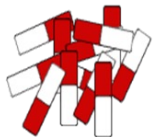
La pandemia silenciosa y la producción de alimentos

Avelino Alvarez-Ordóñez

Departamento de Higiene y Tecnología de los Alimentos, Universidad de León



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EDITORIAL

Science
AAAS

The post-antibiotic era is here

Imagine a world where routine surgery or chemotherapy is considered too dangerous because there are no drugs to prevent or treat bacterial infections. Unless researchers develop new antibiotics and therapeutics, the decimation of modern medicine will soon become a reality. Scientists have long recognized that much stronger incentives for research and development are needed to avoid this scenario. Yet, the rise of "superbugs" has continued, making a pandemic of antibiotic resistance a major threat to global health.

One could blame slowed action against antimicrobial resistance (AMR) on an upstaging by COVID-19. Health and industry sectors deferred prepandemic AMR work to focus on tracking and preventing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission. Worldwide, scientists

sistance between bacteria, new drugs that bolster host immunity against AMR, and microbiota-based therapies. To better track AMR, next-generation diagnostics are needed that use whole-genome and metagenomic sequencing and molecular techniques to detect AMR organisms in humans, animals, and the environment.

Prior to 2020, the United States started paying attention to market-place incentives that would rekindle private investment. In 2013, the US Centers for Disease Control and Prevention (CDC) released its first Antibiotics Resistance Threats report, which prompted a National Action Plan for Combating Antibiotic-Resistant Bacteria in 2015. Fortunately, last October, the strategy was renewed for 5 years, directing federal agencies to spur new drug development. Also, the Pioneering Antimicrobial Subscriptions to End Upsurging Resistance

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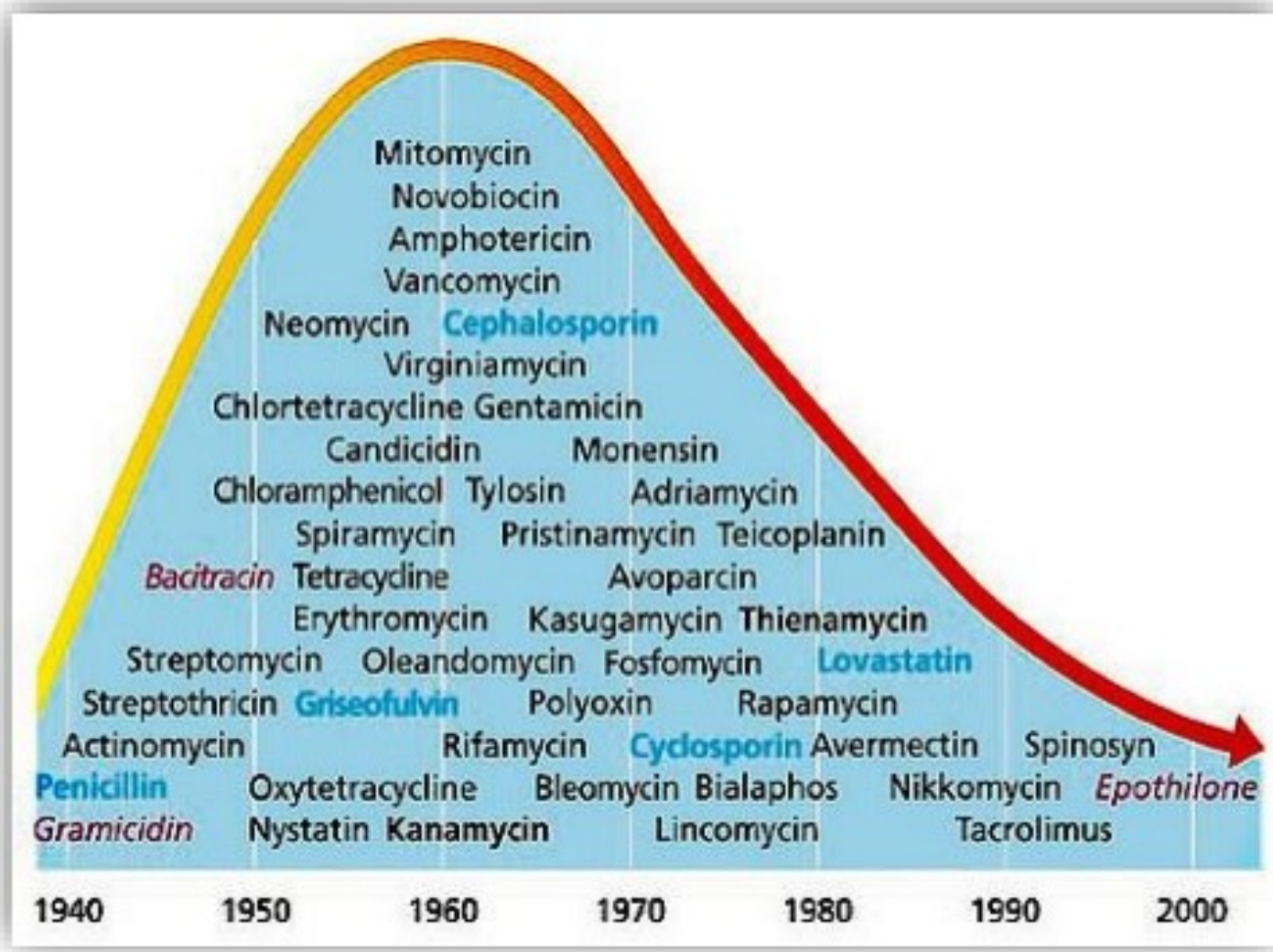

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Penicilina	• 1928 descubrimiento • 1943 uso clínico • 1954 resistencia
Estreptomicina	• 1944 descubrimiento • 1947 uso clínico • 1956 resistencia
Gentamicina	• 1963 descubrimiento • 1967 uso clínico • 1968 resistencia
Fluroquinolonas	• 1978 descubrimiento • 1982 uso clínico • 1985 resistencia

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OPEN ACCESS Freely available online

PLoS one

Antibiotic Resistance Is Prevalent in an Isolated Cave Microbiome

Kirandeep Bhullar[1], Nicholas Waglechner[1], Andrew Pawlowski[1], Kalinka Koteva[1], Eric D. Banks[2], Michael D. Johnston[2], Hazel A. Barton[2], Gerard D. Wright[1]*

1 M.G. DeGroote Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, McMaster University, Hamilton, Ontario, Canada, **2** Department of Biology, University of Akron, Akron, Ohio, United States of America

Abstract

Antibiotic resistance is a global challenge that impacts all pharmaceutically used antibiotics. The origin of the genes associated with this resistance is of significant importance to our understanding of the evolution and dissemination of antibiotic resistance in pathogens. A growing body of evidence implicates environmental organisms as reservoirs of these resistance genes; however, the role of anthropogenic use of antibiotics in the emergence of these genes is controversial. We report a screen of a sample of the culturable microbiome of Lechuguilla Cave, New Mexico, in a region of the cave that has been isolated for over 4 million years. We report that, like surface microbes, these bacteria were highly resistant to antibiotics; some strains were resistant to 14 different commercially available antibiotics. Resistance was detected to a wide range of structurally different antibiotics including daptomycin, an antibiotic of last resort in the treatment of drug resistant Gram-positive pathogens. Enzyme-mediated mechanisms of resistance were also discovered for natural and semi-synthetic macrolide antibiotics via glycosylation and through a kinase-mediated phosphorylation mechanism. Sequencing of the genome of one of the resistant bacteria identified a macrolide kinase encoding gene and characterization of its product revealed it to be related to a known family of kinases circulating in modern drug resistant pathogens. The implications of this study are significant to our understanding of the prevalence of resistance, even in microbiomes isolated from human use of antibiotics. This supports a growing understanding that antibiotic resistance is natural, ancient, and hard wired in the microbial pangenome.

RESEARCH ARTICLE

MICROBIAL ECOLOGY

The microbiome of uncontacted Amerindians

10.1126/sciadv.1500183

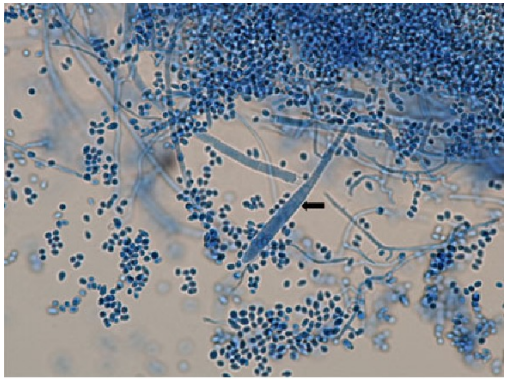
Jose C. Clemente,[1,2]* Erica C. Pehrsson,[3]* Martin J. Blaser,[4,5] Kuldip Sandhu,[5†] Zhan Gao,[5] Bin Wang,[3] Magda Magris,[6] Glida Hidalgo,[6] Monica Contreras,[7] Óscar Noya-Alarcón,[6] Orlana Lander,[8] Jeremy McDonald,[9] Mike Cox,[9] Jens Walter,[10‡] Phaik Lyn Oh,[10] Jean F. Ruiz,[11] Selena Rodriguez,[11] Nan Shen,[1] Se Jin Song,[12] Jessica Metcalf,[12] Rob Knight,[12,13§] Gautam Dantas,[3,14] M. Gloria Dominguez-Bello[5,7,11¶]

Most studies of the human microbiome have focused on westernized people with life-style practices that decrease microbial survival and transmission, or on traditional societies that are currently in transition to westernization. We characterize the fecal, oral, and skin bacterial microbiome and resistome of members of an isolated Yanomami Amerindian village with no documented previous contact with Western people. These Yanomami harbor a microbiome with the highest diversity of bacteria and genetic functions ever reported in a human group. Despite their isolation, presumably for >11,000 years since their ancestors arrived in South America, and no known exposure to antibiotics, they harbor bacteria that carry functional antibiotic resistance (AR) genes, including those that confer resistance to synthetic antibiotics and are syntenic with mobilization elements. These results suggest that westernization significantly affects human microbiome diversity and that functional AR genes appear to be a feature of the human microbiome even in the absence of exposure to commercial antibiotics. AR genes are likely poised for mobilization and enrichment upon exposure to pharmacological levels of antibiotics. Our findings emphasize the need for extensive characterization of the function of the microbiome and resistome in remote nonwesternized populations before globalization of modern practices affects potentially beneficial bacteria harbored in the human body.

Article

Emergence of methicillin resistance predates the clinical use of antibiotics

The discovery of antibiotics more than 80 years ago has led to considerable improvements in human and animal health. Although antibiotic resistance in environmental bacteria is ancient, resistance in human pathogens is thought to be a modern phenomenon that is driven by the clinical use of antibiotics[1]. Here we show that particular lineages of methicillin-resistant *Staphylococcus aureus*—a notorious human pathogen—appeared in European hedgehogs in the pre-antibiotic era. Subsequently, these lineages spread within the local hedgehog populations and between hedgehogs and secondary hosts, including livestock and humans. We also demonstrate that the hedgehog dermatophyte *Trichophyton erinacei* produces two β-lactam antibiotics that provide a natural selective environment in which methicillin-resistant *S. aureus* isolates have an advantage over susceptible isolates. Together, these results suggest that methicillin resistance emerged in the pre-antibiotic era as a co-evolutionary adaptation of *S. aureus* to the colonization of dermatophyte-infected hedgehogs. The evolution of clinically relevant antibiotic-resistance genes in wild animals and the connectivity of natural, agricultural and human ecosystems demonstrate that the use of a One Health approach is critical for our understanding and management of antibiotic resistance, which is one of the biggest threats to global health, food security and development.



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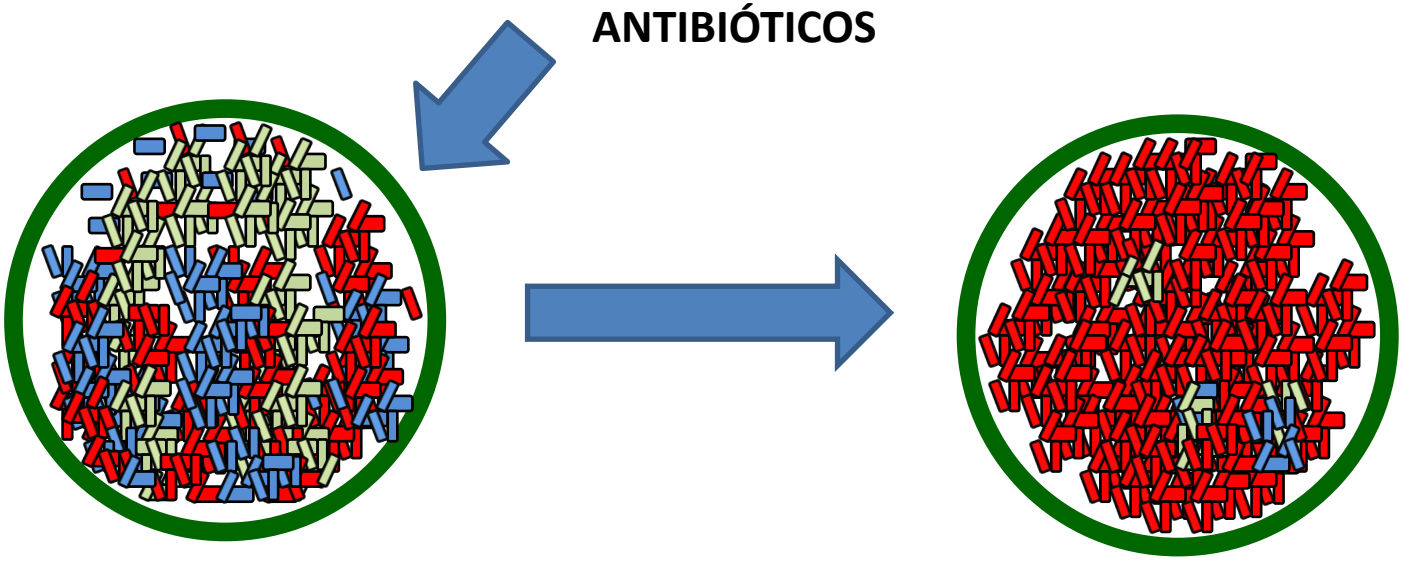

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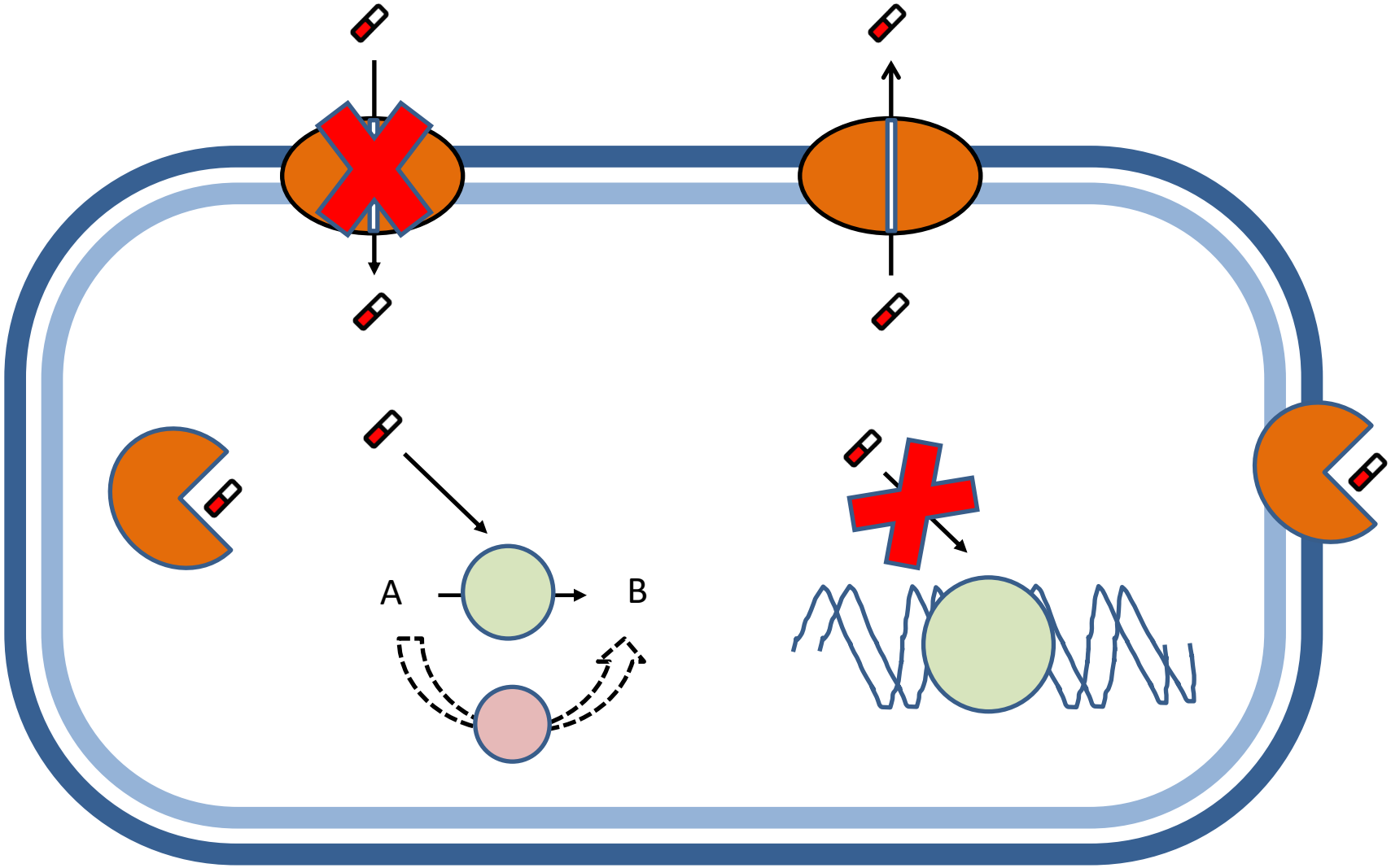

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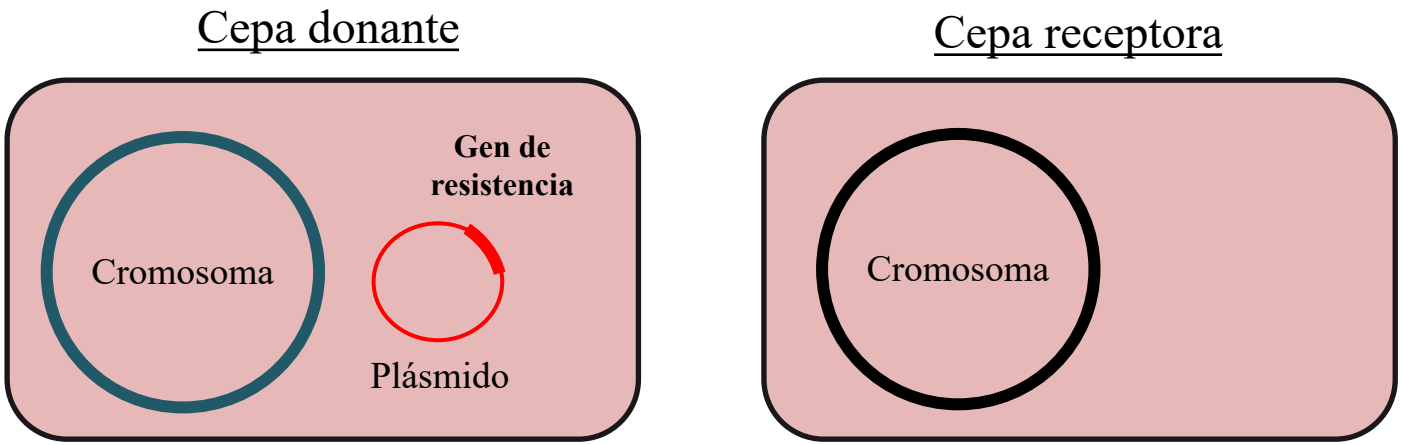
TRANSFERENCIA HORIZONTAL



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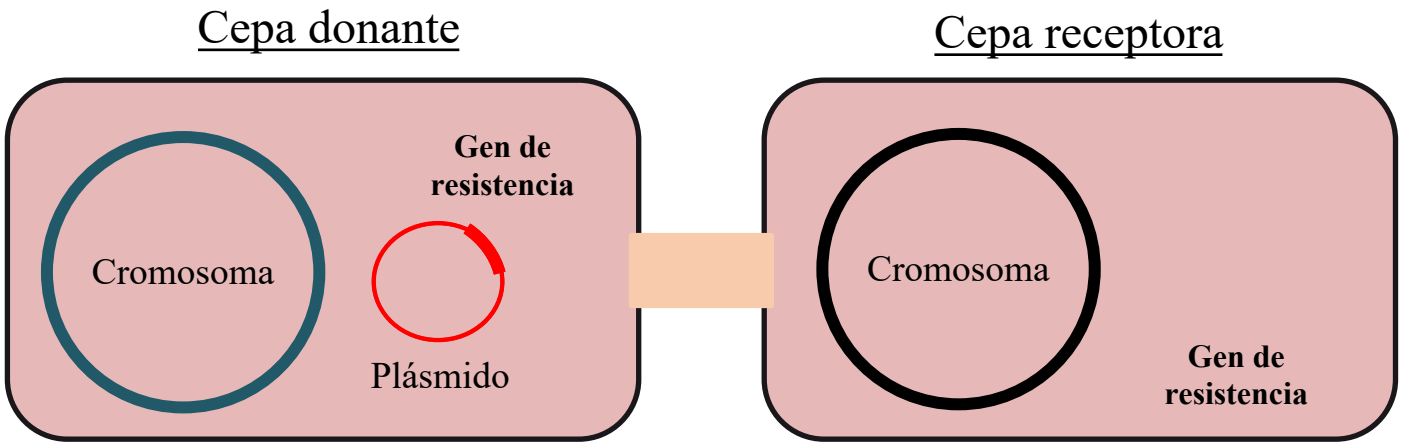
HORIZONTAL TRANSFER



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Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis

*Antimicrobial Resistance Collaborators**

THE LANCET

Lancet 2022; 399: 629–55

Published Online January 20, 2022 https://doi.org/10.1016/S0140-6736(21)02724-0

See Comment page 606

*Collaborators are listed at the end of the paper

Summary

Background Antimicrobial resistance (AMR) poses a major threat to human health around the world. Previous publications have estimated the effect of AMR on incidence, deaths, hospital length of stay, and health-care costs for specific pathogen–drug combinations in select locations. To our knowledge, this study presents the most comprehensive estimates of AMR burden to date.

Methods We estimated deaths and disability-adjusted life-years (DALYs) attributable to and associated with bacterial AMR for 23 pathogens and 88 pathogen–drug combinations in 204 countries and territories in 2019. We obtained

	Associated with resistance				Attributable to resistance			
	Deaths	YLLs	DALYs	YLDs	Deaths	YLLs	DALYs	YLDs
Counts, thousands								
Global	4950 (3620–6570)	189 000 (145 000–245 000)	192 000 (146 000–248 000)	2290 (1520–3450)	1270 (911–1710)	47 600 (35 000–63 400)	47 900 (35 300–63 700)	275 (161–439)
Central Europe, eastern Europe, and central Asia	283 (190–403)	7530 (5240–10 500)	7630 (5320–10 600)	102 (69–140)	73·7 (48·7–105)	1980 (1350–2790)	1990 (1360–2800)	9·95 (4·79–16·8)
High income	604 (434–824)	10 100 (6960–14 200)	10 300 (7040–14 400)	123 (79·7–183)	141 (98·6–197)	2390 (1620–3400)	2410 (1640–3420)	20·2 (12·7–31·2)
Latin America and Caribbean	338 (243–453)	9550 (6770–12 900)	9640 (6830–13 100)	97·2 (63·2–146)	84·3 (60·3–117)	2370 (1660–3310)	2380 (1680–3330)	16 (9·79–24·9)
North Africa and Middle East	256 (174–362)	9970 (6880–13 900)	10 100 (6970–14 000)	116 (73·4–176)	68·3 (45·6–99)	2590 (1770–3700)	2610 (1790–3720)	20·7 (12–33·5)
South Asia	1390 (1030–1830)	58 900 (44 800–76 300)	59 900 (45 700–77 500)	1000 (638–1550)	389 (273–538)	16 000 (11 500–21 600)	16 100 (11 600–21 700)	111 (58·5–188)
Southeast Asia, east Asia, and Oceania	1020 (678–1460)	27 500 (18 700–38 600)	27 900 (19 100–39 100)	437 (256–776)	254 (167–369)	6830 (4620–9840)	6870 (4670–9890)	45·6 (25–80·1)
Sub-Saharan Africa	1070 (847–1340)	65 800 (51 400–83 600)	66 200 (51 800–84 000)	416 (270–599)	255 (196–331)	15 400 (11 700–19 900)	15 500 (11 800–20 000)	51·1 (30·2–81·8)

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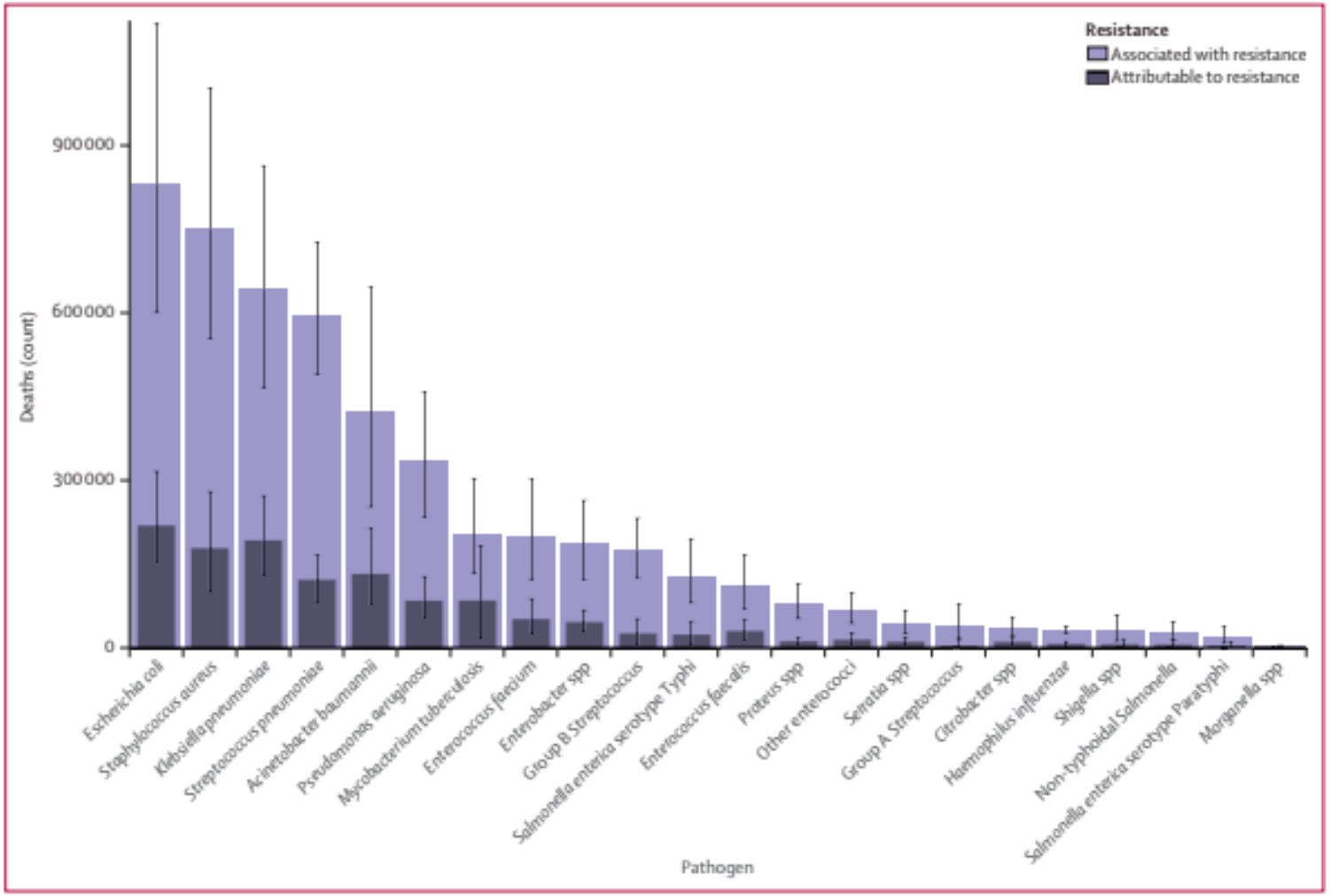

***Figure 4*: Global deaths (counts) attributable to and associated with bacterial antimicrobial resistance by pathogen, 2019**
Estimates were aggregated across drugs, accounting for the co-occurrence of resistance to multiple drugs. Error bars show 95% uncertainty intervals.

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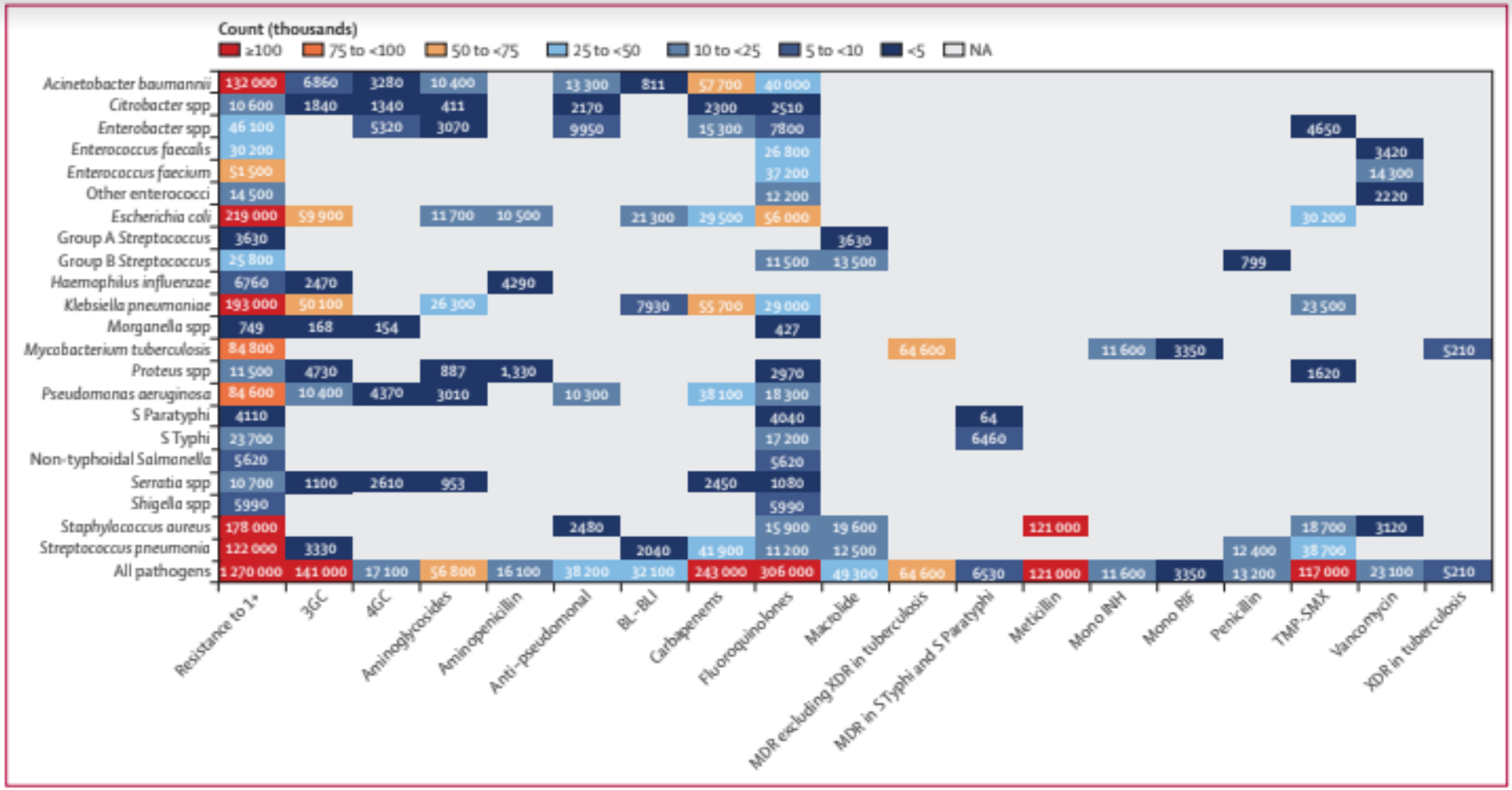

Figure 6: **Global deaths (counts) attributable to bacterial antimicrobial resistance by pathogen-drug combination, 2019**

For this figure, only deaths attributable to resistance, not deaths associated with resistance, are shown due to the very high levels of correlation for resistance patterns between some drugs. 3GC=third-generation cephalosporins. 4GC=fourth-generation cephalosporins. Anti-pseudomonal=anti-pseudomonal penicillin or beta-lactamase inhibitors. BL-BLI=β-lactam or β-lactamase inhibitors. MDR=multidrug resistance. Mono INH=isoniazid mono-resistance. Mono RIF=rifampicin mono-resistance. NA=not applicable. Resistance to 1+=resistance to one or more drug. S Paratyphi=*Salmonella enterica* serotype Paratyphi. S Typhi=*S enterica* serotype Typhi. TMP-SMX=trimethoprim-sulfamethoxazole. XDR=extensive drug resistance.

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American Society for Microbiology
Clinical Microbiology Reviews
Volume 33, Issue 3, 17 June 2020
https://doi.org/10.1128/CMR.00181-19

Review

Antimicrobial Resistance in ESKAPE Pathogens

David M. P. De Oliveira[a,b], Brian M. Forde[a,b], Timothy J. Kidd[a,b], Patrick N. A. Harris[b,c], Mark A. Schembri[a,b], Scott A. Beatson[a,b], David L. Paterson[b,c], and Mark J. Walker[a,b]

[a]School of Chemistry and Molecular Biosciences, The University of Queensland, QLD, Australia
[b]Australian Infectious Diseases Research Centre, The University of Queensland, QLD, Australia
[c]UQ Centre for Clinical Research, The University of Queensland, QLD, Australia

SUMMARY

Antimicrobial-resistant ESKAPE (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter species) pathogens represent a global threat to human health. The acquisition of antimicrobial resistance genes by ESKAPE pathogens has reduced the treatment options for serious infections, increased the burden of disease, and increased death rates due to treatment failure and requires a coordinated global response for antimicrobial resistance surveillance. This looming health threat has restimulated interest in the development of new antimicrobial therapies, has demanded the need for better patient care, and has facilitated heightened governance over stewardship practices.

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World Health Organization

Priority 1: CRITICAL[#]

Acinetobacter baumannii, carbapenem-resistant

Pseudomonas aeruginosa, carbapenem-resistant

Enterobacteriaceae*, carbapenem-resistant, 3rd generation cephalosporin-resistant

Priority 2: HIGH

Enterococcus faecium, vancomycin-resistant

Staphylococcus aureus, methicillin-resistant, vancomycin intermediate and resistant

Helicobacter pylori, clarithromycin-resistant

Campylobacter, fluoroquinolone-resistant

Salmonella *spp.*, fluoroquinolone-resistant

Neisseria gonorrhoeae, 3rd generation cephalosporin-resistant, fluoroquinolone-resistant

Priority 3: MEDIUM

Streptococcus pneumoniae, penicillin-non-susceptible

Haemophilus influenzae, ampicillin-resistant

Shigella *spp.*, fluoroquinolone-resistant

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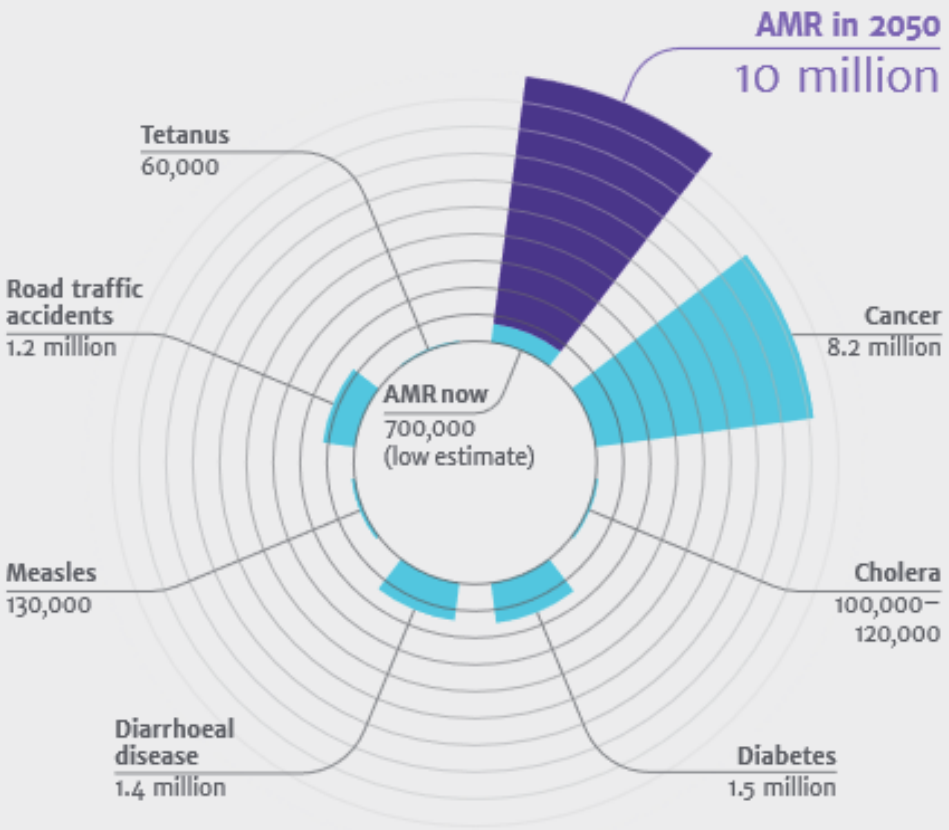
Review on Antimicrobial Resistance

Tackling drug-resistant infections globally

Antimicrobial Resistance: Tackling a crisis for the health and wealth of nations

The Review on Antimicrobial Resistance
Chaired by Jim O'Neill
December 2014

Deaths attributable to AMR every year compared to other major causes of death



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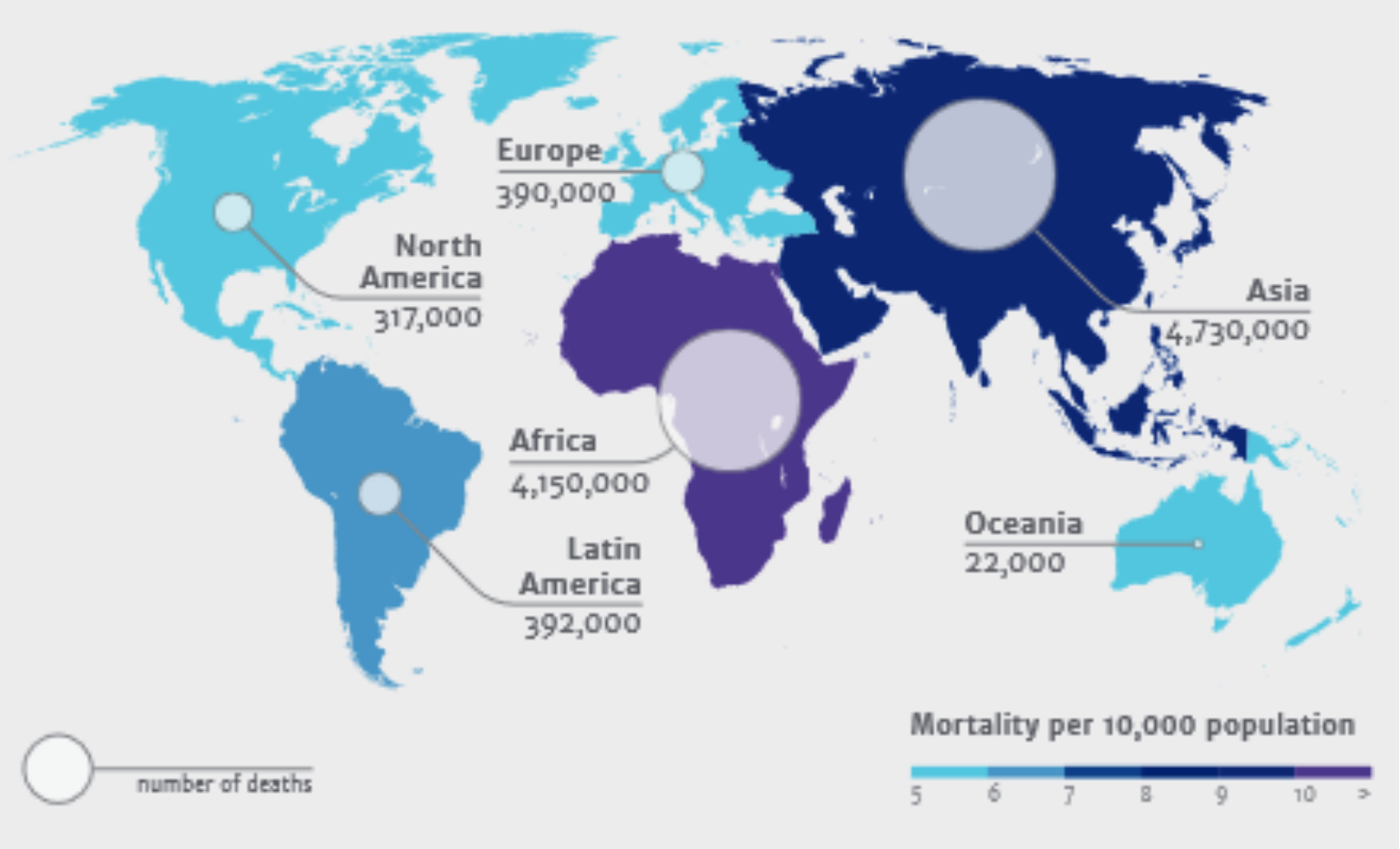

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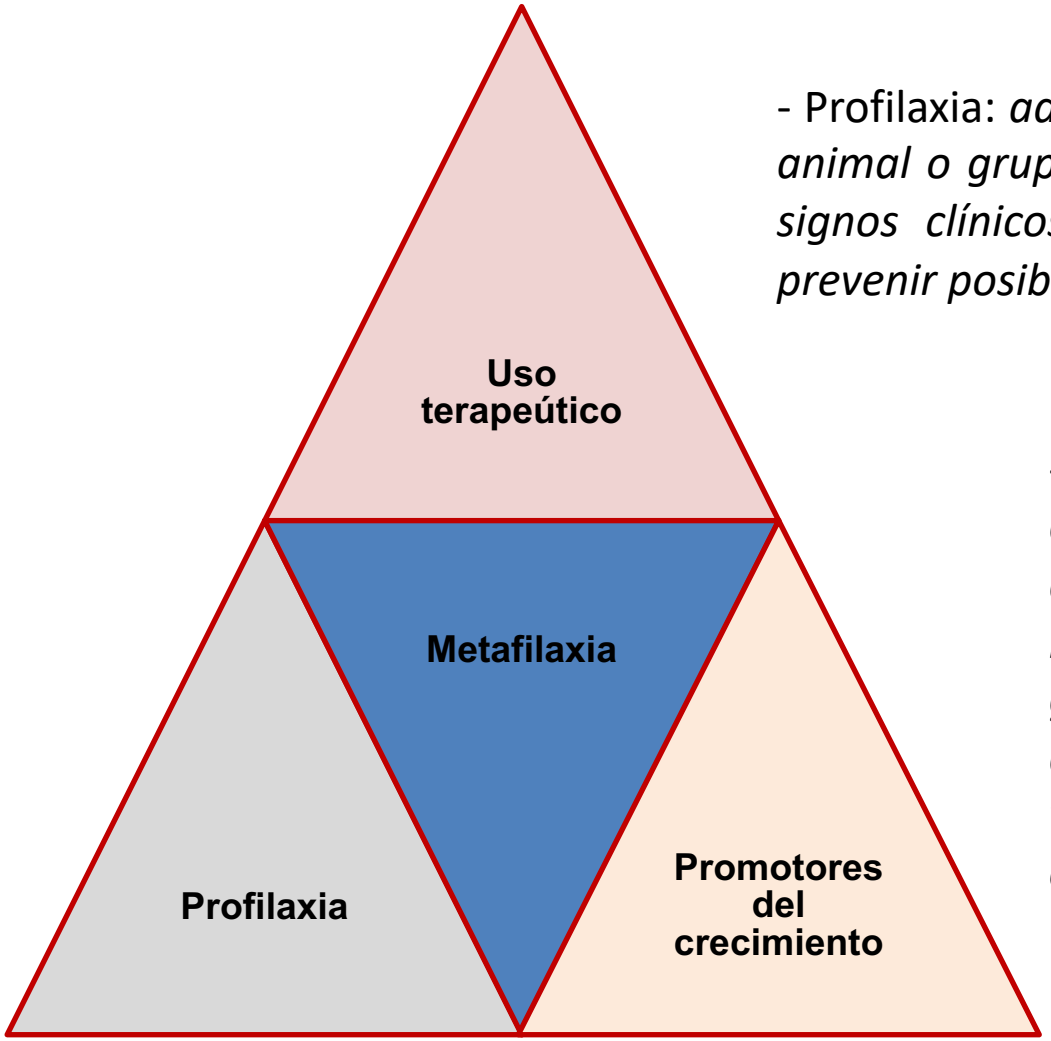
ANTIMICROBIANOS EN ANIMALES



- Profilaxia: *administración de un antimicrobiano a un animal o grupo de animales antes de que aparezcan signos clínicos de enfermedad, con el objetivo de prevenir posibles casos de infección*

- Metafilaxia: *administración de un antimicrobiano a un grupo de animales después del diagnóstico de un proceso infeccioso en alguno de los animales del grupo, con el objetivo de tratar a los animales enfermos y controlar la transmisión de la infección a animales en contacto estrecho*

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¿Impacto del uso de antimicrobianos en la prevalencia de bacterias resistentes y genes de resistencia?

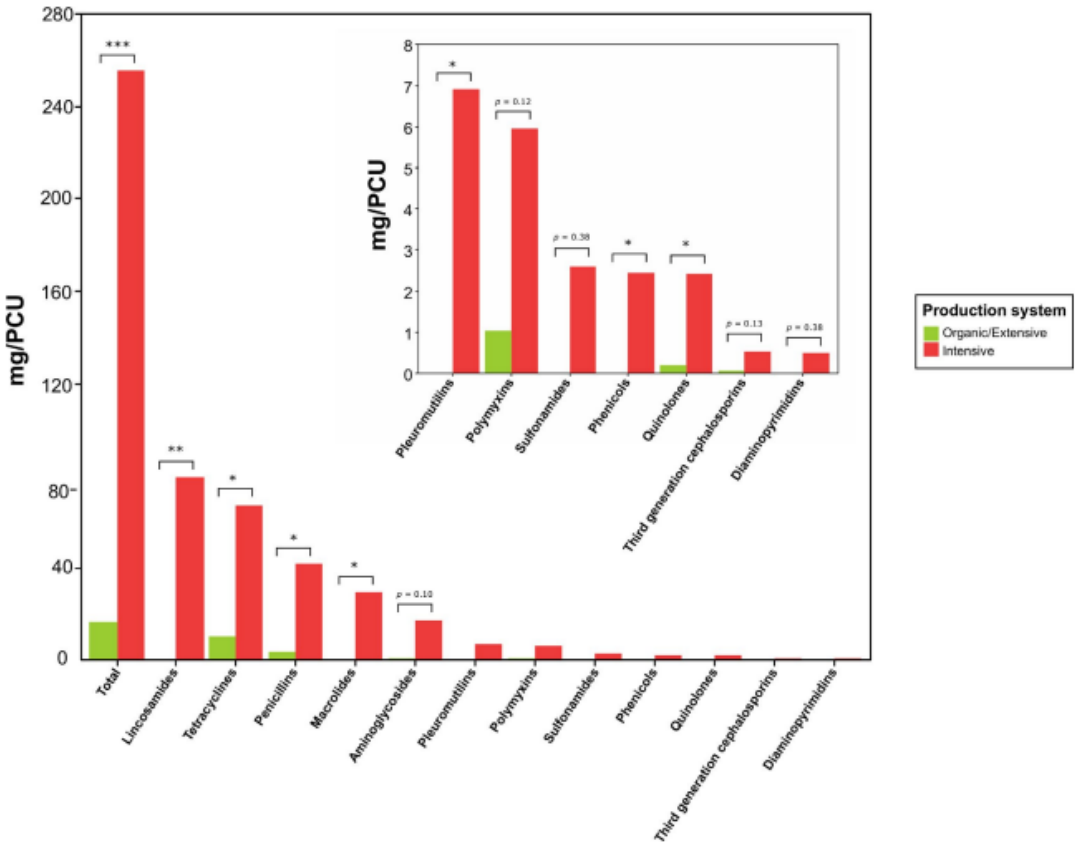
Received: 30 December 2019 | Revised: 3 August 2020 | Accepted: 7 November 2020
DOI: 10.1111/zph.12790

ORIGINAL ARTICLE

WILEY

Effect of antimicrobial use and production system on *Campylobacter* spp., *Staphylococcus* spp. and *Salmonella* spp. resistance in Spanish swine: A cross-sectional study

Oscar Mencía-Ares[1] | Héctor Argüello[1] | Héctor Puente[1] | Manuel Gómez-García[1] | Avelino Álvarez-Ordóñez[2,3] | Edgar G. Manzanilla[4,5] | Ana Carvajal[1] | Pedro Rubio[1]



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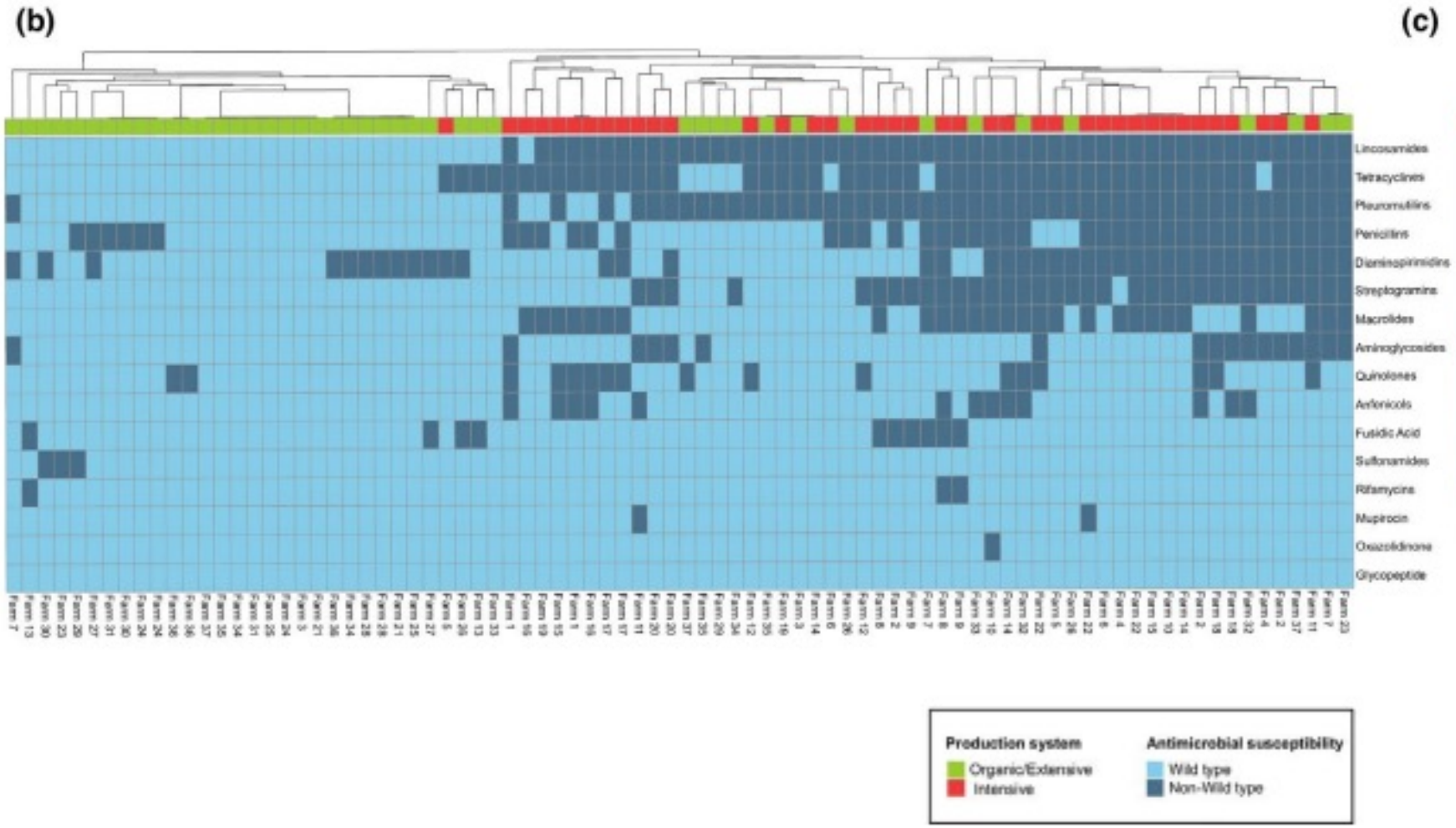

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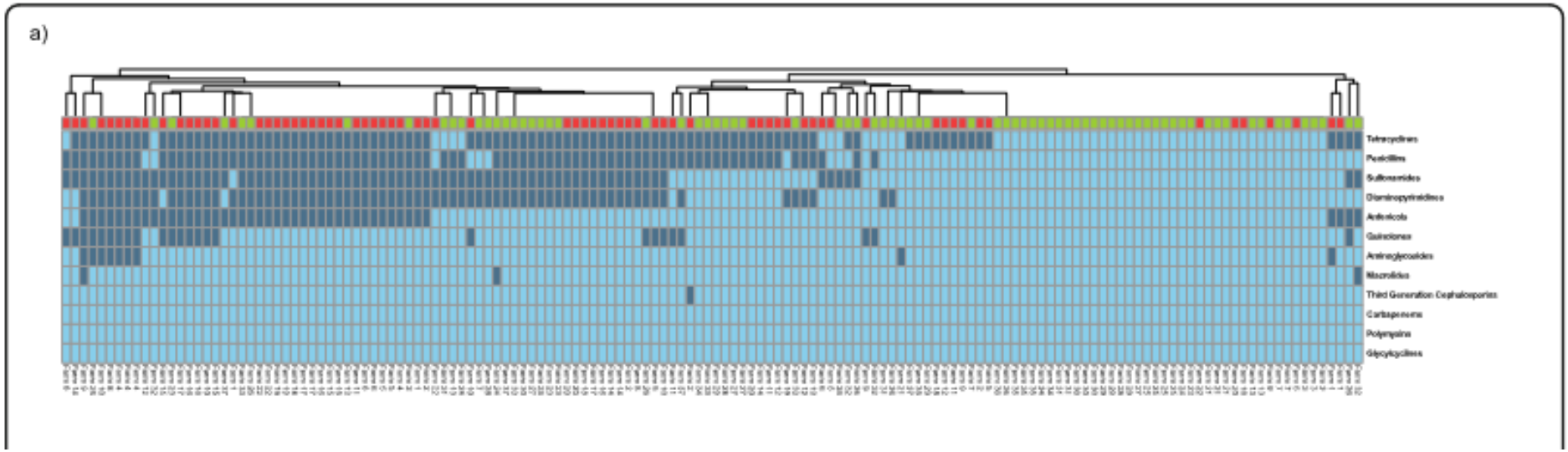
Mencía-Ares *et al. Porcine Health Management* (2021) 7:27
https://doi.org/10.1186/s40813-021-00206-1

Porcine Health Management

RESEARCH Open Access

Antimicrobial resistance in commensal *Escherichia coli* and *Enterococcus* spp. is influenced by production system, antimicrobial use, and biosecurity measures on Spanish pig farms

Oscar Mencía-Ares[1*], Héctor Argüello[1], Héctor Puente[1], Manuel Gómez-García[1], Edgar G. Manzanilla[2,3], Avelino Álvarez-Ordóñez[4,5], Ana Carvajal[1] and Pedro Rubio[1]



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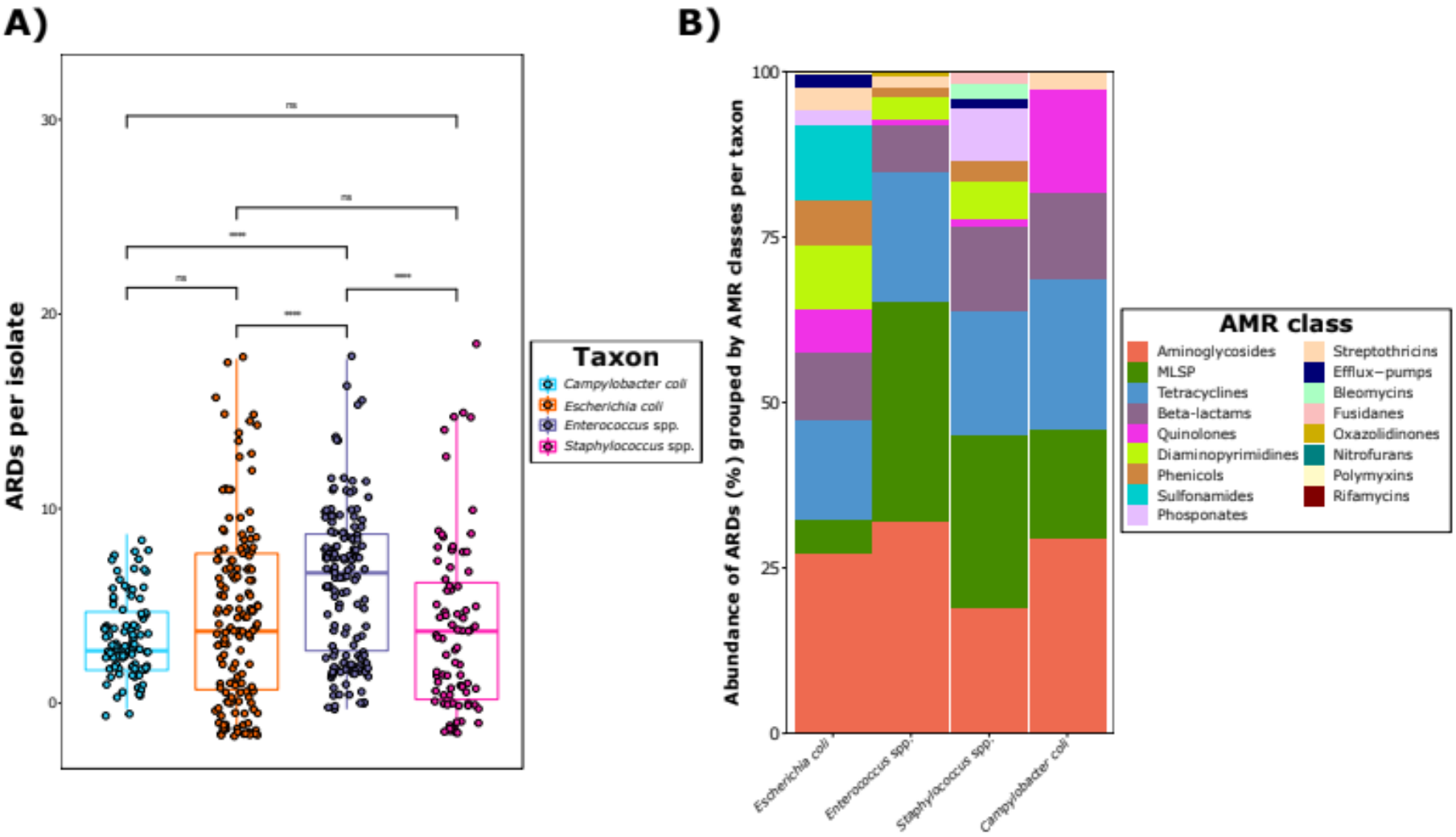

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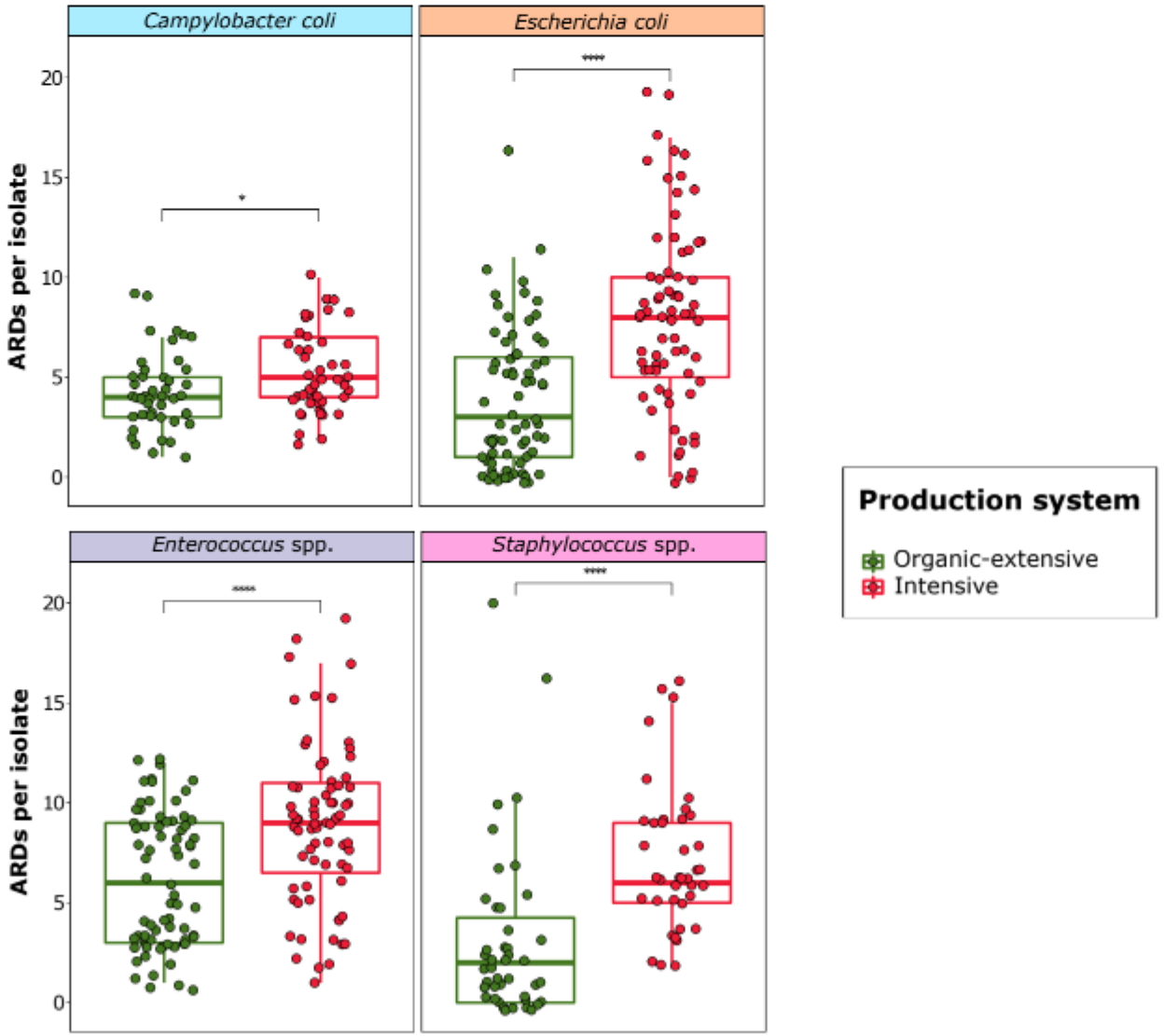

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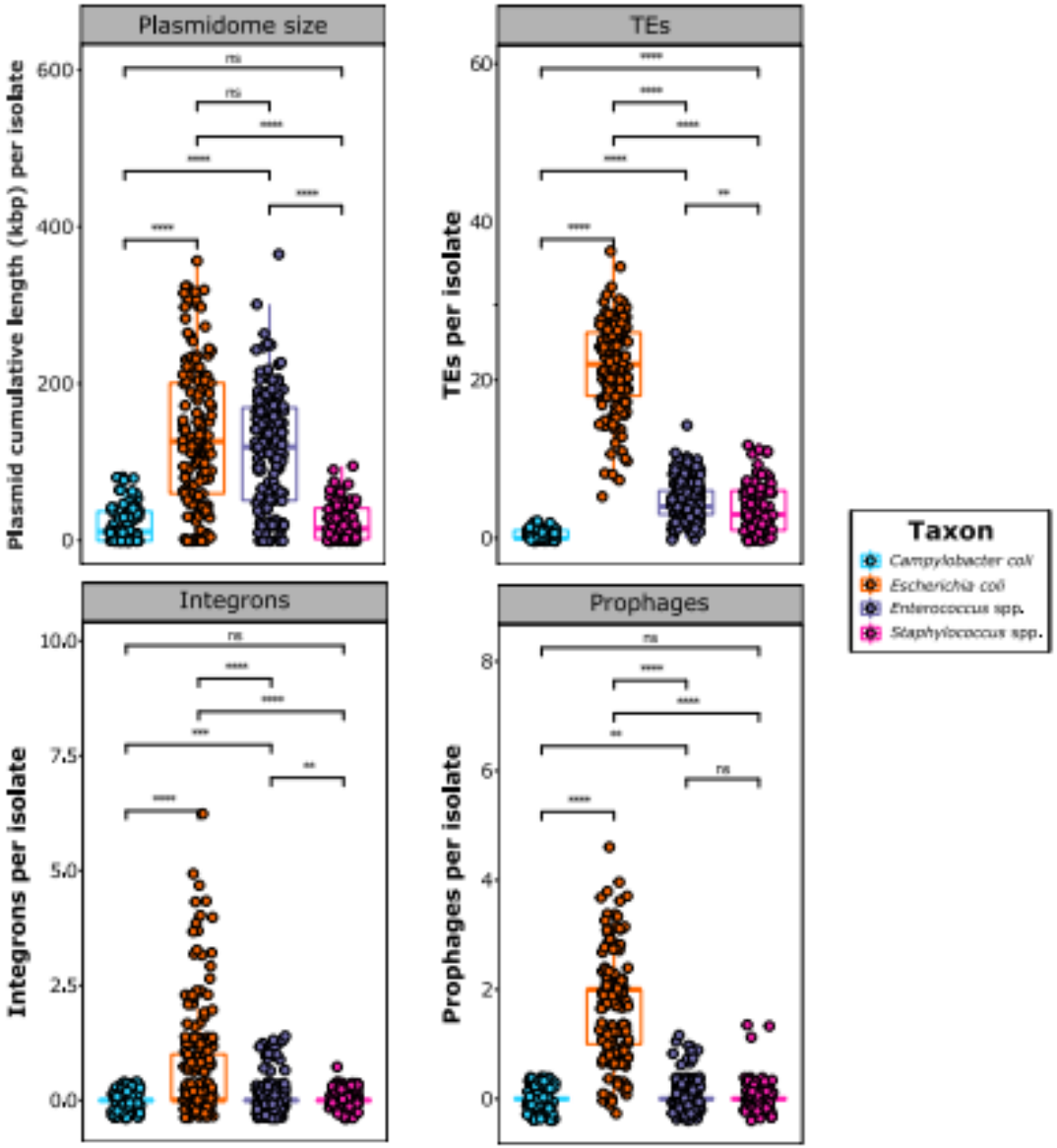

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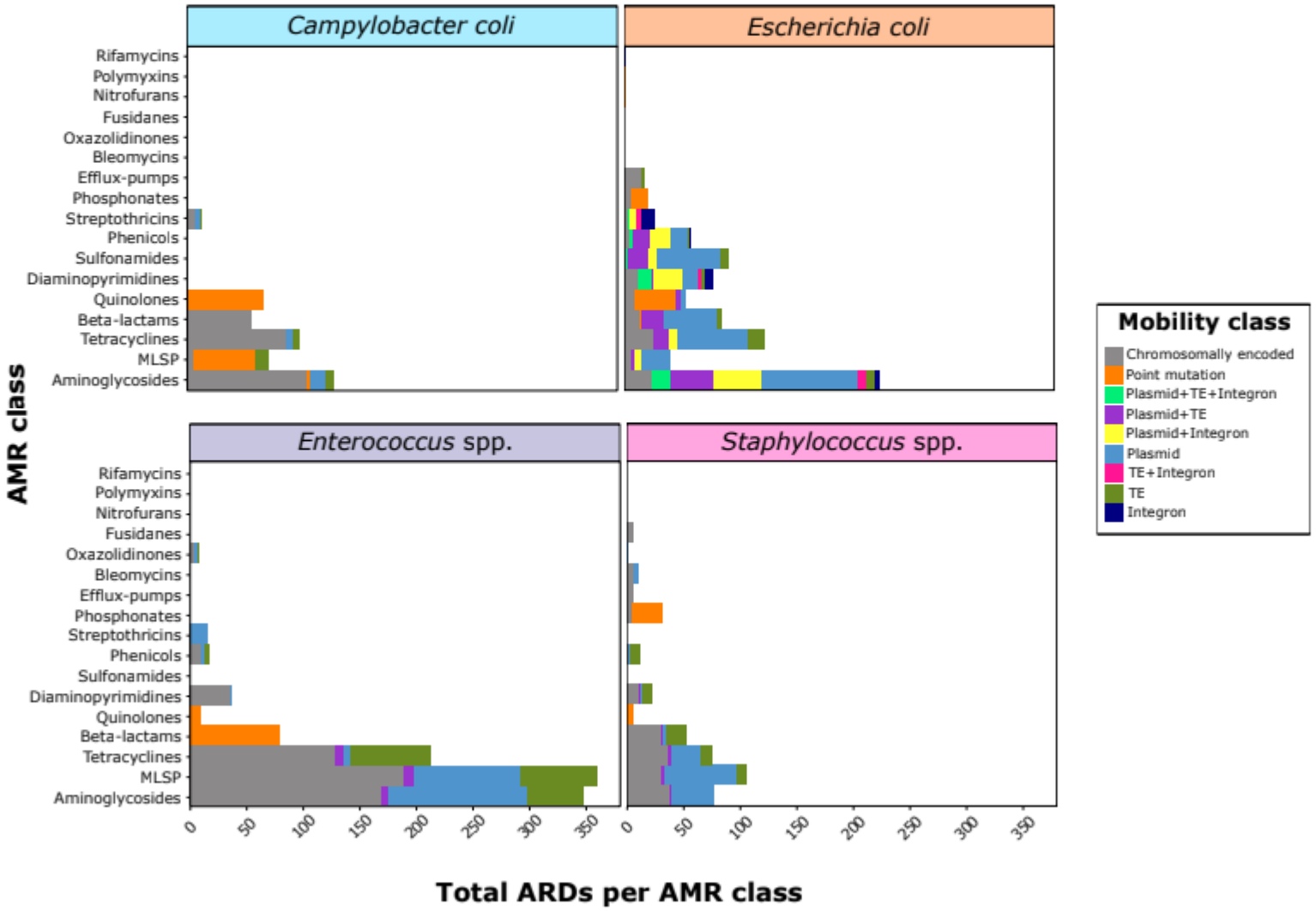

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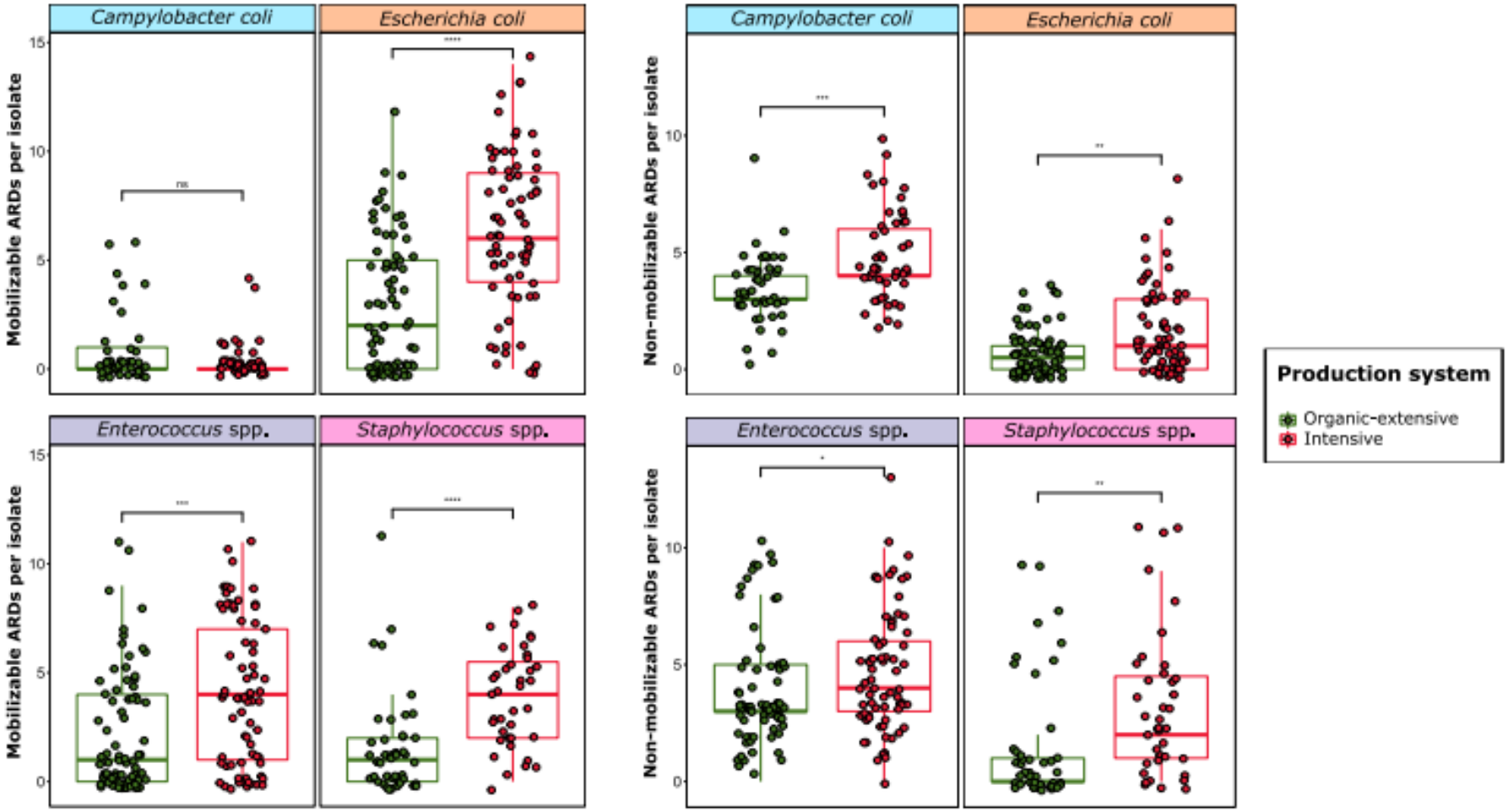

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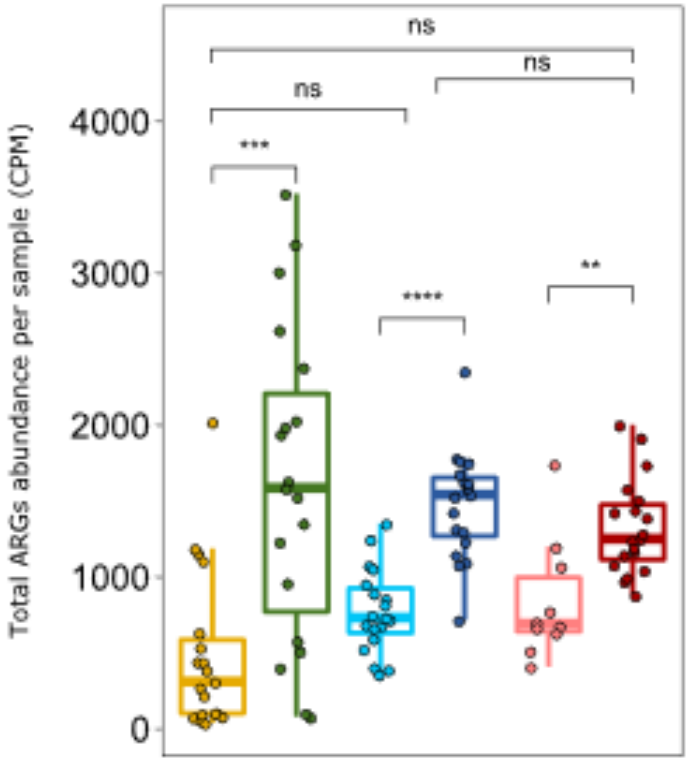
Mencía-Ares *et al. Microbiome* (2020) 8:164
https://doi.org/10.1186/s40168-020-00941-7

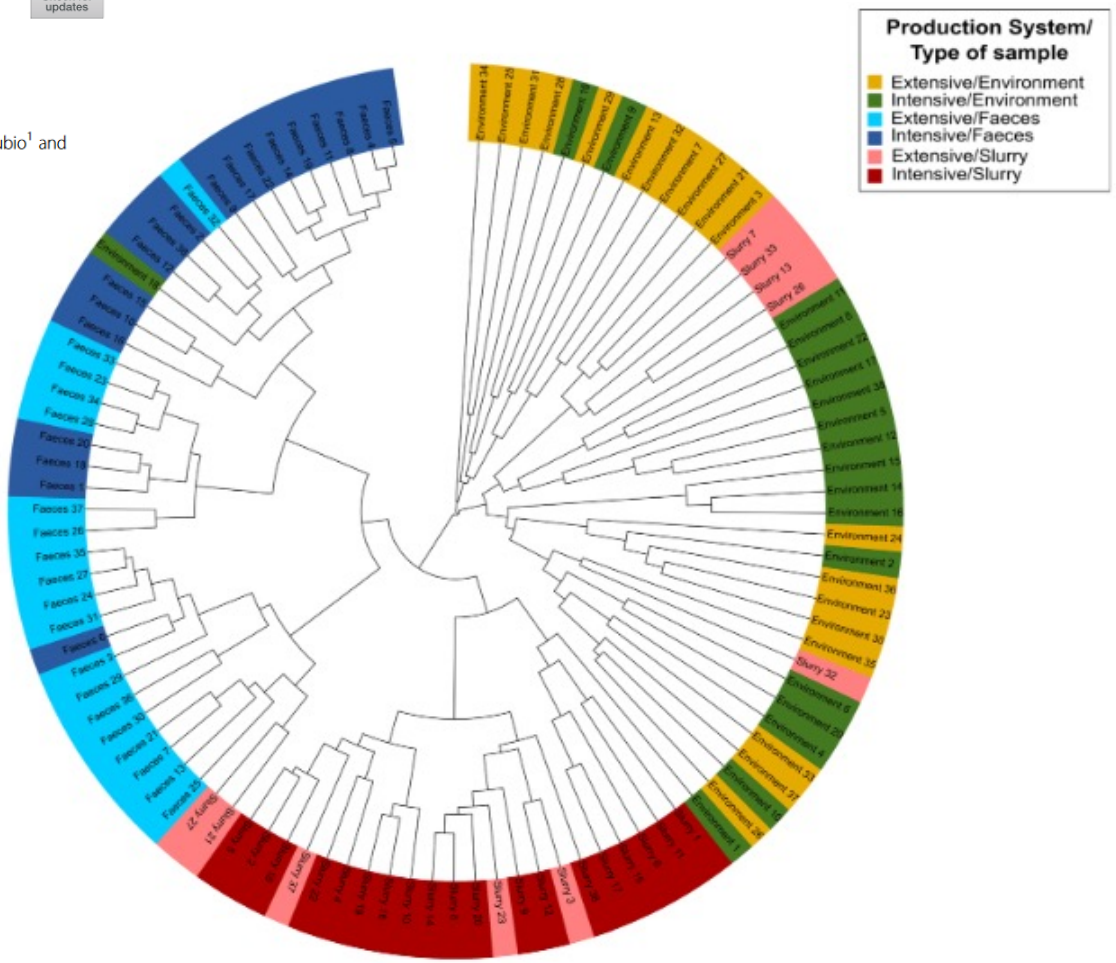
Microbiome

RESEARCH Open Access

Antimicrobial use and production system shape the fecal, environmental, and slurry resistomes of pig farms

Oscar Mencía-Ares[1], Raúl Cabrera-Rubio[2,3], José Francisco Cobo-Díaz[4,5], Avelino Álvarez-Ordóñez[4,5], Manuel Gómez-García[1], Héctor Puente[1], Paul D. Cotter[2,3,6], Fiona Crispie[2,3], Ana Carvajal[1*], Pedro Rubio[1] and Héctor Argüello[1]





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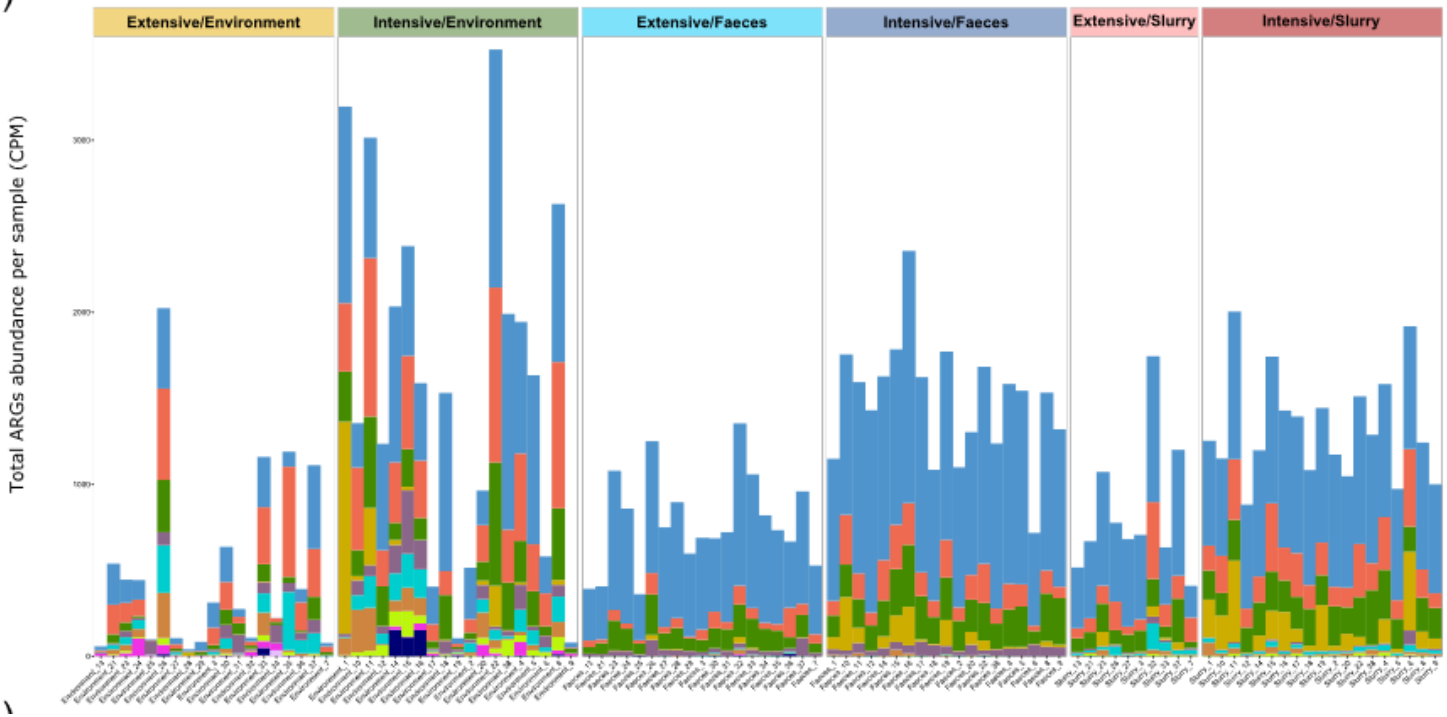

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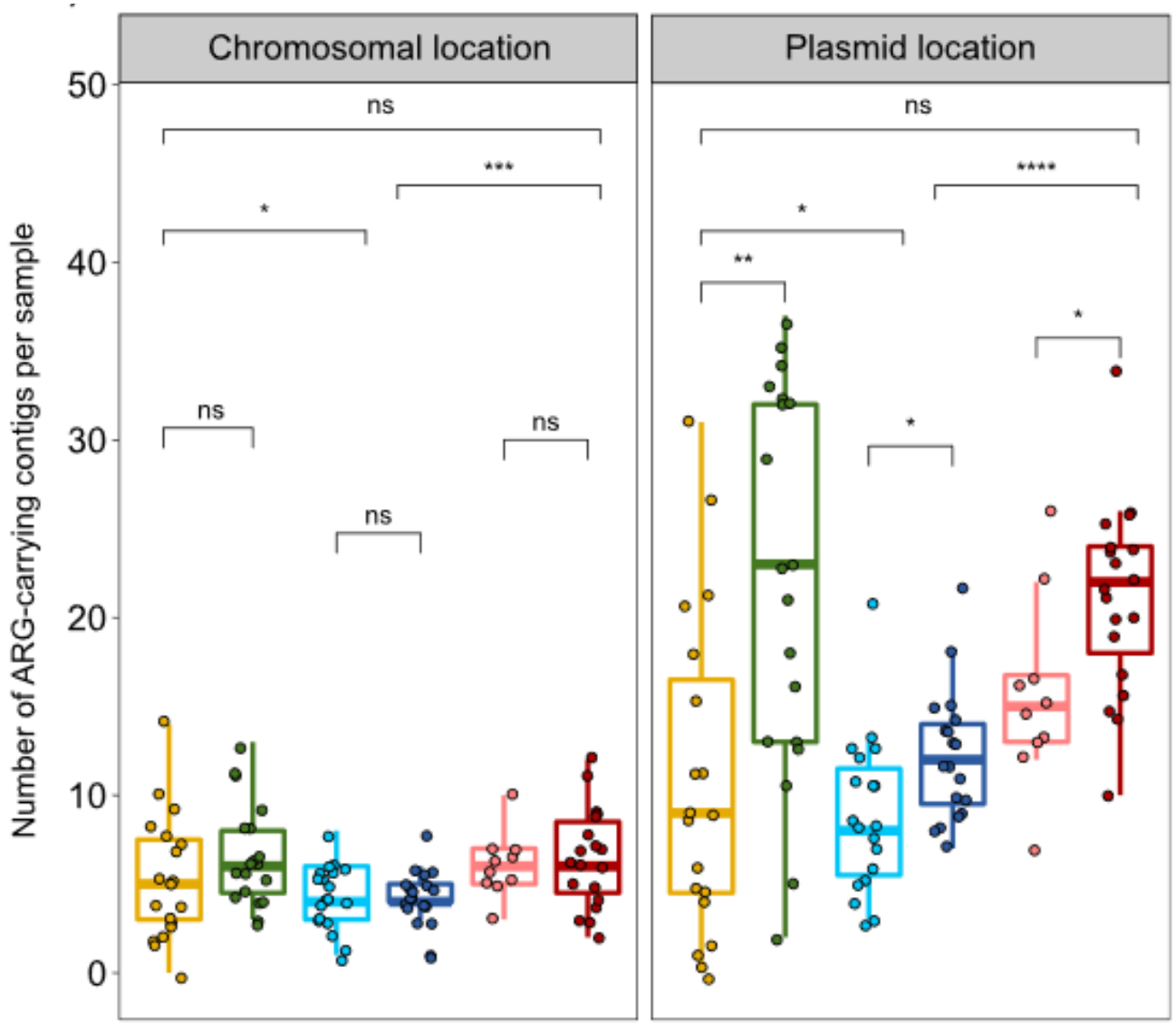

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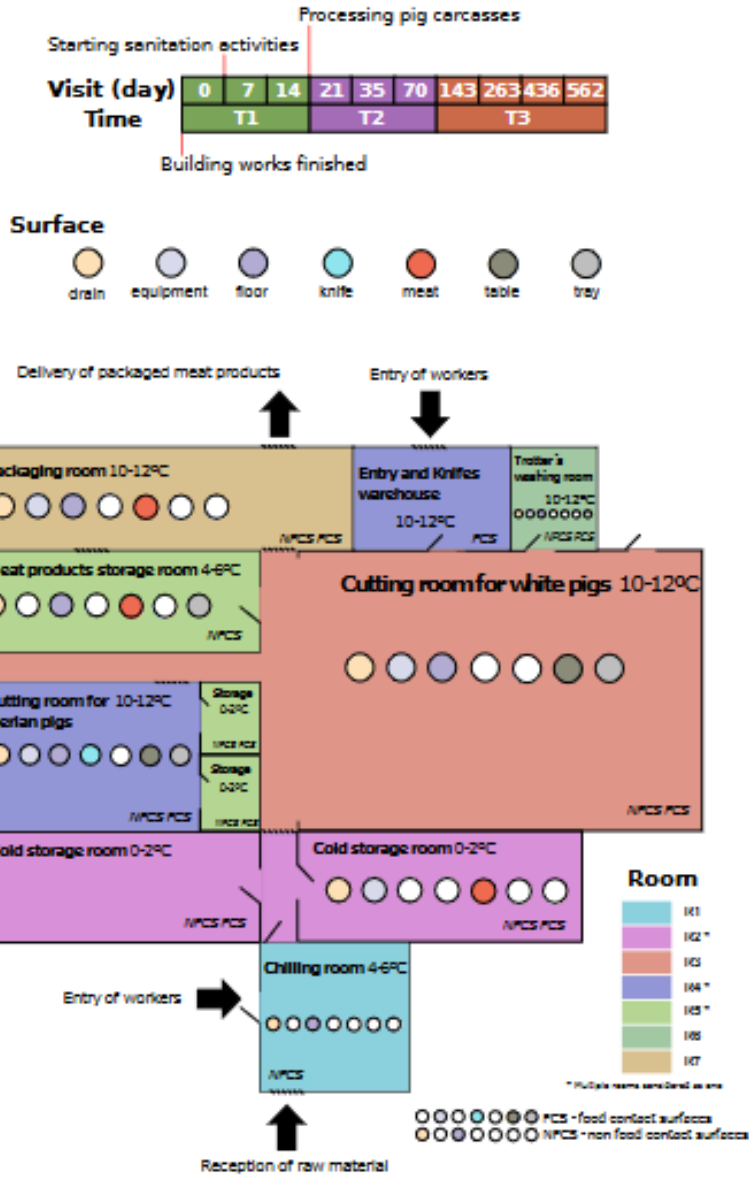
Cobo-Díaz et al. Microbiome (2021) 9:204
https://doi.org/10.1186/s40168-021-01131-9

Microbiome

RESEARCH Open Access

Microbial colonization and resistome dynamics in food processing environments of a newly opened pork cutting industry during 1.5 years of activity

José F. Cobo-Díaz[1†], Adrián Alvarez-Molina[1†], Elena A. Alexa[1,2†], Calum J. Walsh[3,4], Oscar Mencía-Ares[5], Paula Puente-Gómez[1], Eleni Likotrafiti[6], Paula Fernández-Gómez[1], Bernardo Prieto[1,7], Fiona Crispie[3], Lorena Ruiz[8,9], Montserrat González-Raurich[1,7], Mercedes López[1,7], Miguel Prieto[1,7], Paul Cotter[3,4] and Avelino Alvarez-Ordóñez[1,7*]



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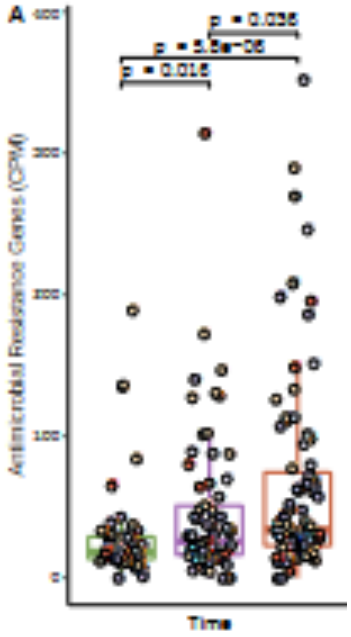

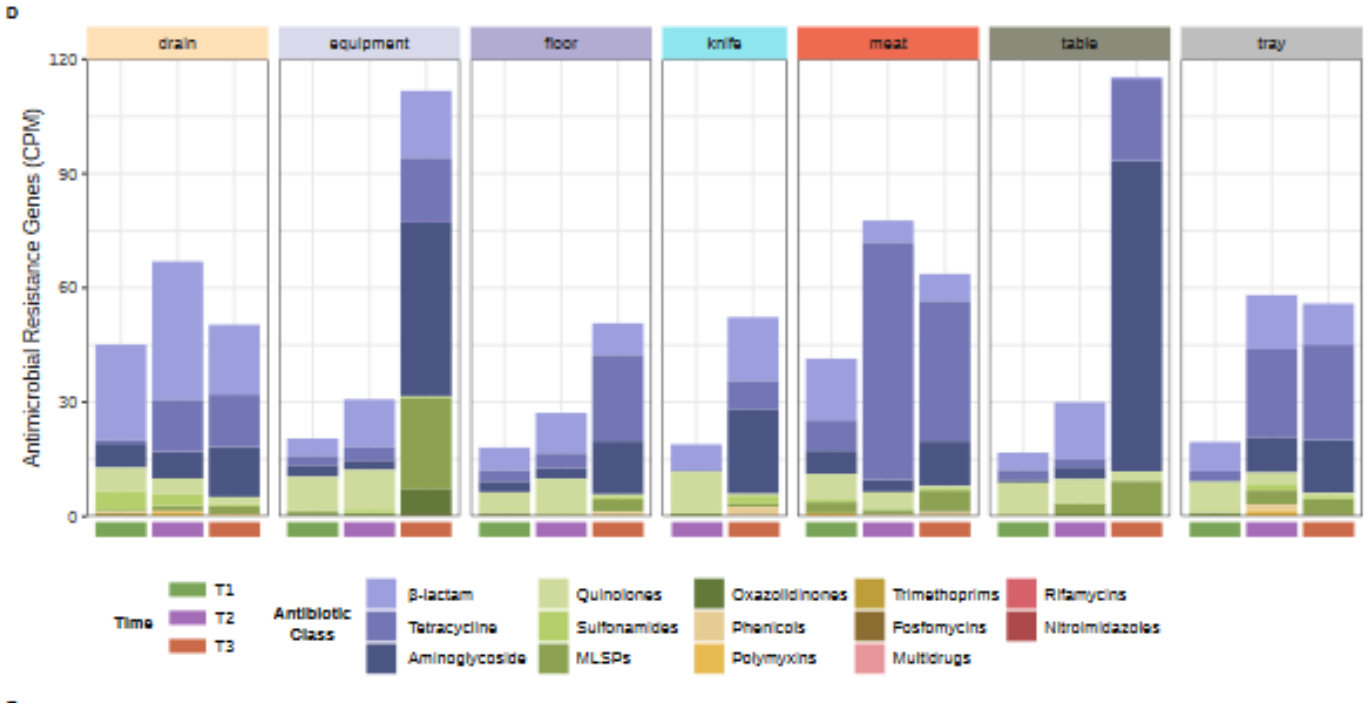

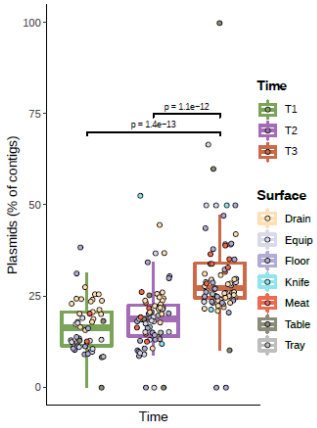

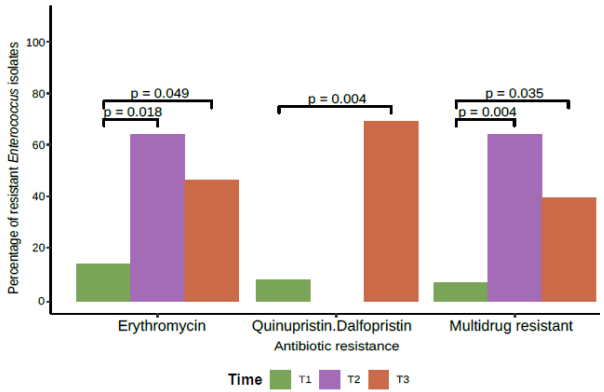

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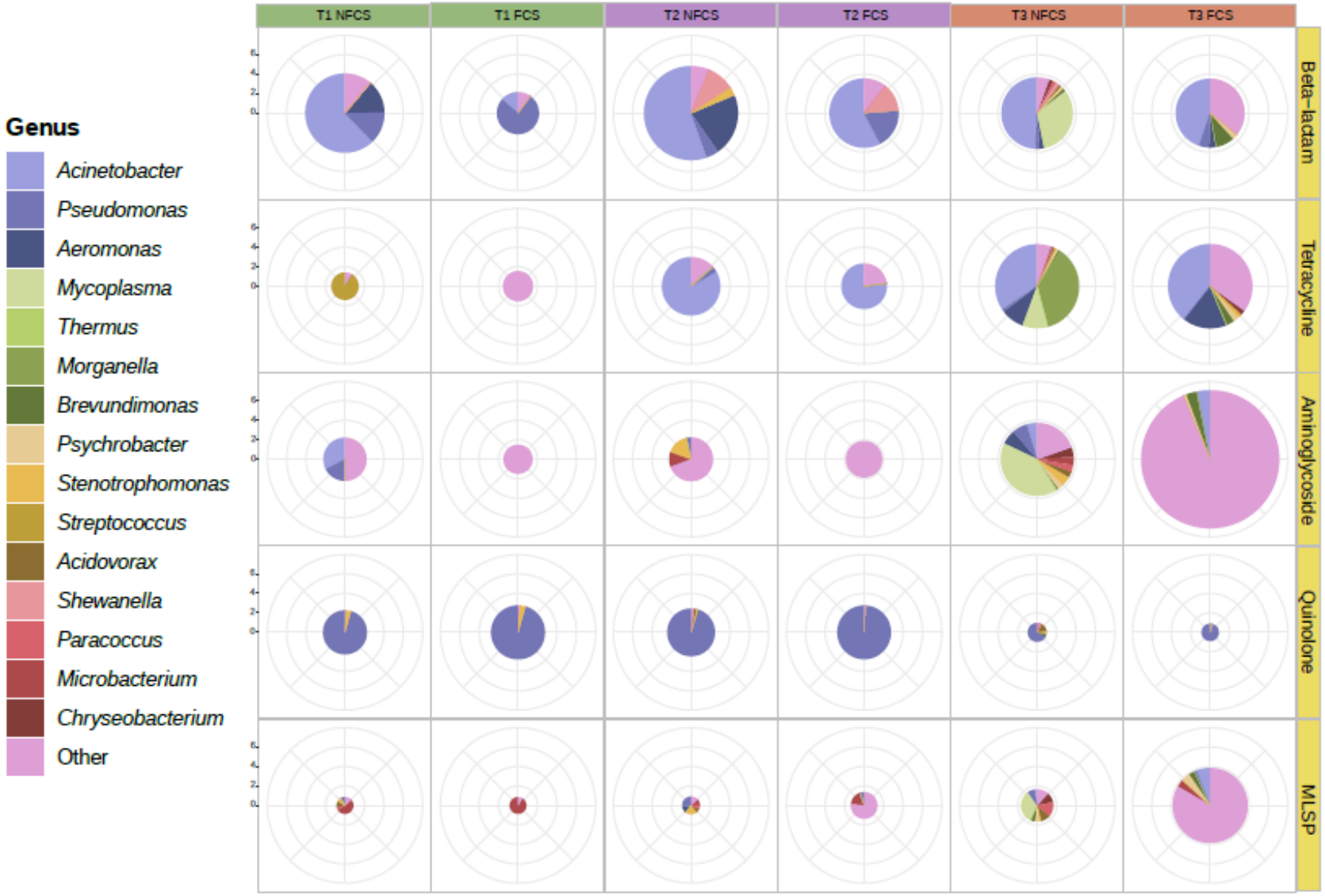

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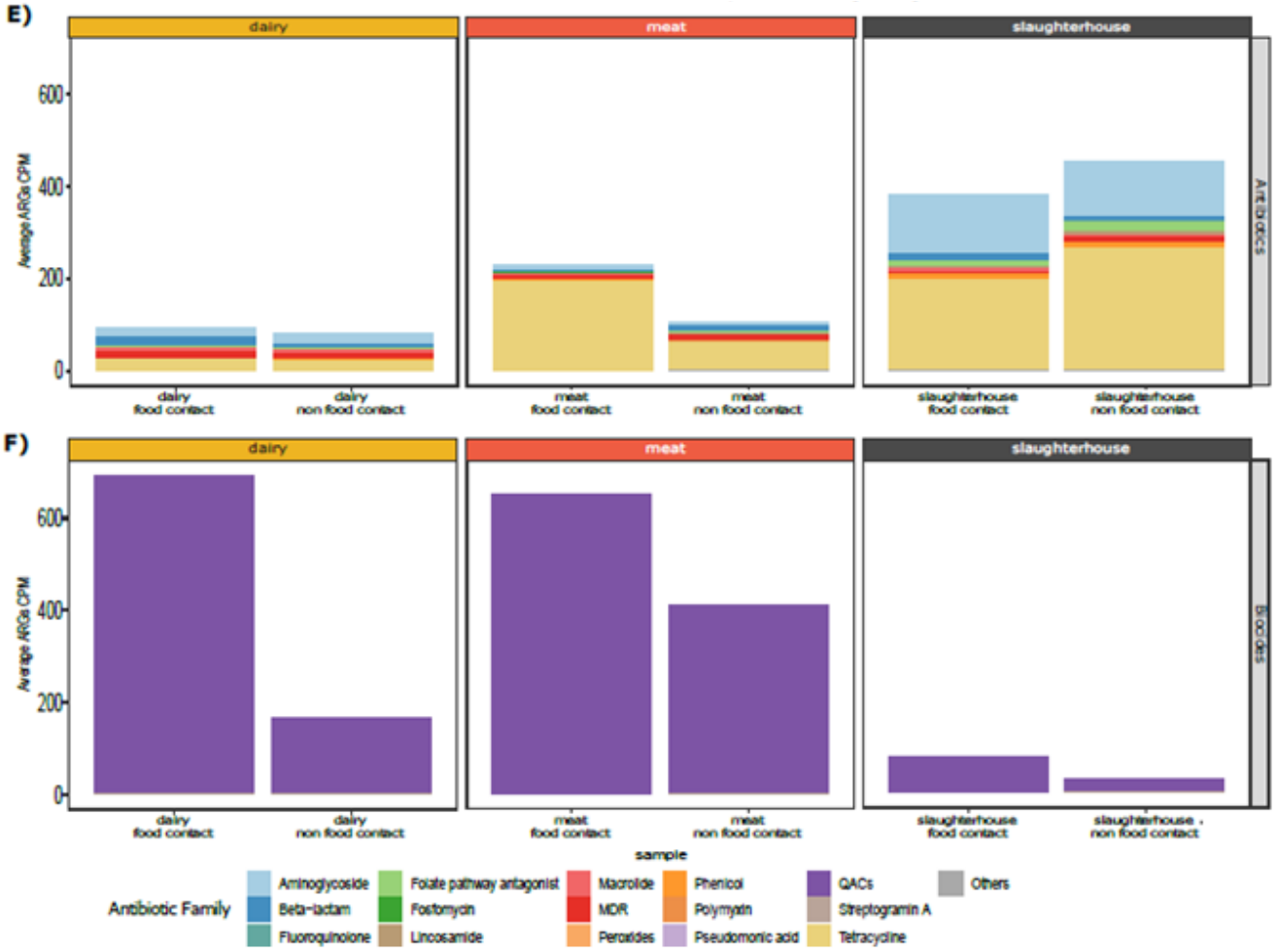
¿Son las industrias alimentarias un reservorio de bacterias resistentes y genes de resistencia?



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Microbiome Applications for Sustainable food systems through Technologies and EnteRprise

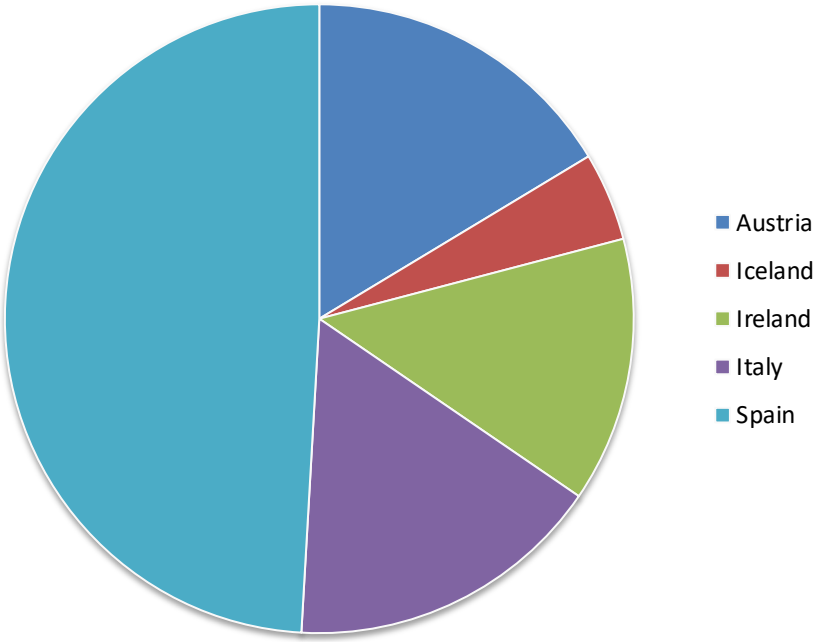
- **Task 4.1. Testing of microbiome mapping workflows and tools in the food industry**

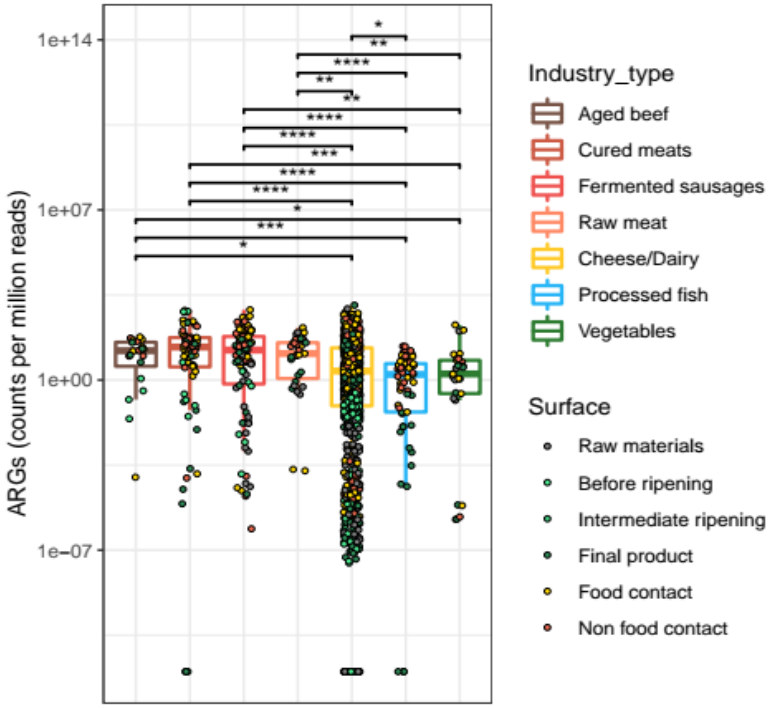
Develop and validate a complete microbiome analysis approach, from sampling to DNA extraction, microbiota detection and data analysis for food and environmental microbiome testing by food processors with the aim to enhance food quality and safety.

Inter-laboratory validation strategy to develop Standard Operation Procedures (SOPs) to be directly applied in food industries

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 818368

- De diciembre de 2019 a abril de 2021
- 114 industrias
- > 2,000 muestras





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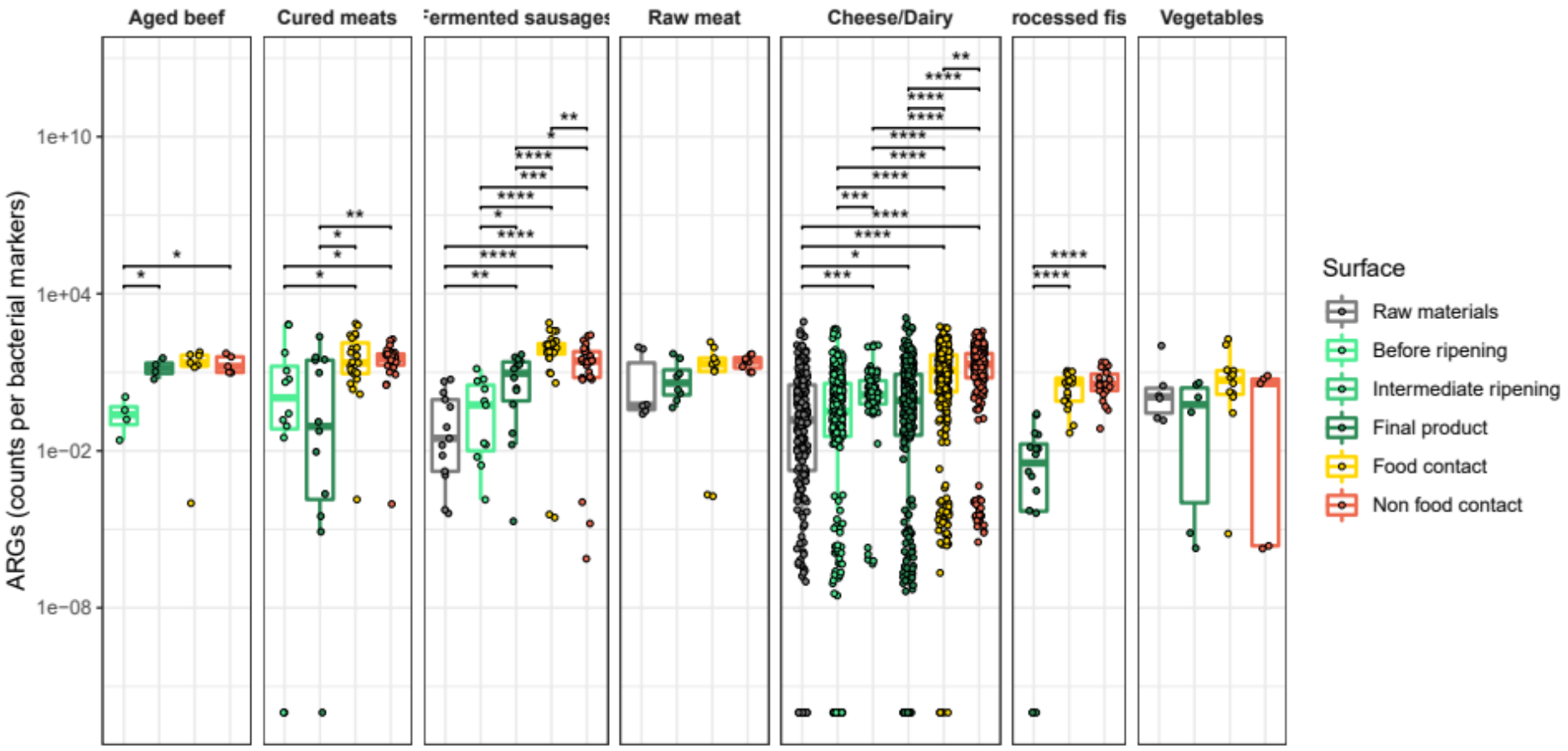

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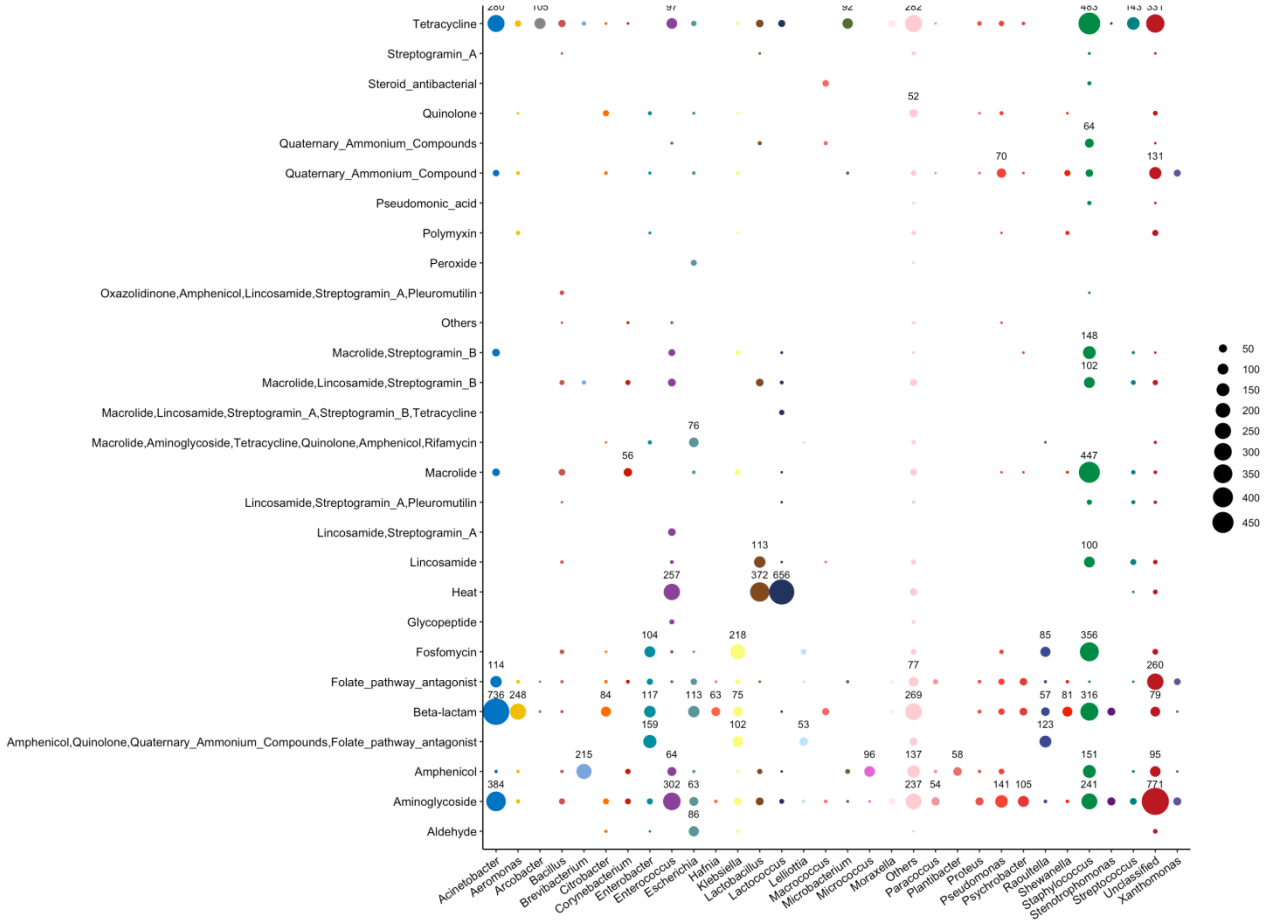

Staphylococcus, genes asociados con resistencia a:

- Tetraciclinas
- Macrolidos
- Fosfomicina
- Beta-lactámicos
- Aminoglucósidos
- Varios otros más

Acinetobacter, principalmente asociados con:

- Beta-lactámicos
- Tetraciclinas
- Aminoglucósidos

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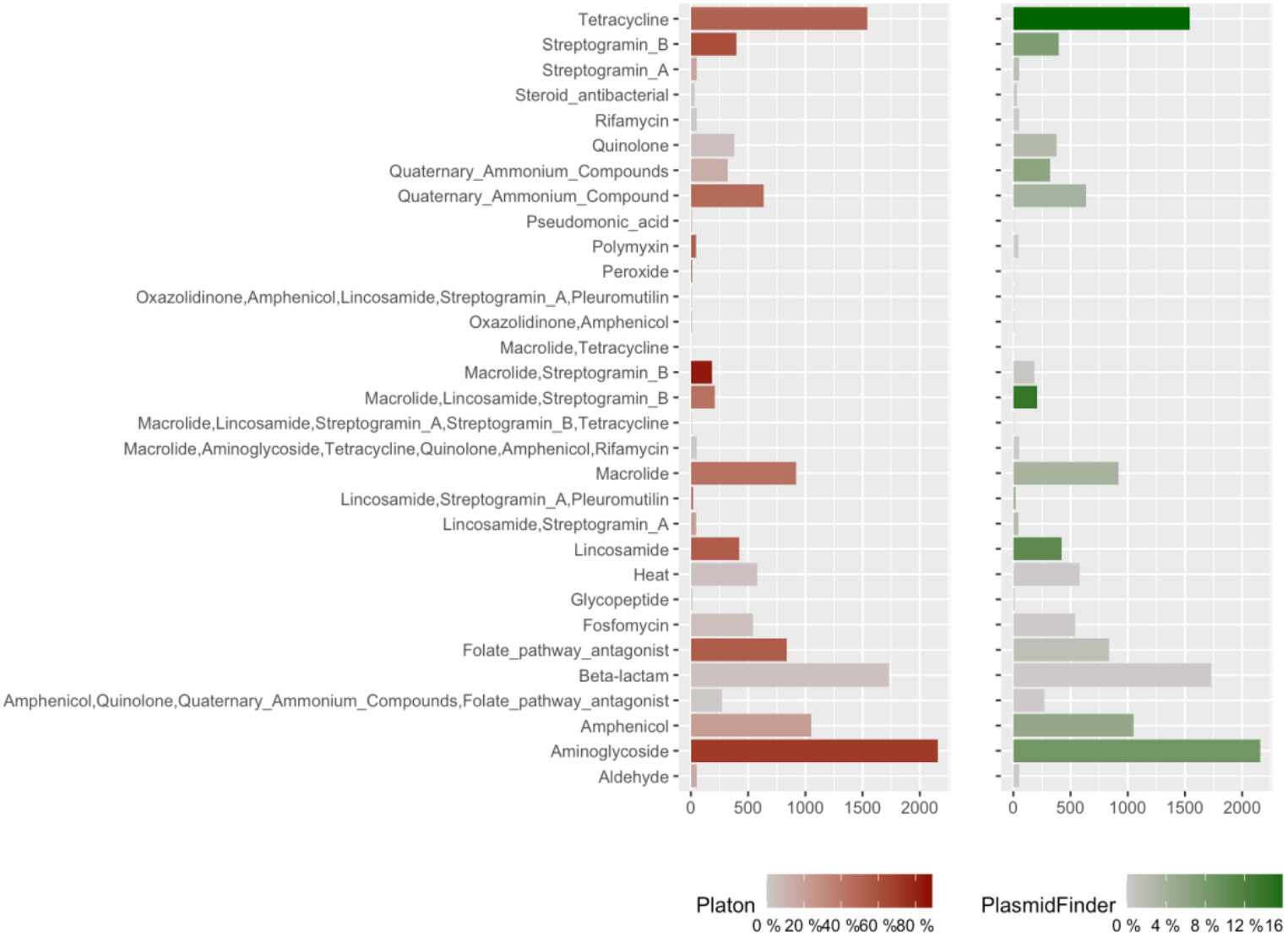

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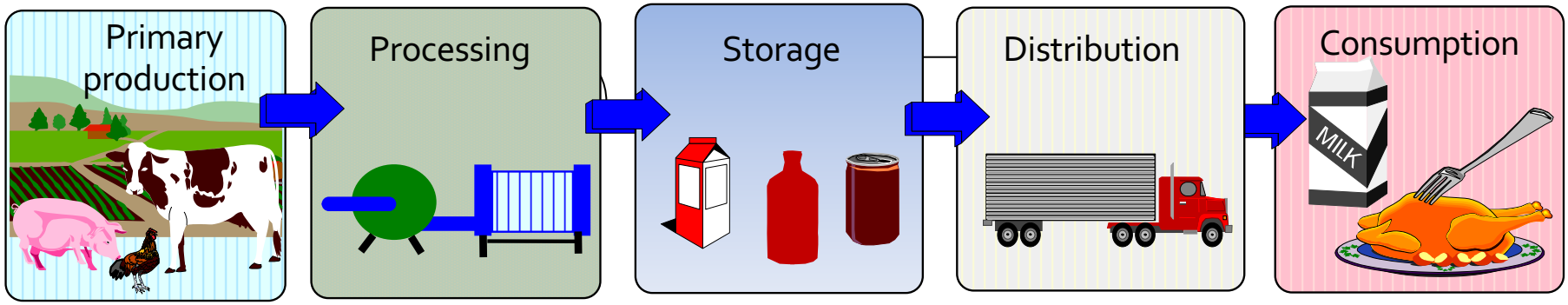
PRESIONES SELECTIVAS



Refrigeration

Pasteurization

High pressures

Bacteriocins

Organic acids

Dehidratation

Radiations

Freezing

UV light

Sterilization

Disinfectants

Alkali

Acidification

Sal

Bile

Microwaves

Gastric fluid

Additives

Vaccuum packaging

Modified atmosphere packaging

Antimicrobial compounds

Detergents

Nitrates and nitrities

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- Alcohols
- Aldehydes
- Chlorine and chlorine releasing agents (sodium hypochlorite, clorhexidine)
- Iodine
- Peroxygen compounds (hydrogen peroxide, peracetic acid)
- Phenolic type compounds
- Quaternary ammonium compounds (benzalkonium chloride)
- Bases (sodium hydroxide, potasium hydroxide)
- Acids (mineral and organic acids)

Improper use

Sub-optimal concentrations

Resistance development

- Cracks and crevices
- Presence of organic matter
- Erroneous formulation
- Inappropriate storage
- Inadequate distribution
- Application to wet surfaces
- Rinsing of frequently disinfected areas

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Check for updates

Artificial sweeteners stimulate horizontal transfer of extracellular antibiotic resistance genes through natural transformation

Zhigang Yu[1], Yue Wang[1], Ian R. Henderson[2] and Jianhua Guo[1]✉

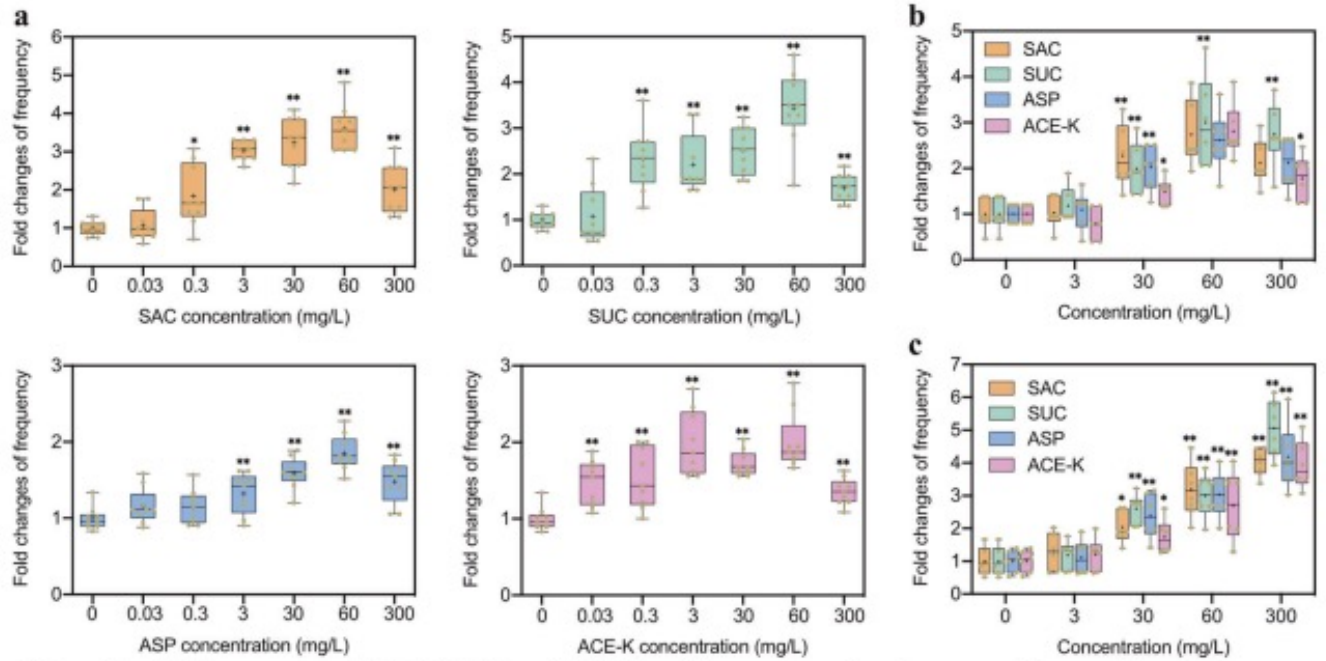

Fig. 1 Effects of artificial sweeteners (SAC, SUC, ASP, and ACE-K) on the transformation frequency of extracellular ARGs to competent cells. a Fold changes of transformation frequency of pWH1266 plasmid in *A. baylyi* ADP1 under different concentrations of artificial sweeteners. At high concentrations (> 0.3 mg/L), artificial sweeteners promote the transformation ($N = 9$; ANOVA, $p < 0.05$). **b** Fold changes of transformation frequency of pWH1266 plasmid in *Bacillus subtilis* under exposure to different concentrations of artificial sw0eeteners ($N = 6$). **c** Fold changes of transformation frequency of *gfp*-encoded pKJK5 plasmid in mice faecal bacteria under exposure to different concentrations of artificial sweeteners ($N = 6$). Significant differences between individual sweetener-treated groups and the control (0 mg/L of sweeteners) were tested with Independent-sample *t* test, $*p < 0.05$ and $**p < 0.01$.

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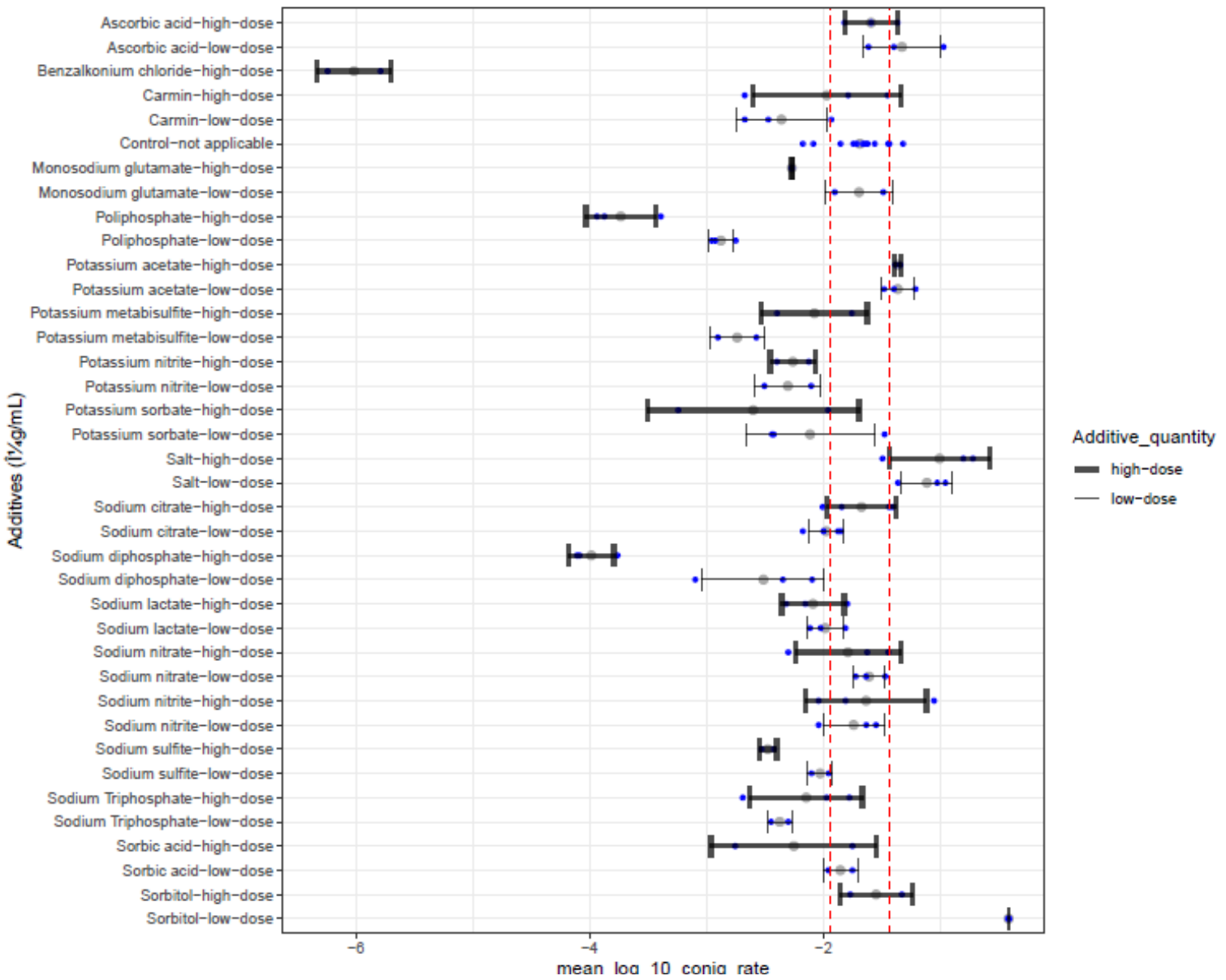

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Conclusiones

- **El elevado uso de antimicrobianos en granjas de producción intensiva se asocia directamente con un mayor riesgo de dispersión de resistencias**

- **Determinados nichos ambientales en industrias alimentarias se ven colonizados y actúan como reservorios de bacterias resistentes**

- **Otras presiones selectivas en la cadena alimentaria pueden influir en la emergencia y transmisión de resistencias a antimicrobianos**

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Acknowledgments

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Dr. P.D. Cotter
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MENU

THE TIMES
saturday october 15 2022

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Saturday October 15 2022, 12.01am, The Times

Patients will be able to obtain antibiotics from pharmacies without seeing a doctor under new plans aimed at reducing the need for GP appointments.

Thérèse Coffey, the health secretary, has pushed to make antibiotics more freely available and has said that she has previously handed out her own supplies of the medicines to friends and family who were feeling unwell.

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Governing Global Antimicrobial Resistance: 6 Key Lessons From the Paris Climate Agreement

Isaac Weldon, MSc, Susan Rogers Van Katwyk, PhD, Gian Luca Burci, Dr Giur, Thana C. de Campos, DPhil, Mark Eccleston-Turner, PhD, Helen R. Fryer, DPhil, Alberto Giubilini, PhD, Thomas Hale, PhD, Mark Harrison, DPhil, Stephanie Johnson, PhD, Claas Kirchhelle, DPhil, Kelley Lee, DPhil, Kathleen Liddell, DPhil, Marc Mendelson, PhD, Gorik Ooms, PhD, James Orbinski, MD, MSc, MA, Laura J. V. Piddock, PhD, John-Arne Røttingen, MD, PhD, Julian Savulescu, PhD, Andrew C. Singer, PhD, A. M. Viens, PhD, Clare Wenham, PhD, Mary E. Wiktorowicz, PhD, MSc, Shehla Zaidi, MD, PhD, and Steven J. Hoffman, JD, PhD, LLI

TABLE 1— Comparing the Paris Climate Agreement With Existing Global AMR Efforts

Essential Elements	Paris Climate Agreement	Current Global AMR Efforts
1. Collective global goal	Keep global temperature rise below 1.5°C above preindustrial levels or at least well below 2°C	No consensus on what a collective global goal could look like
2. A focus on social and economic transformation	Implementation of the Paris Agreement requires social and economic transformation to decarbonize national economies.	AMR discourse has historically emphasized individual behavior instead of social and economic transformation.
3. Nationally determined contributions pledged, reviewed, and ratcheted every 5 years	All parties must communicate their nationally determined contributions every 5 years and, during revisions, aim for maximally ambitious goals. Nationally determined contributions are reviewed to ensure the distribution of responsibilities is fair and that countries are ambitious in their goals. All parties must regularly provide information on activities and outcomes using methods that are articulated by the Intergovernmental Panel on Climate Change.	All WHO member states committed to having national action plans for AMR. Even though this commitment is not legally binding, more than 100 countries have published plans, and many are under development. However, there are no specified review, intensification, or accountability mechanisms, and little financial, technical, and infrastructural support is provided for achieving necessary policies. WHO, FAO, and OIE conduct self-assessment surveys on national AMR activities, but there is no regular reporting or standard methodology for reporting outcomes.
4. Annual multistakeholder forum	The annual Conference of the Parties to the UNFCCC serves as a multistakeholder meeting place for advancing the Paris Agreement.	AMR is normally discussed every 3 years at the World Health Assembly, but there is no formal or regular meeting focused on AMR and no permanent forum for multistakeholder discussions on AMR across sectors.
5. Global scientific stock taking every 5 years	Requirement to assess the best available science every 5 years; this stock-taking exercise will help ensure that the Paris Agreement's ongoing efforts are in line with scientific best practices.	No relevant comparison
6. International legal framework	The Paris Agreement is a legally binding instrument of the UNFCCC. The UNFCCC provides a broader legal framework for the Paris Agreement.	No international legal framework, although the constituting instruments of the WHO, FAO, OIE, or UN could serve as the broader legal framework for a legally binding AMR agreement

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REGULATION (EU) 2019/6 OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL

of 11 December 2018

on veterinary medicinal products and repealing Directive 2001/82/EC

(Text with EEA relevance)

- **Se prohibe el uso profiláctico de antimicrobianos en grupos de animales**

- **Se restringe el uso metafiláctico de antimicrobianos en grupos de animales**

- **Se reservan algunos antimicrobianos exclusivamente para el uso en medicina humana**

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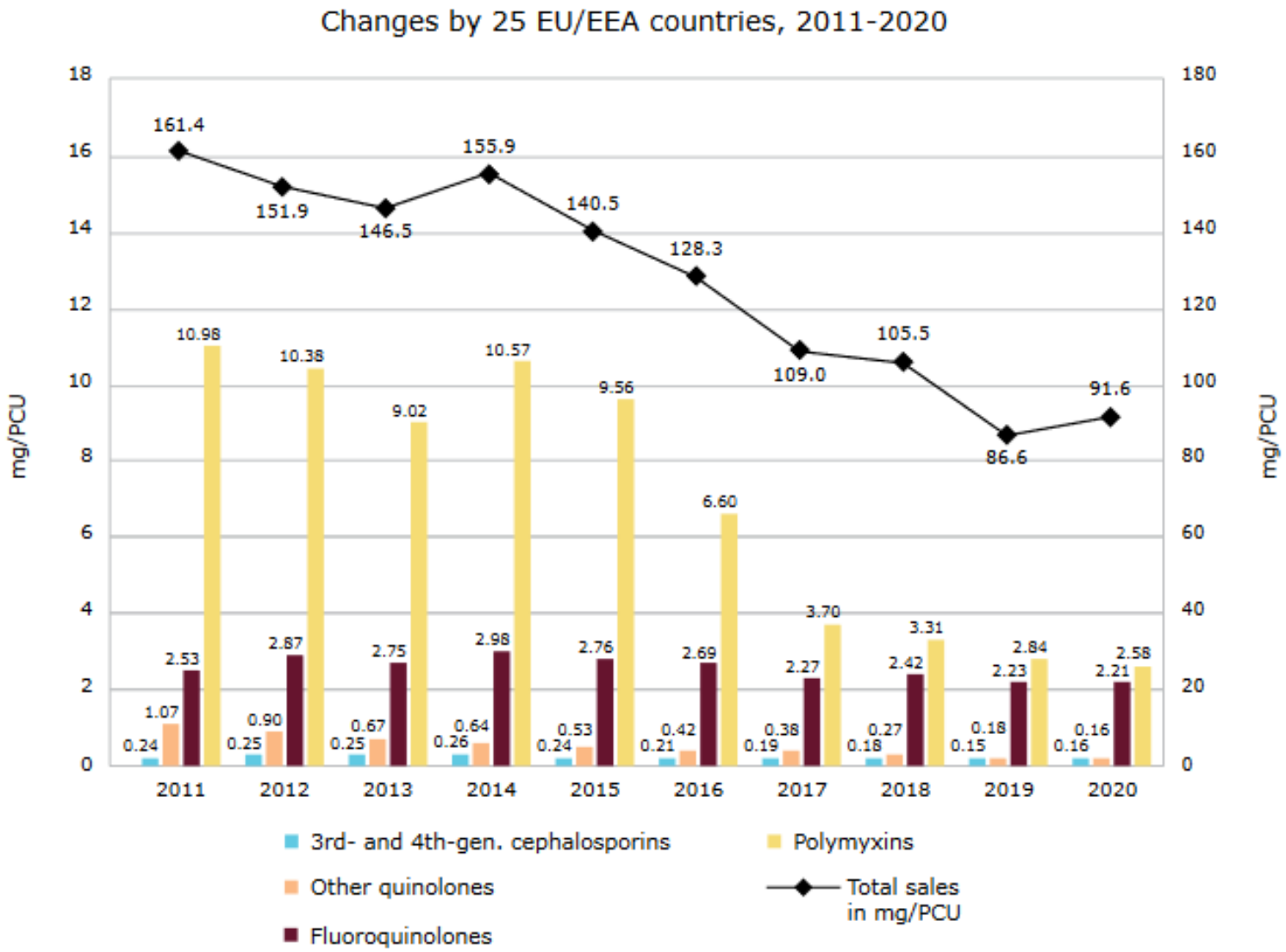

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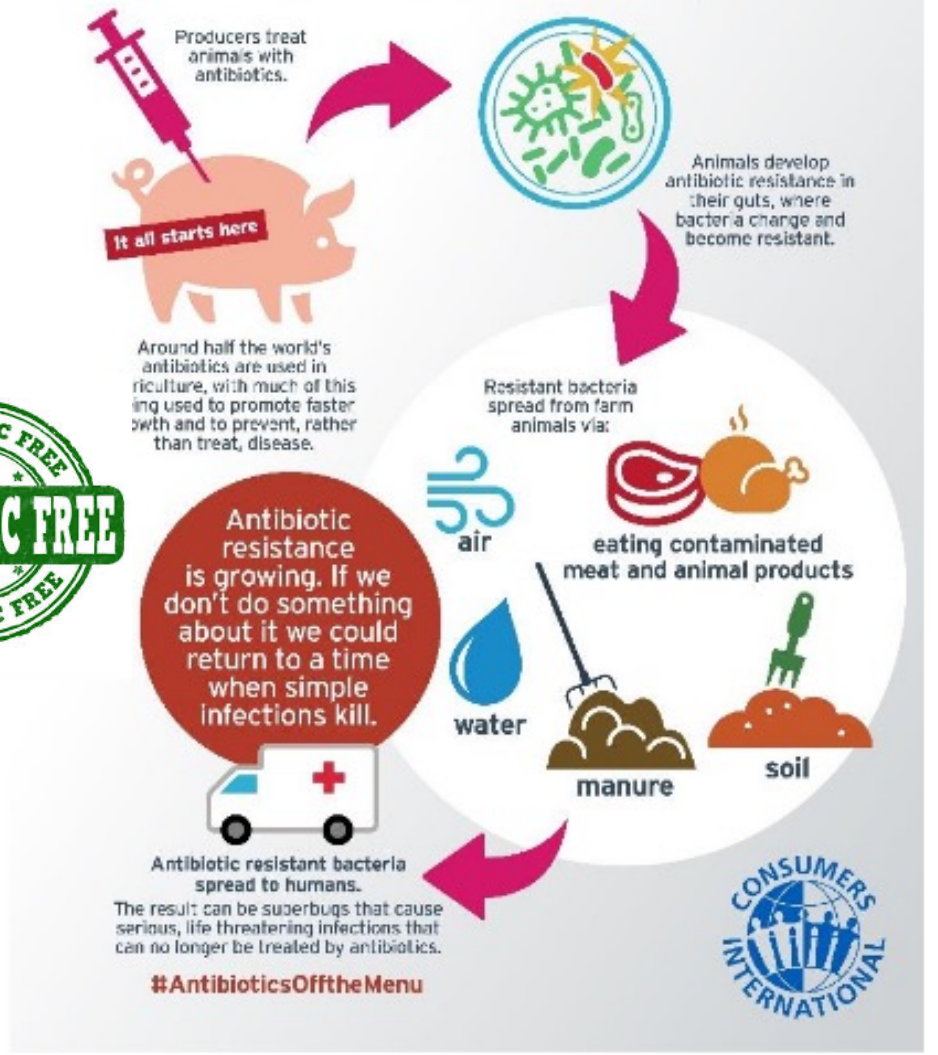
ANTIBIÓTICOS FUERA DEL MENÚ

CÓMO PUEDEN AYUDAR LAS CADENAS DE RESTAURANTES GLOBALES A ABORDAR LA RESISTENCIA A LOS ANTIBIÓTICOS

ANTIBIOTIC FREE



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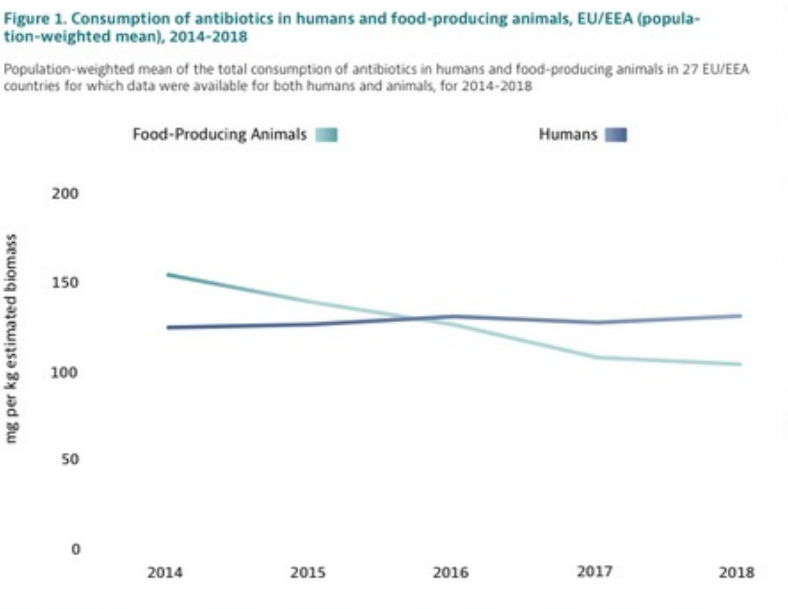
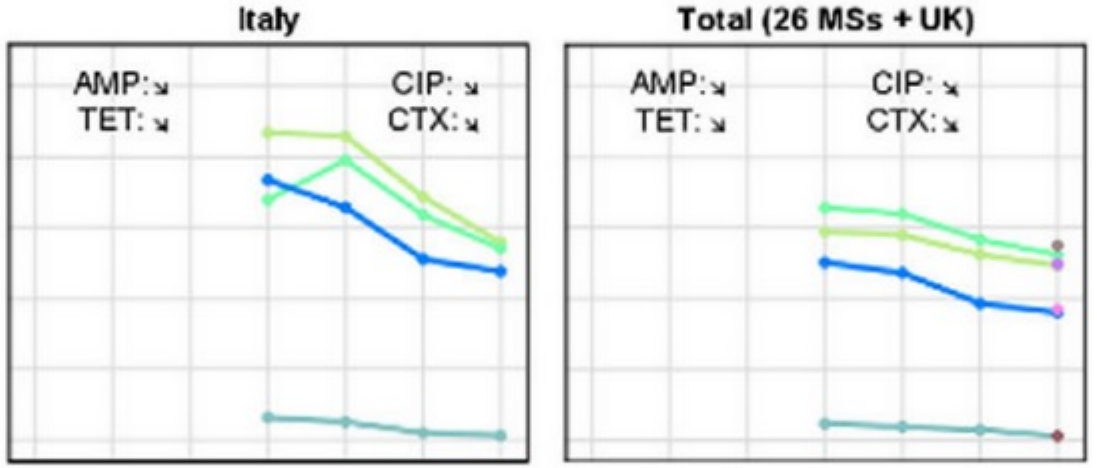
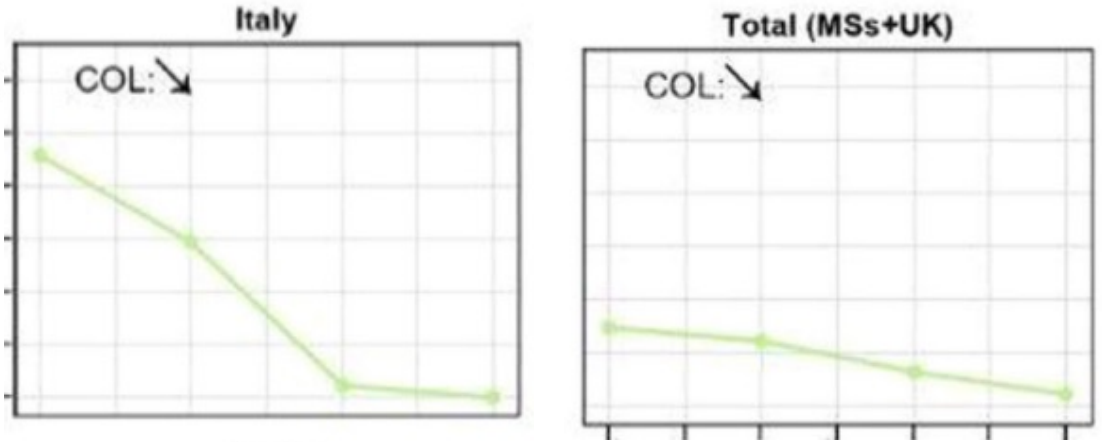
E. coli - broilers





E. coli - colistin



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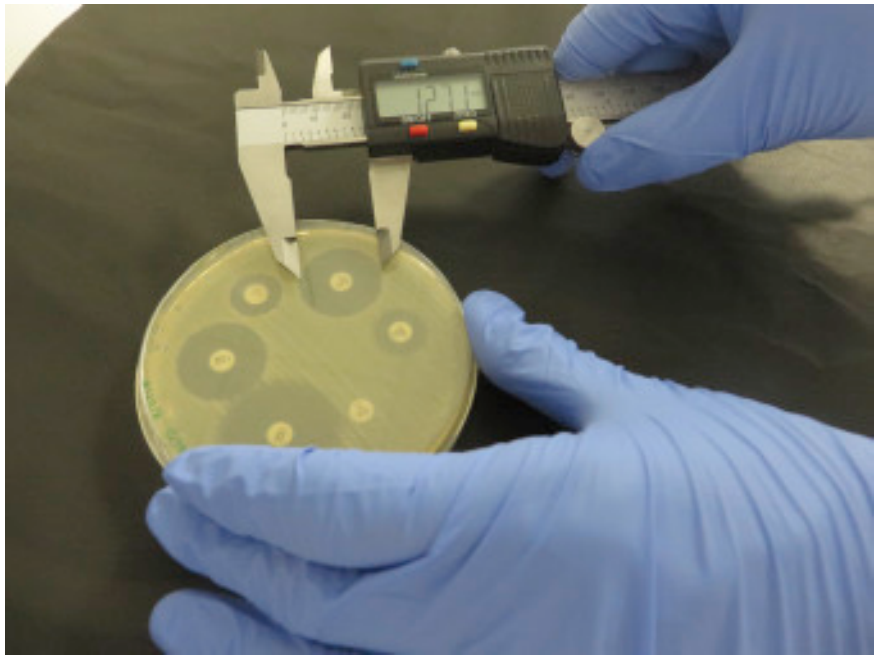

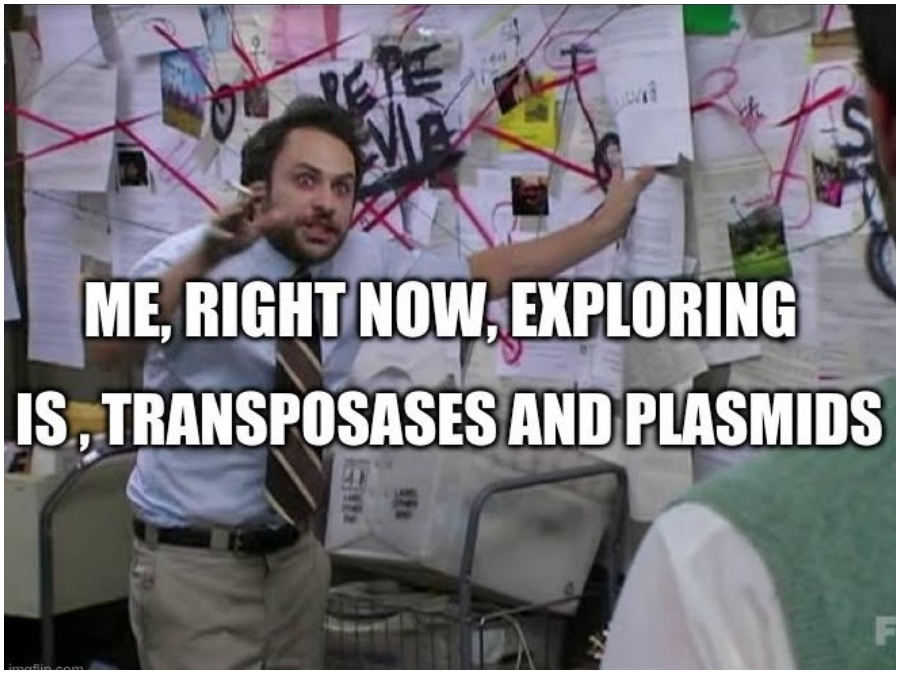

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Antibiotic resistance in the environment

D. G. Joakim Larsson[1,2]✉ *and Carl-Fredrik Flach*[1,2]

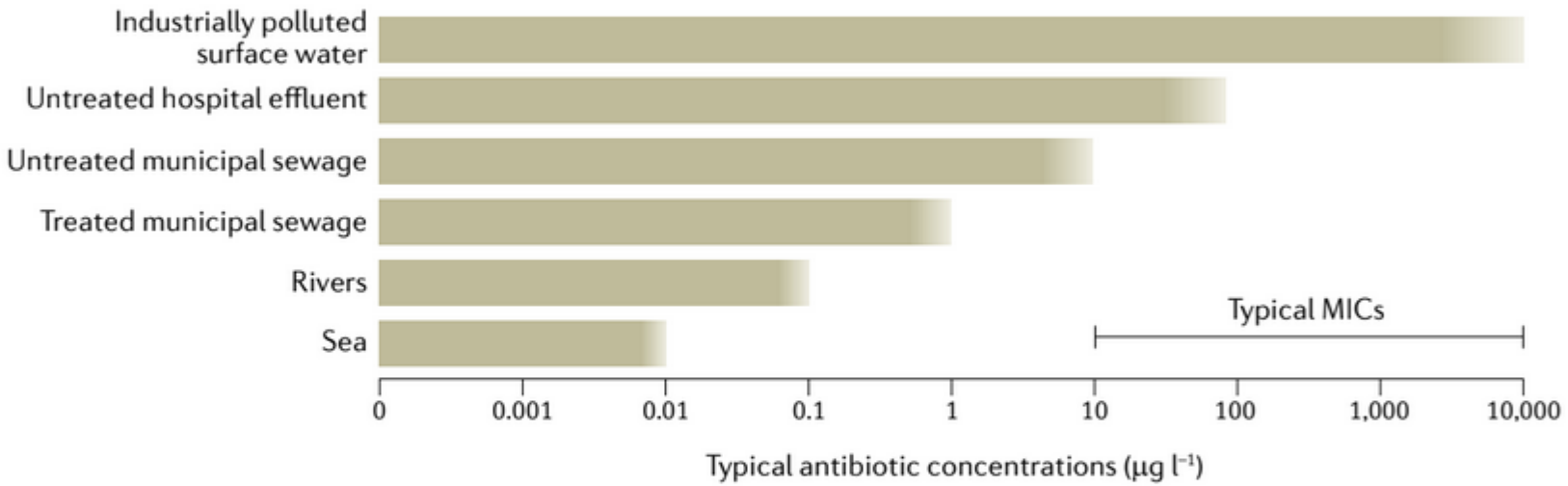

Fig. 2 | **Antibiotic concentrations in selected aquatic environments.** Different types of sources of antibiotic pollution

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Wastewater treatment plants

Sampling site	Gen									
	bla$_{CTX-M}$	*bla*$_{TEM}$	*catA1*	*cmlA*	*qnrA*	*qnrB*	*sul1*	*sul2*	*tetA*	*tetB*
	(β-lactámicos)		(Cloranfenicol)		(Quinolonas)		(Sulfametoxazol)		(Tetraciclinas)	
Influent	69,23	92,31	100,00	100,00	46,15	76,92	84,62	100,00	100,00	100,00
Effluent	61,54	92,31	92,31	92,31	23,08	46,15	61,54	92,31	61,54	84,62
Influent	72,73	100,00	81,81	100,00	63,64	72,73	90,90	100,00	100,00	100,00
Effluent	54,55	81,81	81,81	100,00	36,36	54,55	72,73	81,81	27,27	72,73
Influent	72,73	100,00	100,00	100,00	45,45	81,82	100,00	100,00	100,00	81,82
Effluent	36,36	90,90	90,90	100,00	0,00	72,73	72,73	100,00	72,73	72,73
Influent	72,73	90,90	100,00	100,00	36,36	63,64	90,90	100,00	90,90	63,64
Effluent	9,90	54,55	63,63	100,00	9,09	54,55	81,81	100,00	36,36	54,55

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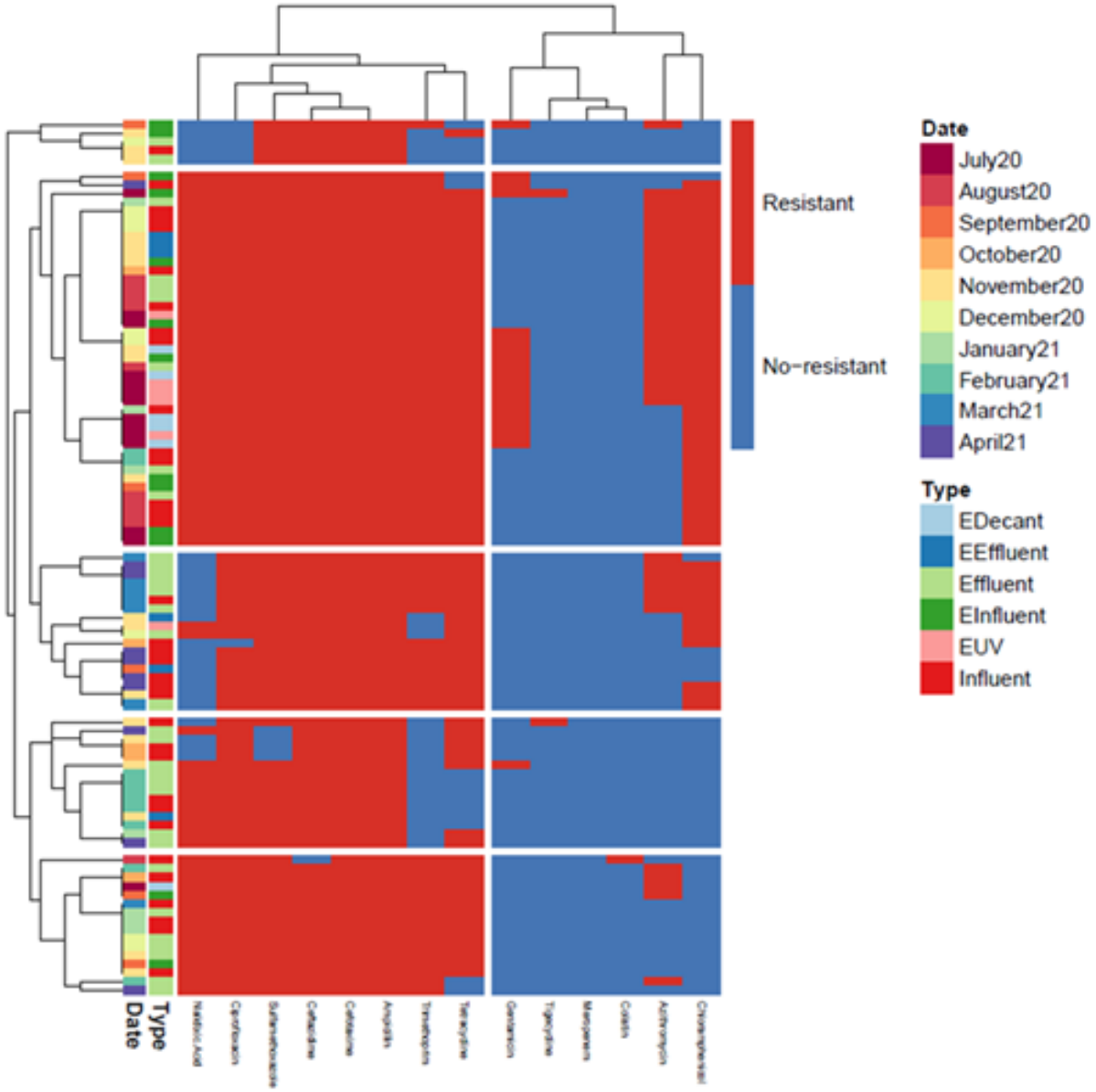

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