenomics, quantitative polymerase chain reaction (qPCR), and cultivation. For the purpose of comparison, we also quantified ARG and ARB in the inlets of municipal treatment plants with and without connection to airports. As expected, airplane sewage contained an extraordinarily rich set of mobile ARG, and the relative abundances of genes were mostly increased

compared to typical raw sewage of municipal origin. Moreover, combined resistance against third-generation cephalosporins, fluorochinolones, and aminoglycosides was unusually common (28.9%) among *Escherichia coli* isolated from airplane sewage. This percentage exceeds the one reported for German clinical isolates by a factor of 8. Our findings suggest that airplane-borne sewage can effectively contribute to the fast and global spread of antibiotic resistance.



RESEARCH

Open Access



The structure and diversity of human, animal and environmental resistomes

Chandan Pal^{1,2}, Johan Bengtsson-Palme^{1,2}, Erik Kristiansson^{2,3} and D. G. Joakim Larsson^{1,2*}



Many ARGs are widespread across environments

Out of the 325 horizontally transferable ARG types analysed, 203 ARG types were detected at least once in this

14 % of the detected ARGs were found in both humans and at least one external environment.

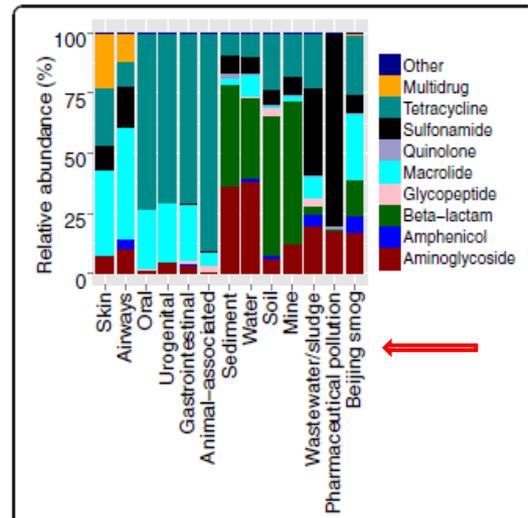


Fig. 3 Bar graph showing the relative abundance of resistance genes to different classes of antibiotics across environments

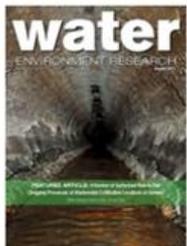
Biocide and metal resistance genes are most common in external environments

The relative abundances of biocide and metal resistance genes were, in contrast to ARGs, higher in most external environments than in human and animal microbiomes (Fig. 1b). Similarly, the richness of biocide and metal resistance genes was higher in all investigated external environments than in human body sites and animals, with Beijing smog having the highest richness of biocide and metal resistance genes (Fig. 1e). Within the human microbiome, oral and skin habitats showed higher richness of biocide/metal resistance genes than other body sites did. There was a strong correlation between the richness of biocide/metal resistance genes and the genus richness (Spearman's correlation coefficient = 0.469, $p < 0.001$) (Fig. 2c). We observed no correlation between the richness of ARGs and biocide/metal resistance genes (Spearman's correlation coefficient = -0.015, $p = 0.645$), even after controlling for the effect of taxonomic richness (partial correlation coefficient = -0.056, $p = 0.097$) (Additional file 1: Figure S4).

The Invisible Killer

*This compelling book is a must-read for all!
Damian Carrington, *The Guardian*

The Rising
Global
Threat of Air
Pollution – and
How We Can
Fight Back
Gary Fuller



Survival and antibiotic resistance of bacteria in artificial snow produced from contaminated water

Authors: Anna Lenart-Boroń; Justyna Prajsnar; Piotr Boroń

Source: Water Environment Research

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This study shows microbiological contamination of water in two main Podhale rivers, whose resources are used for artificial snowing, and the resulting snow contamination. 31 *E. coli* strains were isolated from snow at two ski stations in the studied region, their antimicrobial resistance was determined and the presence of extended-spectrum β -lactamase (ESBL) genes was searched for. The results indicate that waters of both rivers are severely contaminated, resulting in contamination of artificial snow, with among others thermotolerant *E. coli*. *E. coli* isolated from snow were most frequently resistant to ampicillin (74.19%) and amoxicillin/clavulanate (51.61% isolates). Aminoglycosides and 3rd generation cephalosporins were most efficient among the tested antimicrobials. Some bacterial strains were multi-drug resistant and three strains exhibited ESBL mechanism. Molecular analyses showed the presence of ESBL genes in the same three strains. Genetic variation among *E. coli* indicates that only some genotypes are able to survive the artificial snowing process.

Keywords: antimicrobial resistance; artificial snow; ESBL; *Escherichia coli*

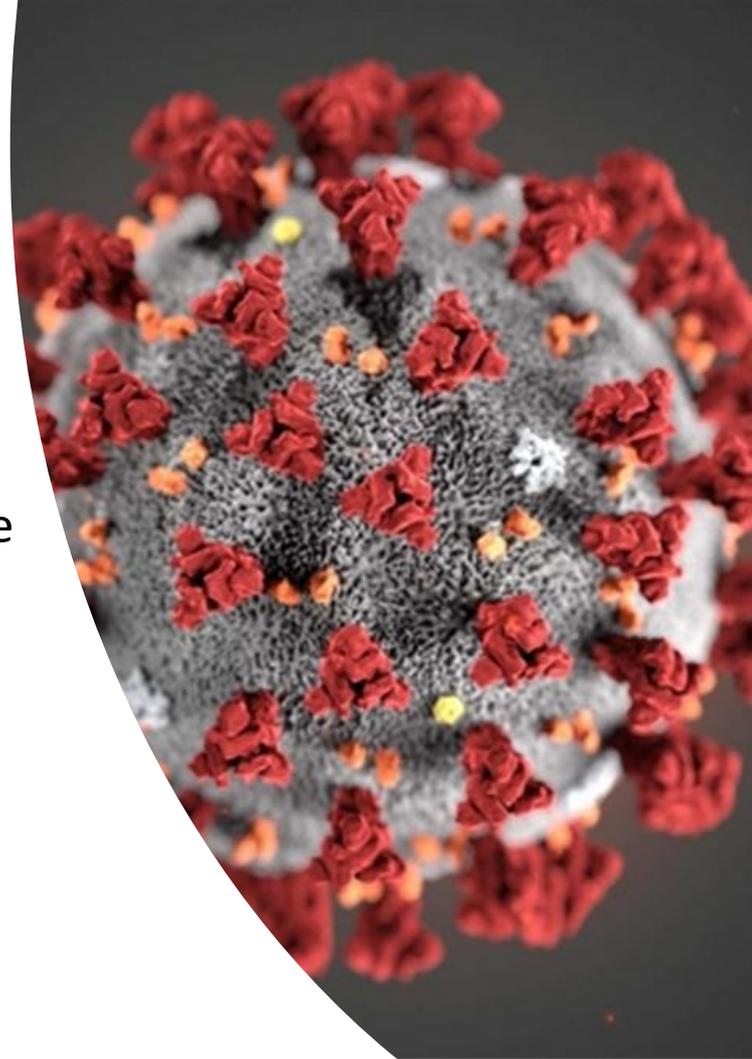


Integrated Surveillance System Data/Information for Action

- Prevalence of AMR in different reservoirs
- AMR trends over time
- Association between AMR and Use of antimicrobial agents
- Guide evidence-based policies and guidelines to control antimicrobial use in human and animals
- Identify and evaluate the effectiveness of interventions to contain the emergence and spread of resistant bacteria, or even new viruses or threats

How surveillance can improve health outcomes

- **Locally:** allow healthcare professionals to make better informed clinical decisions to ensure better patients outcomes
 - ASP, PRP, PPP
- **Nationally:** guide policy and ensure appropriate and timely public health interventions
 - PNCAR, scientific societies,
- **Globally:** provide early warnings of emerging threats and data to identify and act on long-term trends
 - WHO, CDC





MISSION REPORT

ECDC country visit to Italy to discuss antimicrobial resistance issues

9-13 January 2017

Conclusions

Observations from this ECDC country visit confirm that the AMR situation in Italian hospitals and regions poses a major public health threat to the country. The levels of carbapenem-resistant *Enterobacteriaceae* (CRE) and *Acinetobacter baumannii* have now reached hyper-endemic levels and, together with methicillin-resistant *Staphylococcus aureus* (MRSA), this situation causes Italy to be one of the Member States with the highest level of resistance in Europe.

During conversations in Italy, ECDC often gained the impression that these high levels of AMR appear to be accepted by stakeholders throughout the healthcare system, as if they were an unavoidable state of affairs.

The factors that contribute negatively to this situation seem to be:

- Little sense of urgency about the current AMR situation from most stakeholders and a tendency by many stakeholders to avoid taking charge of the problem;
- Lack of institutional support at national, regional and local level;
- Lack of professional leadership at each level;
- Lack of accountability at each level;
- Lack of coordination of the activities between and within levels.

If the current trends of carbapenem resistance and colistin resistance in gram-negative bacteria such as *Klebsiella pneumoniae* and *A. baumannii* are not reversed, key medical interventions will be compromised in the near future. Untreatable infections following organ transplantation, intensive care or major surgical interventions are now a significant possibility in many Italian hospitals.

Infections caused by resistant bacteria are associated with increased morbidity, mortality, length of hospital stay, and costs.⁹ If unrelenting attention to infection control practices is crucial, the administration of antimicrobials should no longer be considered a single's pledge, as clearly demonstrated by these recent Italian experiences. AMPs are rightly aimed at a more appropriate prescription of antimicrobials and trigger a virtuous circle through tight collaborative efforts and ever-improving educational plans: we are bound to be geared up in helping caregivers avoid collateral damage related to antimicrobial misuse while ultimately improving patient safety. In Italy, we should really start thinking about effective antimicrobial policies rather than deeming antimicrobial resistance and inappropriate antimicrobial therapy as our inescapable fate.

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One World, One Medicine, One Health

