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French Agency for Food, Environmental and Health Safety

Challenges related to the environmental dimension of AMR

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Scientific Director on AMR, Anses

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The story of NDM-1

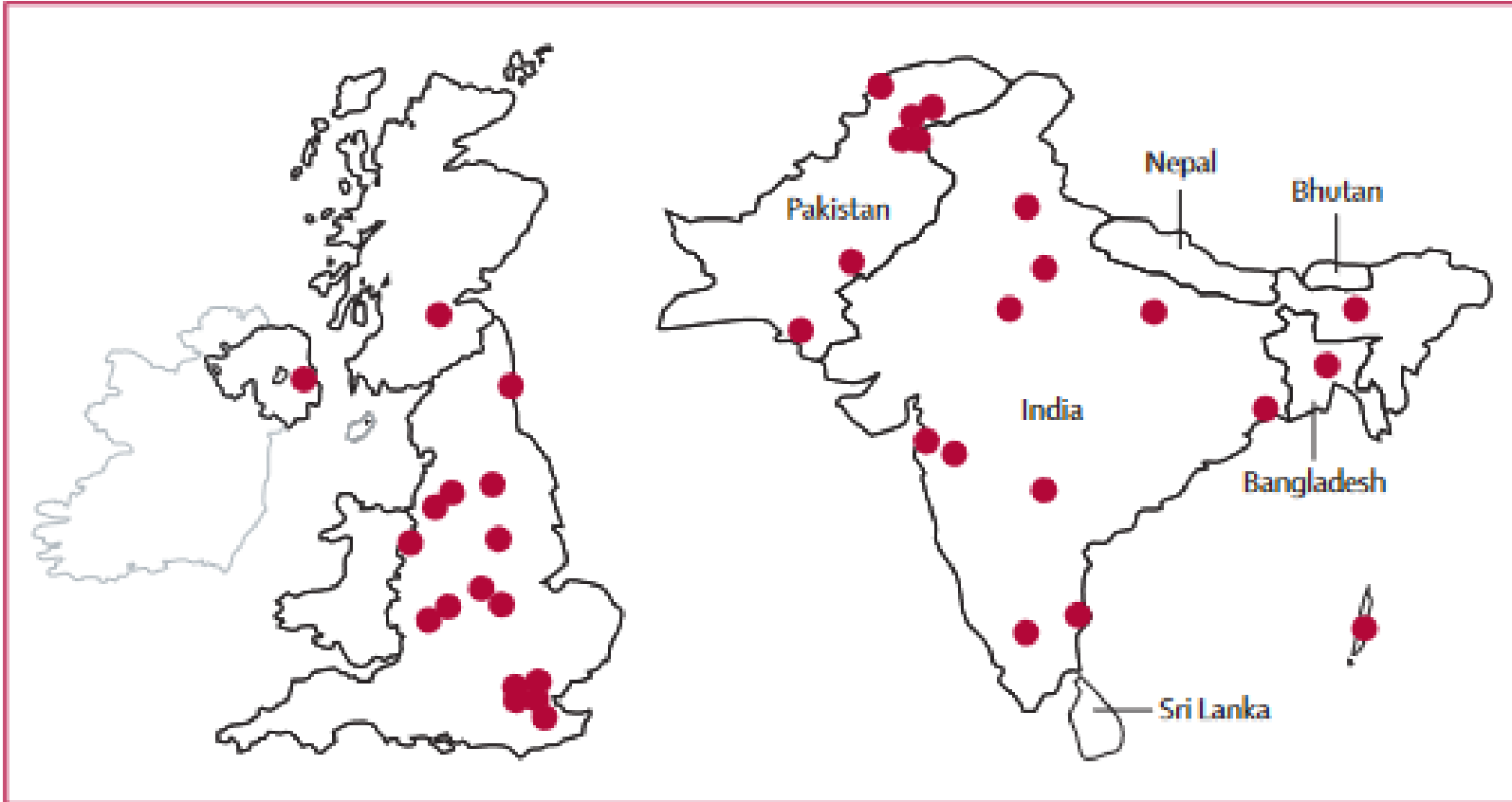


Figure 5: Distribution of NDM-1-producing Enterobacteriaceae strains in Bangladesh, Indian, Pakistan, and the UK

New Delhi Metallo-Beta-Lactamase-1 (NDM-1)

Has emerged in 2008 in the Indian subcontinent

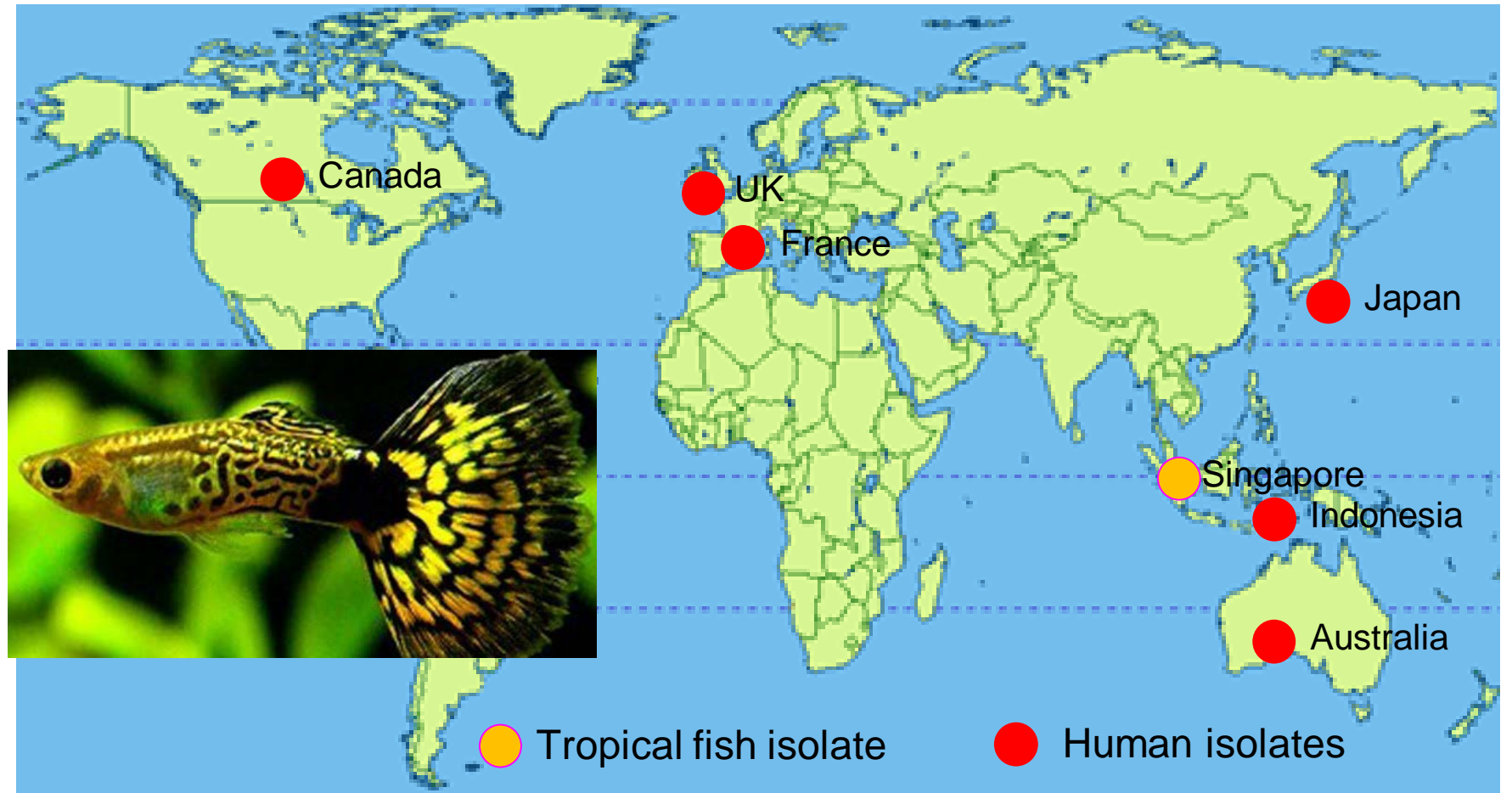
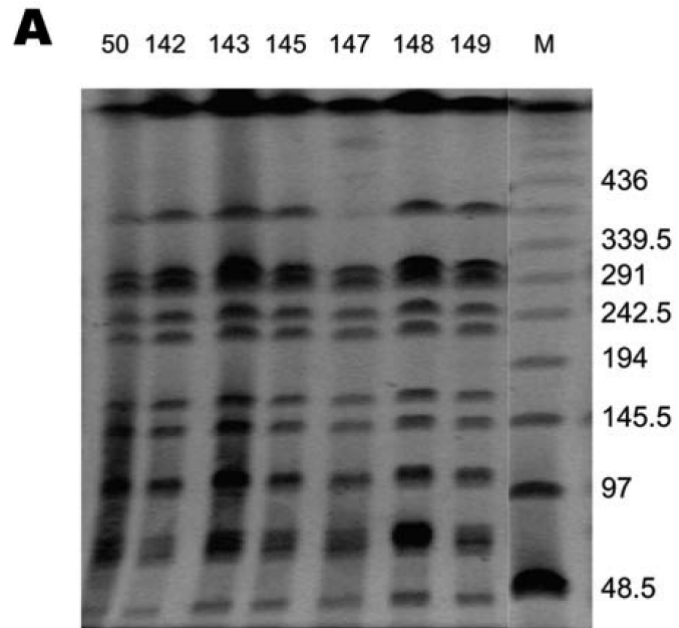
Spread to UK (medical tourism) and worldwide

NDM-1 genes found in **surface and tap waters** in 2010 in India, and **in the environment** in Bangladesh

In 2019, NDM-1 found in **nutrient-rich Arctic soil** of a remote Norwegian archipelago

The story of *Poecilia reticulata* (guppy)

Aquariums as reservoirs of multidrug resistant *Salmonella* Paratyphi B



The story of *mecC*-MRSA

Meticillin-resistant *Staphylococcus aureus* with a novel *mecA* homologue in human and bovine populations in the UK and Denmark: a descriptive study

Laura García-Alvarez, Matthew T G Halden, Heather Lindsay, Cerian R Webb, Derek F J Brown, Martin D Curran, Enid Walpole, Karen Brooks, Derek J Pickard, Christopher Teale, Julian Parkhill, Stephen D Bentley, Giles F Edwards, E Kirsty Girvan, Angela M Kearns, Bruno Pichon, Robert L R Hill, Anders Rhod Larsen, Robert L Skov, Sharon J Peacock, Duncan J Maskell, Mark A Holmes

www.thelancet.com/infection Published online June 3, 2011 DOI:10.1016/S1473-3099(11)70126-8

2011



theguardian

New strain of MRSA superbug may have spread from cattle to humans

Newly discovered MRSA strain found in cattle on 3% of dairy farms in the UK and caused 12 infections in people last year

Ian Sample, science correspondent
The Guardian, Friday 3 June 2011

The story of *mecC*-MRSA

2013

Detection of *mecC*-Positive *Staphylococcus aureus* (CC130-MRSA-XI) in Diseased European Hedgehogs (*Erinaceus europaeus*) in Sweden

Stefan Monecke^{1,2*}, Dolores Gavier-Widen^{3,4}, Roland Mattsson³, Lena Rangstrup-Christensen³, Alexandros Lazaris⁵, David C. Coleman⁵, Anna C. Shore^{5,6}, Ralf Ehricht¹



2017

High occurrence of *mecC*-MRSA in wild hedgehogs (*Erinaceus europaeus*) in Sweden

Björn Bengtsson^{a,*}, Lotta Persson^b, Kerstin Ekström^a, Helle Ericsson Unnerstad^a, Henrik Uhlhorn^a, Stefan Börjesson^a

2019

European hedgehogs (*Erinaceus europaeus*) as a natural reservoir of methicillin-resistant *Staphylococcus aureus* carrying *mecC* in Denmark

Sophie Lund Rasmussen^{1*}, Jesper Larsen², Rien E. van Wijk³, Owen R. Jones⁴, Thomas Bjørneboe Berg^{1,5}, Øystein Angen², Anders Rhod Larsen²

The story of *mecC*-MRSA

Emergence of methicillin resistance predates the clinical use of antibiotics

<https://doi.org/10.1038/s41586-021-04265-w>

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 Check for updates

Jesper Larsen^{1,59,63}, Claire L. Raisen^{2,55}, Xiaoliang Ba², Nicholas J. Sadgrove³, Guillermo F. Padilla-González², Monique S. J. Simmonds⁴, Igor Loncaric⁴, Heidrun Kerschner⁵, Petra Apfalter⁵, Rainer Hartl⁵, Ariane Deplano⁵, Stien Vandendriessche^{6,48}, Barbora Černá Bolfiková⁷, Pavel Hulva^{8,9}, Maiken C. Arendrup¹, Rasmus K. Hare¹, Céline Barnadas^{1,10}, Marc Stegger¹, Raphael N. Sieber¹, Robert L. Skov¹¹, Andreas Petersen¹, Øystein Angen¹, Sophie L. Rasmussen^{12,13}, Carmen Espinosa-Gongora¹⁴, Frank M. Aarestrup¹⁵, Laura J. Lindholm¹⁶, Suvi M. Nykäsenoja¹⁷, Frederic Laurent¹⁸, Karsten Becker¹⁹, Birgit Walther^{20,47}, Corinna Kehrenberg²¹, Christiane Cuny²², Franziska Layer²², Guido Werner²², Wolfgang Witte²², Ivonne Stamm²³, Paolo Moroni^{24,48}, Hannah J. Jørgensen²⁵, Herminia de Lencastre^{26,27}, Emilia Cercenado²⁸, Fernando Garcia-Garrote^{28,49}, Stefan Börjesson^{29,50}, Sara Hæggman³⁰, Vincent Perreten³¹, Christopher J. Teale³², Andrew S. Waller^{33,51,52}, Bruno Pichon³⁴, Martin D. Curran³⁵, Matthew J. Ellington^{35,53}, John J. Welch³⁶, Sharon J. Peacock³⁷, David J. Seilly², Fiona J. E. Morgan^{2,54}, Julian Parkhill², Nazreen F. Hadjirin², Jodi A. Lindsay³⁸, Matthew T. G. Holden³⁹, Giles F. Edwards⁴⁰, Geoffrey Foster⁴¹, Gavin K. Paterson⁴², Xavier Didelot⁴³, Mark A. Holmes^{2,56}, Ewan M. Harrison^{37,44,45,56} & Anders R. Larsen^{1,56}

mecC-MRSA was driven by natural selection by dermatophyte *Trichophyton erinacei* producing penicillin and colonizing hedgehogs



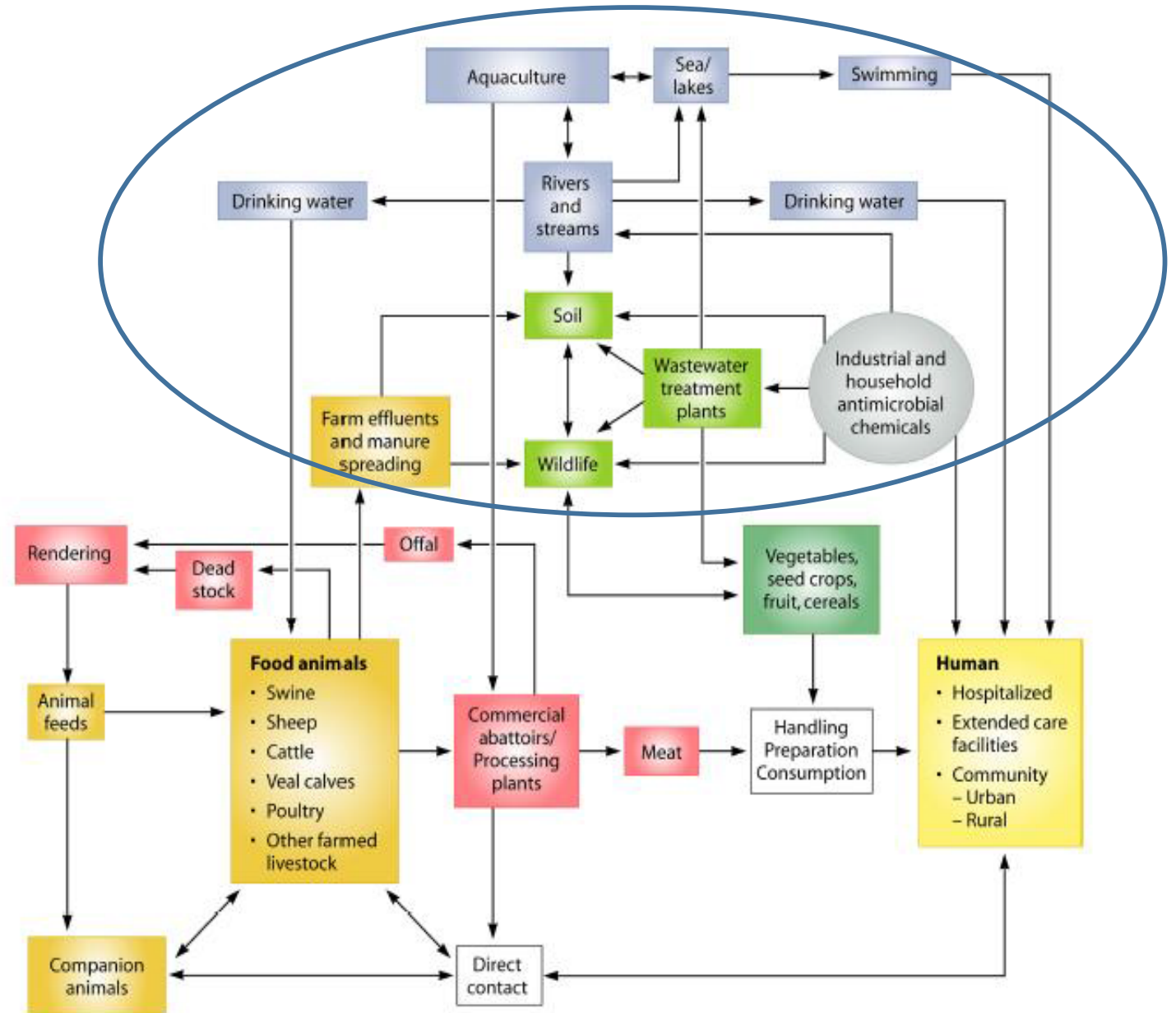
AMR is One Health

Need for an integrated and holistic multi-sectoral approach



AMR is One Health

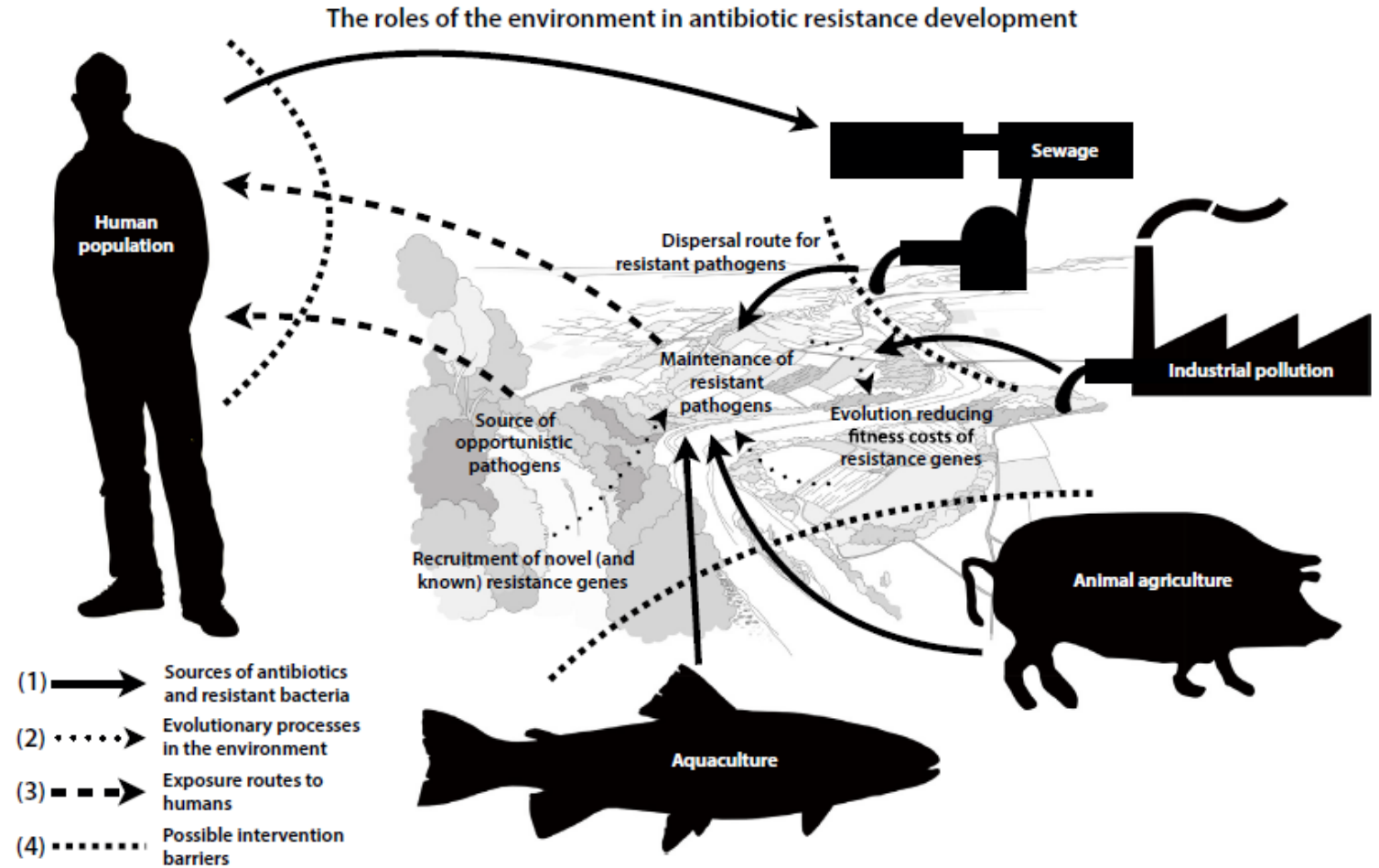
What definition for “the environment “ ?



The complex interplay between different sectors in the spread of antimicrobial resistance (from Davies & Davies, Microbiol Mol Biol Rev. 2010)

Dual aspect of the environment

Source of ...
Polluted by ...



(from Larsson et al, Environment International, 2018)

Antibiotics and AMR were present in the environment well before anthropogenic use

DOMAIN 11 ANTIBIOTIC MECHANISMS AND RESISTANCE

Ancient Antibiotics, Ancient Resistance

NICHOLAS WAGLECHNER,^a ELIZABETH J. CULP,^a AND
GERARD D. WRIGHT^a

^aM.G. DeGrootte Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, David Braley Centre for Antibiotic Discovery, McMaster University, Hamilton, Ontario, L8S 4K1, Canada

Nicholas Waglechner and Elizabeth J. Culp These authors contributed equally to this work.

The role of antibiotics in nature

What concentrations of antibiotics are bacteria exposed to in nature ?

Dating the origin of antibiotics

AMR in environmental isolates is far more diverse than that observed in pathogens

Antibiotics and AMR were present in the environment well before anthropogenic use



Antimicrobial peptide from frog skin

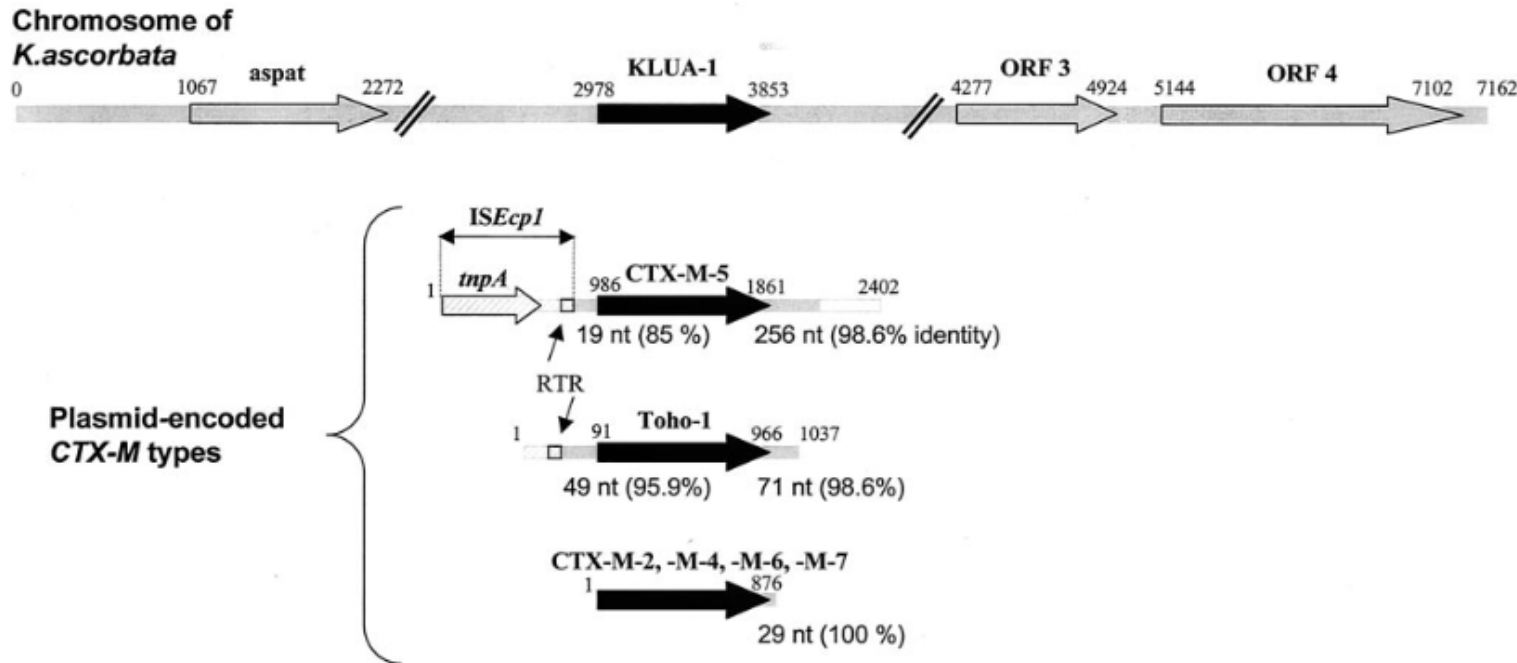
Rollins-Smith et al, Bioch Bioph Research Comm 2002



Teixobactin produced by *Eleftheria terrae*

Ling et al, Nature 2015

AMR genes in clinics have progenitors in nature



The epidemic spread of CTX-M beta-lactamases

AMR genes are actually pleiotropic in environmental isolates

It also questions the commonly held notion that AMR genes mobilization is in response to human antibiotic use

Coevolution of antibiotics and AMR genes in a co-evolutionary setting

β -Lactamases of *Kluyvera ascorbata*, Probable Progenitors of Some Plasmid-Encoded CTX-M Types

Christel Humeniuk,¹ Guillaume Arlet,² Valerie Gautier,² Patrick Grimont,³
 Roger Labia,⁴ and Alain Philippon^{1*}

The pandemic expansion of CTX-M enzymes



Contents lists available at SciVerse ScienceDirect

International Journal of Medical Microbiology

journal homepage: www.elsevier.com/locate/ijmm



Mini review

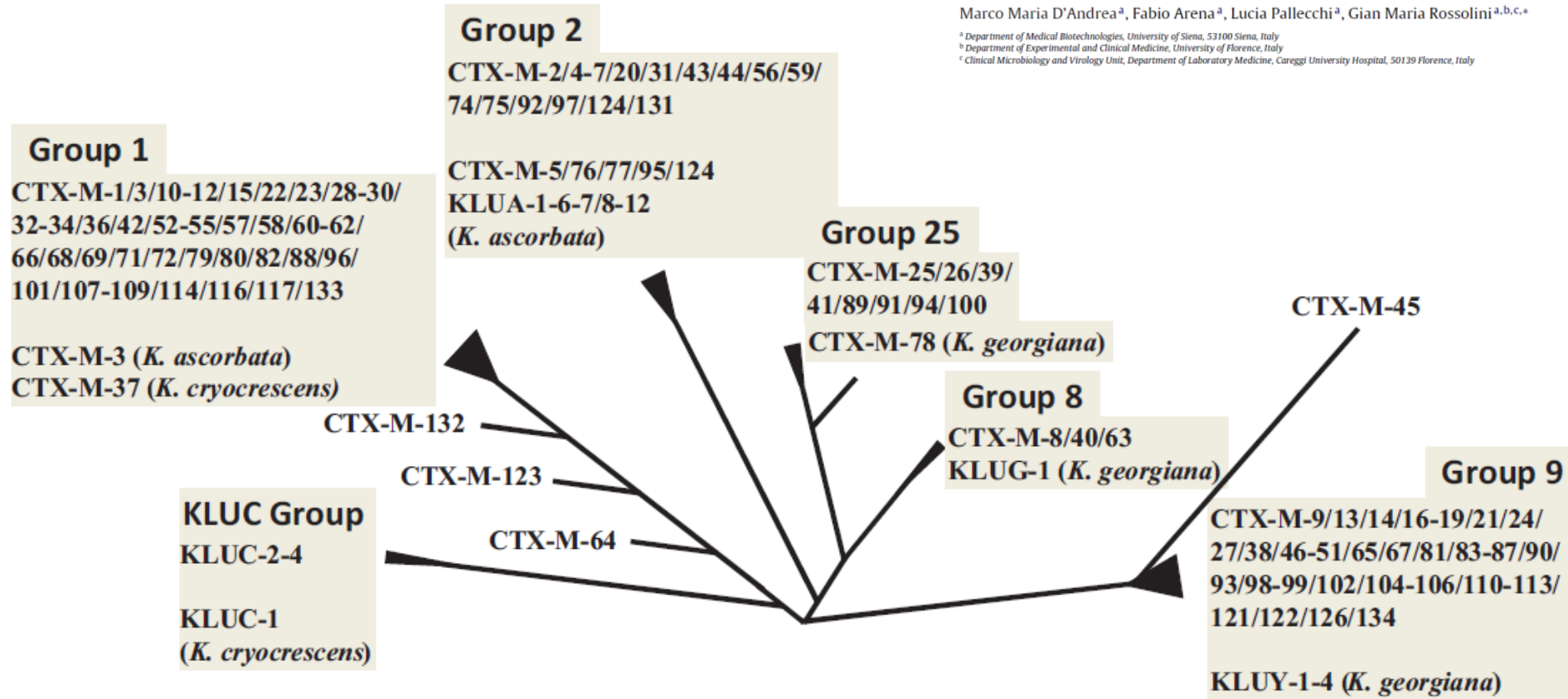
CTX-M-type β -lactamases: A successful story of antibiotic resistance

Marco Maria D'Andrea^a, Fabio Arena^a, Lucia Pallecchi^a, Gian Maria Rossolini^{a,b,c,*}

^a Department of Medical Biotechnologies, University of Siena, 53100 Siena, Italy

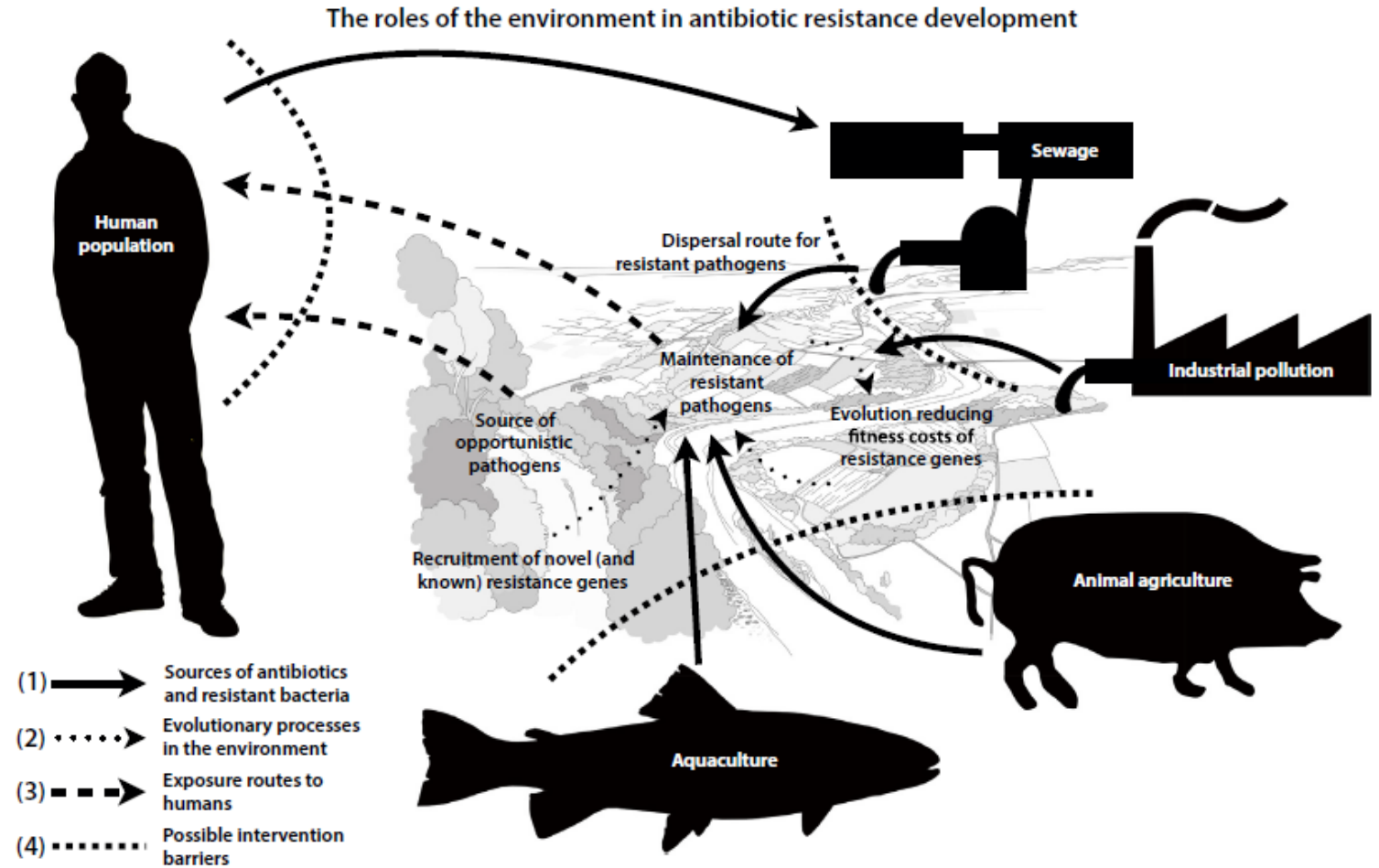
^b Department of Experimental and Clinical Medicine, University of Florence, Italy

^c Clinical Microbiology and Virology Unit, Department of Laboratory Medicine, Careggi University Hospital, 50139 Florence, Italy



Dual aspect of the environment

Source of ...
Polluted by ...



(from Larsson et al, Environment International, 2018)

Pollution with (anthropogenic-related) AMR

ESBL *E. coli*



Hernandez PLoS One 2013



Blaak AEM 2014



Bréchet CID 2014



Hartmann Frontiers 2012



Mani AAC 2018



Yaici JAC 2017



Kola JAC 2012



Van Hoek IJFM 2015

Pollution with (anthropogenic-related) AMR



Bizerte Lagoon

KPC-3-producing ST167 *Escherichia coli* from mussels bought at a retail market in Tunisia

Yosra Mani^{1†}, Wejdene Mansour^{1,2†}, Hedi Mammeri³⁻⁵, Erick Denamur⁴⁻⁶, Estelle Saras⁷, Nouredine Boujâafar^{1,8}, Olfa Bouallègue^{1,9}, Jean-Yves Madec^{7*} and Marisa Haenni⁷

JAC 2017

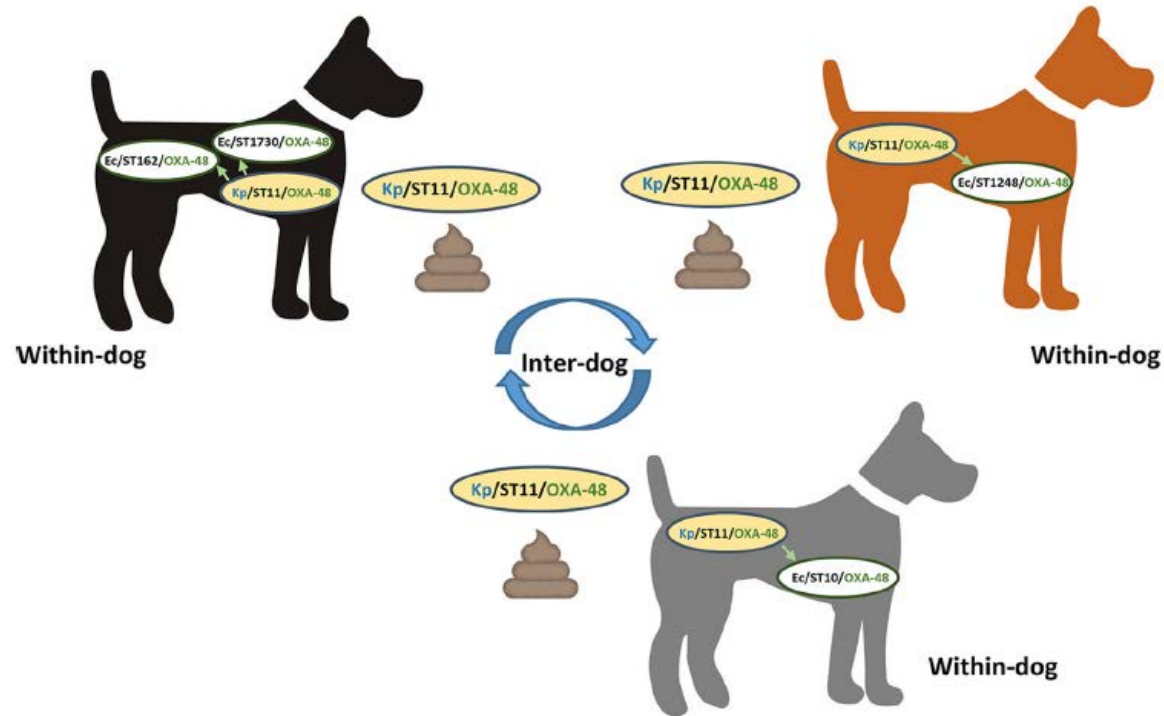
Spread of bla_{CTX-M-15}-Producing *Enterobacteriaceae* and OXA-23-Producing *Acinetobacter baumannii* Sequence Type 2 in Tunisian Seafood

Yosra Mani,³ Wejdene Mansour,^{2,b} Agnese Lupo,^c Estelle Saras,^c Olfa Bouallègue,^{3,d} Jean-Yves Madec,^c Marisa Haenni^c

AAC 2018



Pollution with (anthropogenic-related) AMR



Spread of the *bla*_{OXA-48}/IncL Plasmid within and between Dogs in City Parks, France

Marisa Haenni,^a Véronique Métayer,^a Agnese Lupo,^a Antoine Drapeau,^a Jean-Yves Madec^a

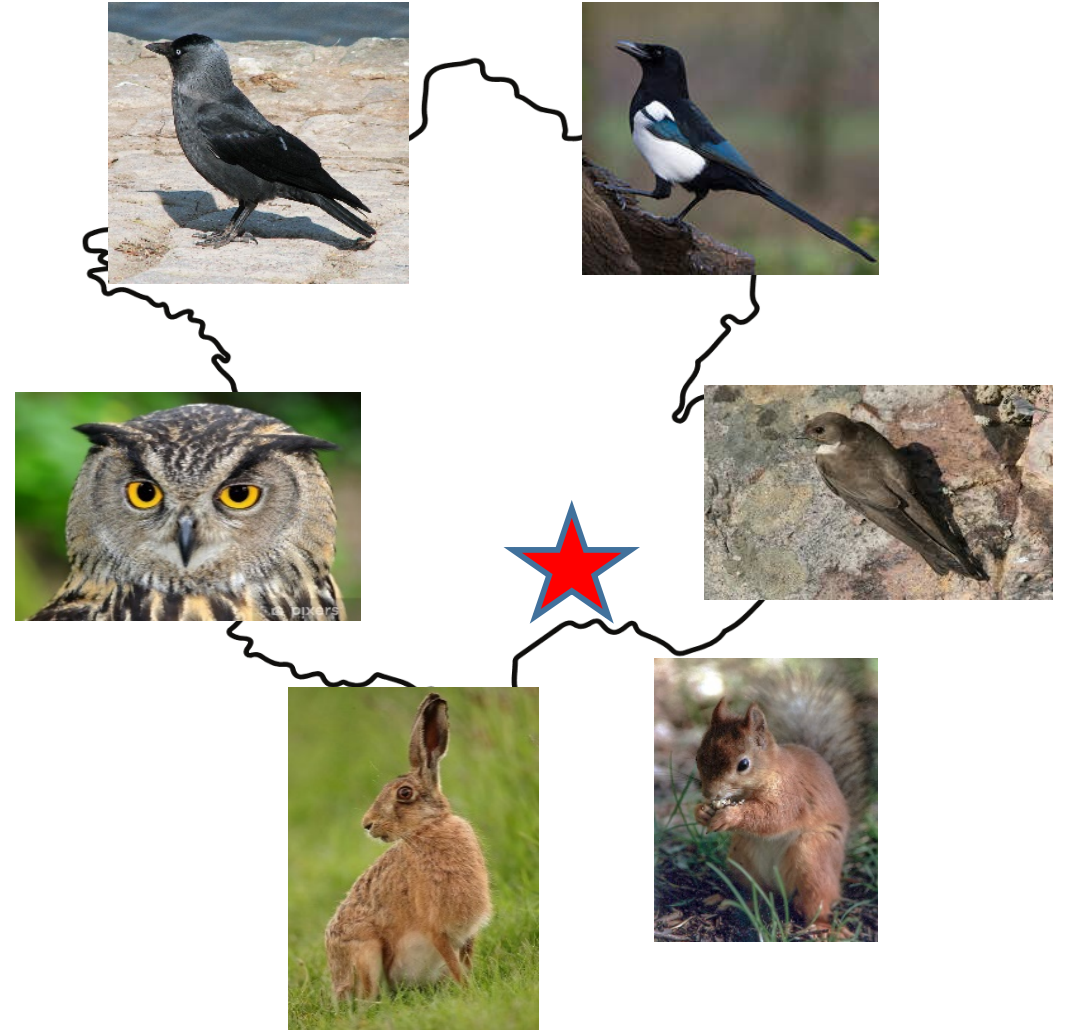
Pollution with (anthropogenic-related) AMR

Over 400 wild animals at wildlife rescue center (France)

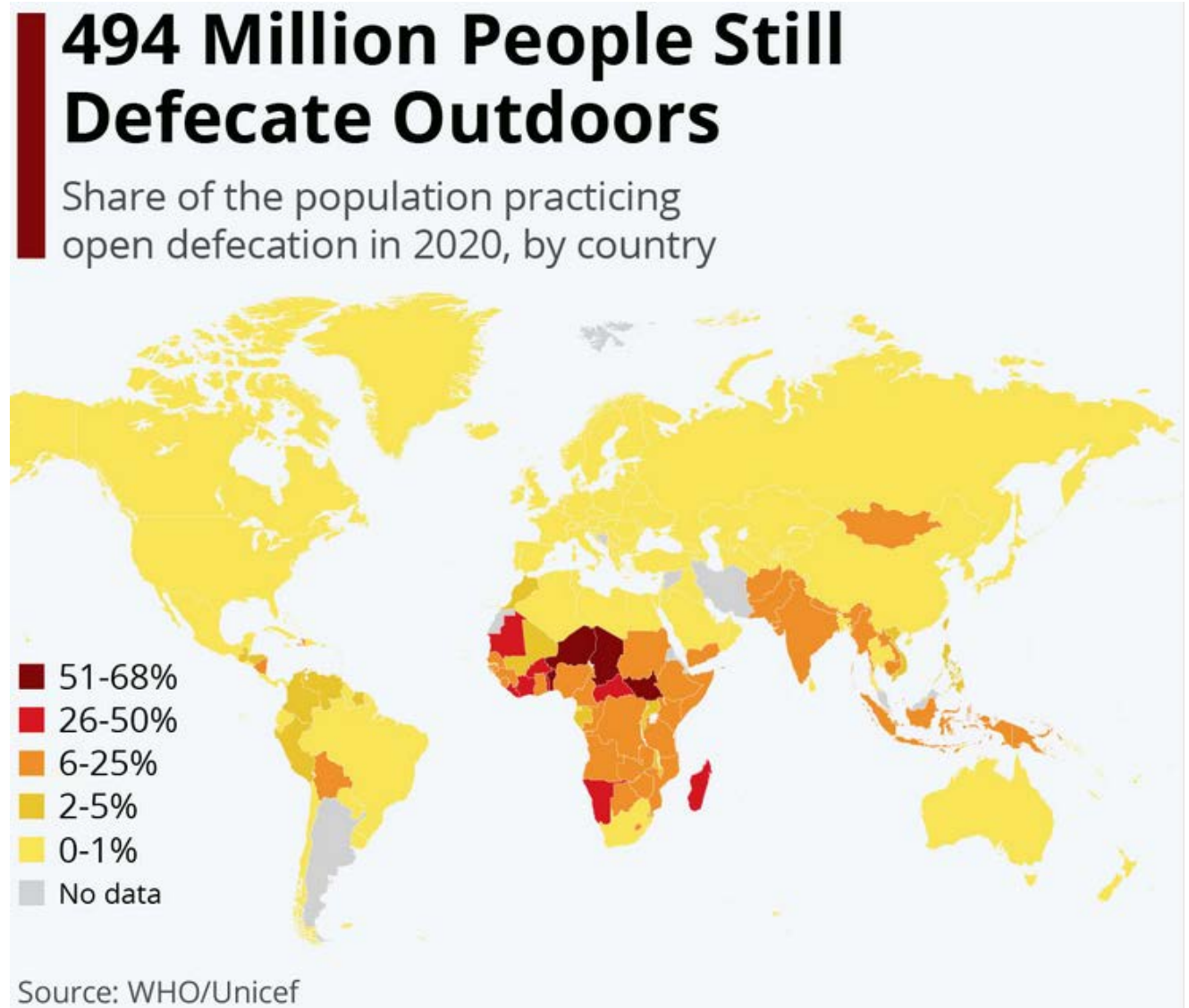
25% of animals acquired ESBL during their stay

Limited number of ESBL clones, one dominant ESBL plasmid

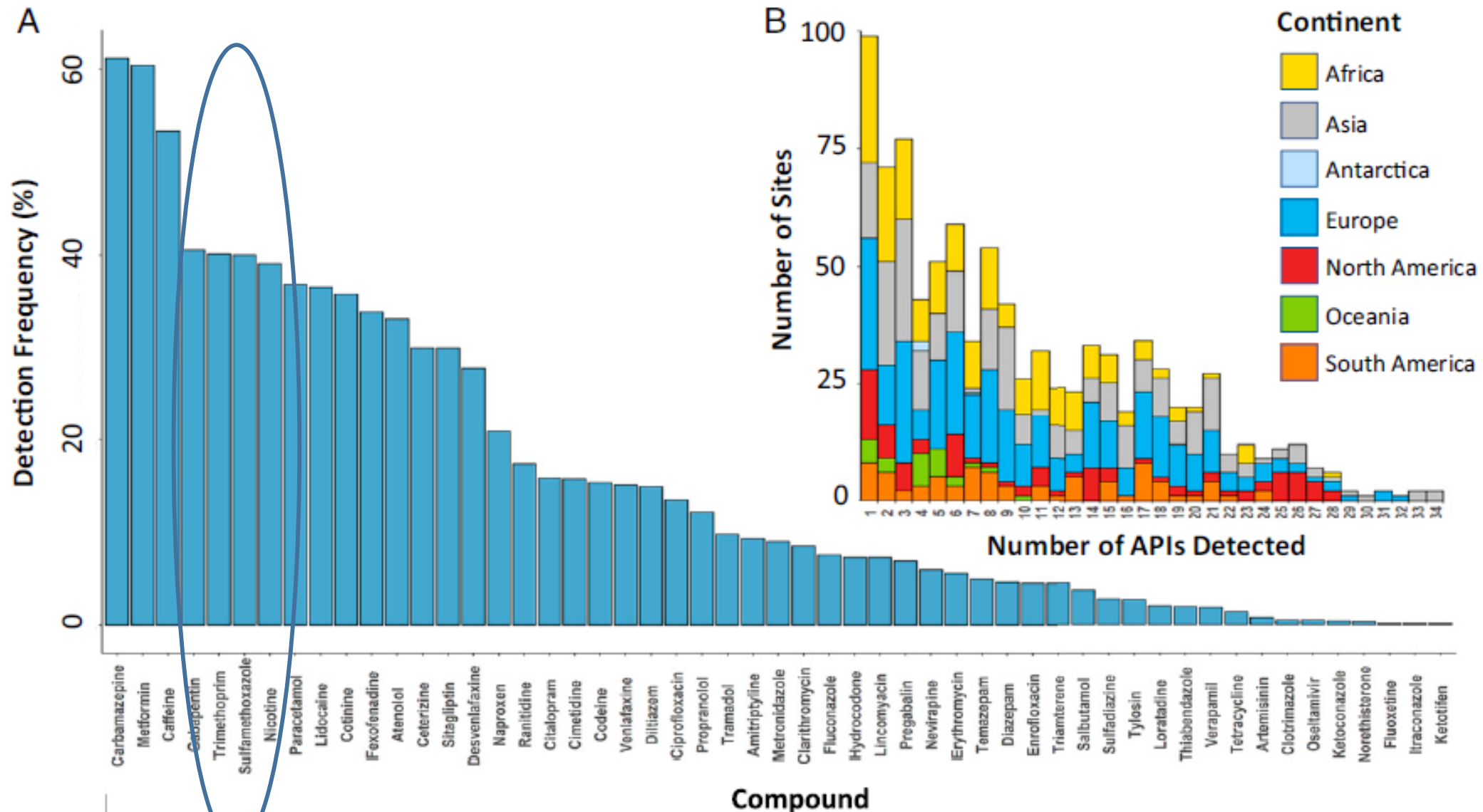
It questions the ecological impact **when animals are released in nature** after recovery



Wastewater is a major issue for AMR



Pollution with pharmaceuticals



Pollution with pharmaceuticals



Sulfonamides dominant in sewage in tropical Asia

Sulfamethazine and oxytetracyclines dominant in livestock and aquaculture waste

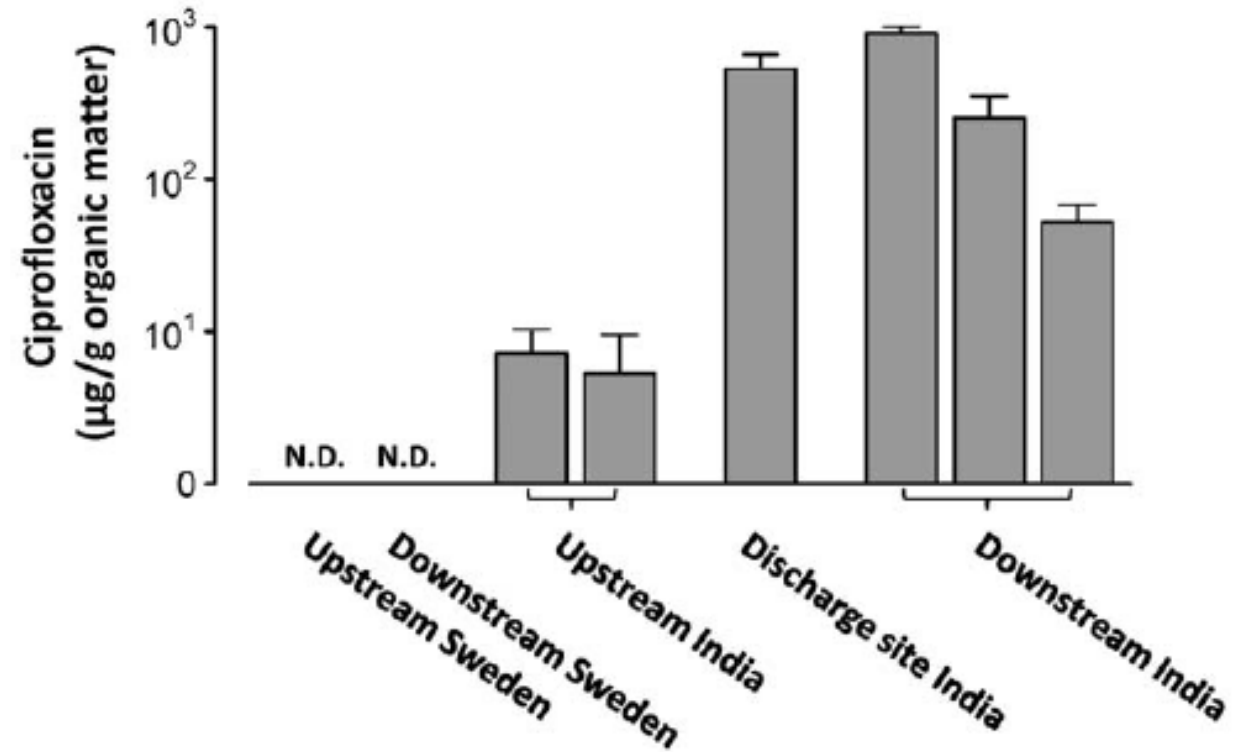
12 tons/year of sulfamethoxazole is supplied from Mekong river to South China sea

Shimizu et al, Sci of the Total Environment, 2013

Pollution with pharmaceuticals



Resistance in Antibiotic-Contaminated Sediments



Kristiansson et al, PLoS One, 2021

Pollution with pharmaceuticals



Contents lists available at [ScienceDirect](#)

Environment International

journal homepage: www.elsevier.com/locate/envint

Environmental contamination in a high-income country (France) by antibiotics, antibiotic-resistant bacteria, and antibiotic resistance genes: Status and possible causes

Marisa Haenni^a, Christophe Dagot^b, Olivier Chesneau^c, Delphine Bibbal^d, Jérôme Labanowski^e, Michèle Vialette^f, Damien Bouchard^g, Fabrice Martin-Laurent^h, Louisiane Calsatⁱ, Sylvie Nazaret^j, Fabienne Petit^{k,l}, Anne-Marie Pourcher^m, Anne Togolaⁿ, Morgane Bachelot^o, Edward Topp^p, Didier Hocquet^{q,r,*}



Fluoroquinolones and trimethoprim
at higher risk of AMR selection

Effluents of wastewater treatment
plants as a major source of antibiotics
pollution

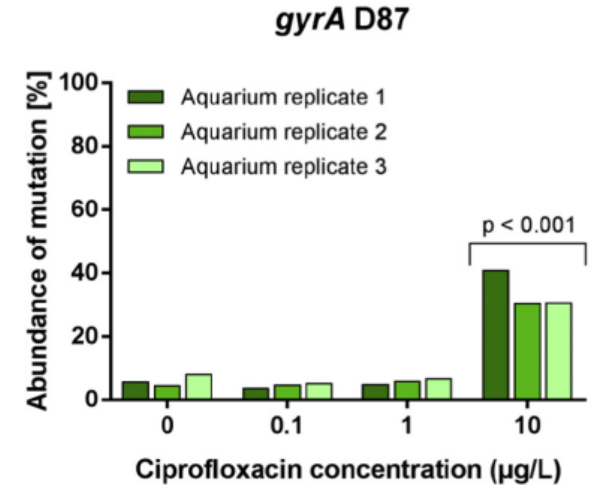
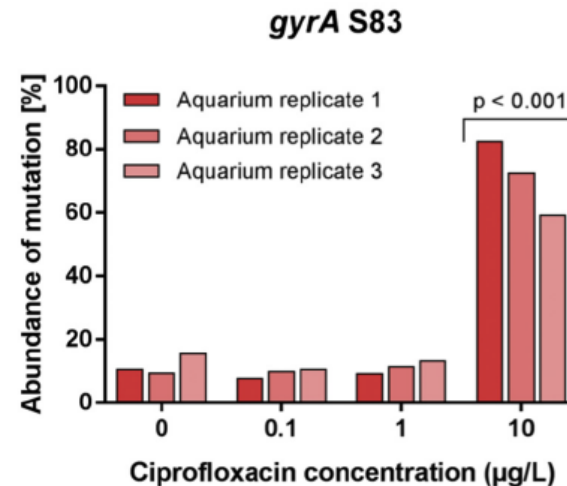
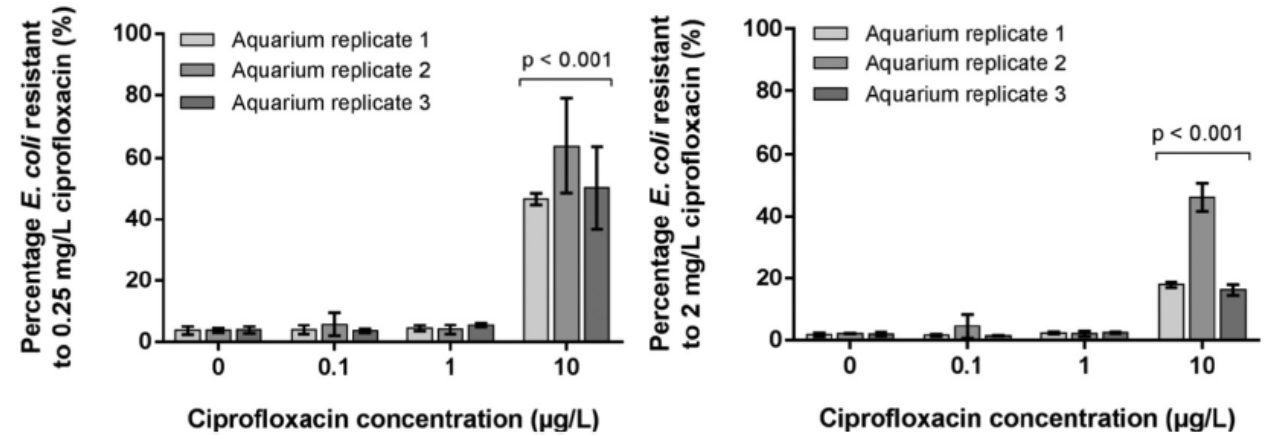
Proposed list of indicators

Harmonization of methods and
sampling strategies

Pollution with pharmaceuticals

What levels of antibiotics are needed to select AMR in complex bacterial communities ?

CIP-R *E. coli* grown in complex aquatic biofilms with different CIP concentrations



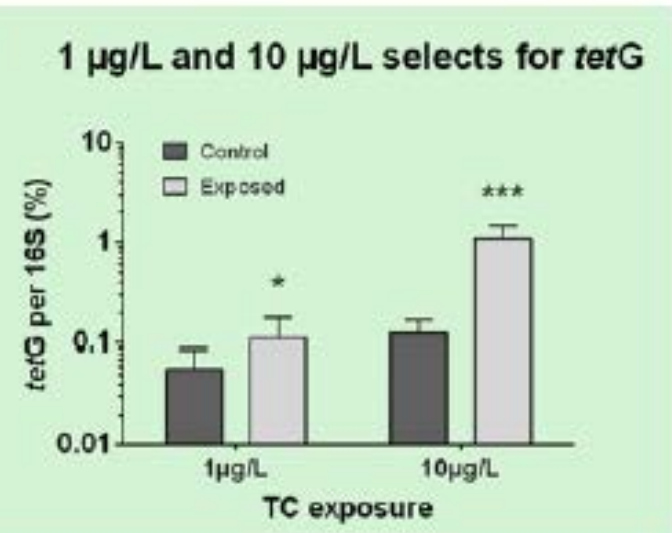
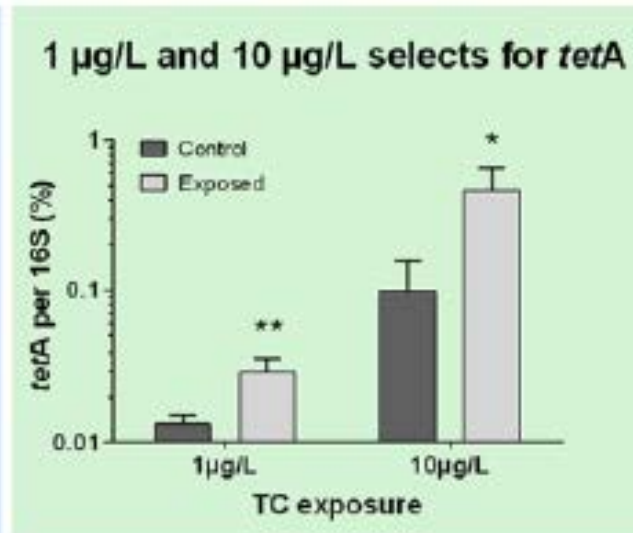
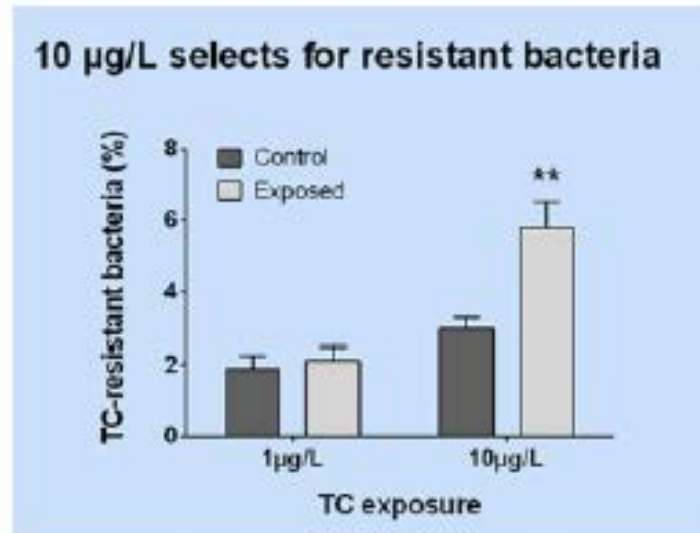
Pollution with pharmaceuticals

What levels of antibiotics are needed to select AMR in complex bacterial communities ?

One $\mu\text{g}/\text{mL}$ of tetracycline selects *tetA* and *tetG* genes in freshwater biofilms

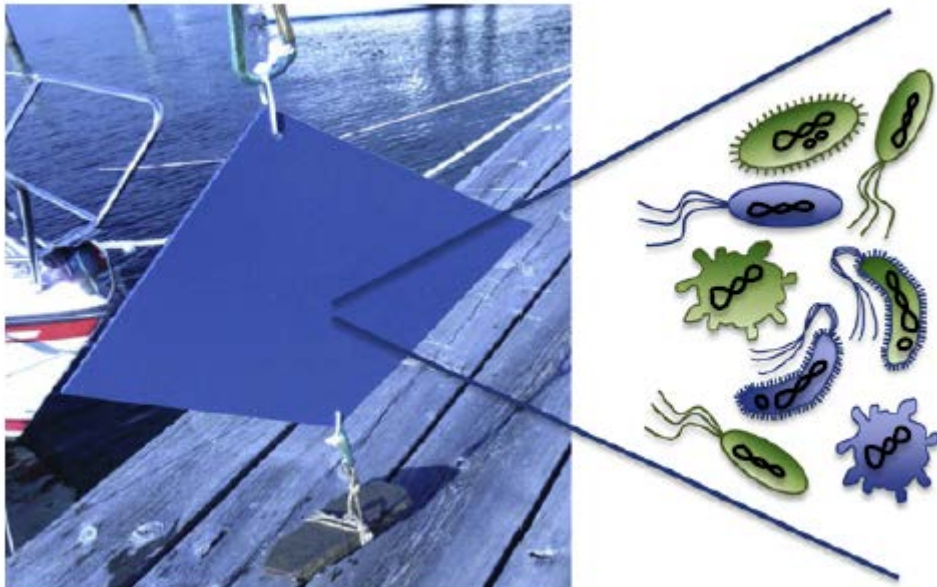
Ten $\mu\text{g}/\text{mL}$ of tetracycline selects for phenotypic resistance

Selective concentrations overlap with those reported in sewage treatment plants

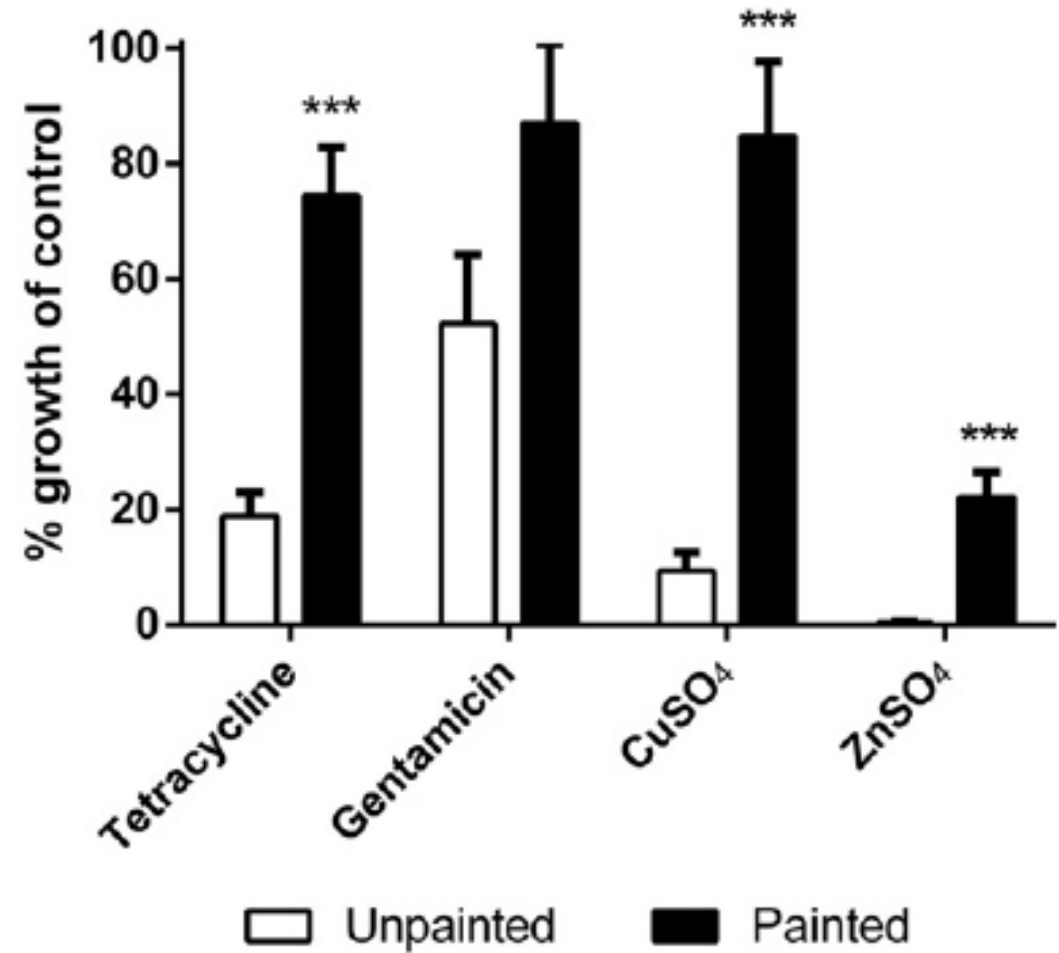


Pollution with pharmaceuticals

AMR from marine biofilms on **painted** and unpainted surfaces



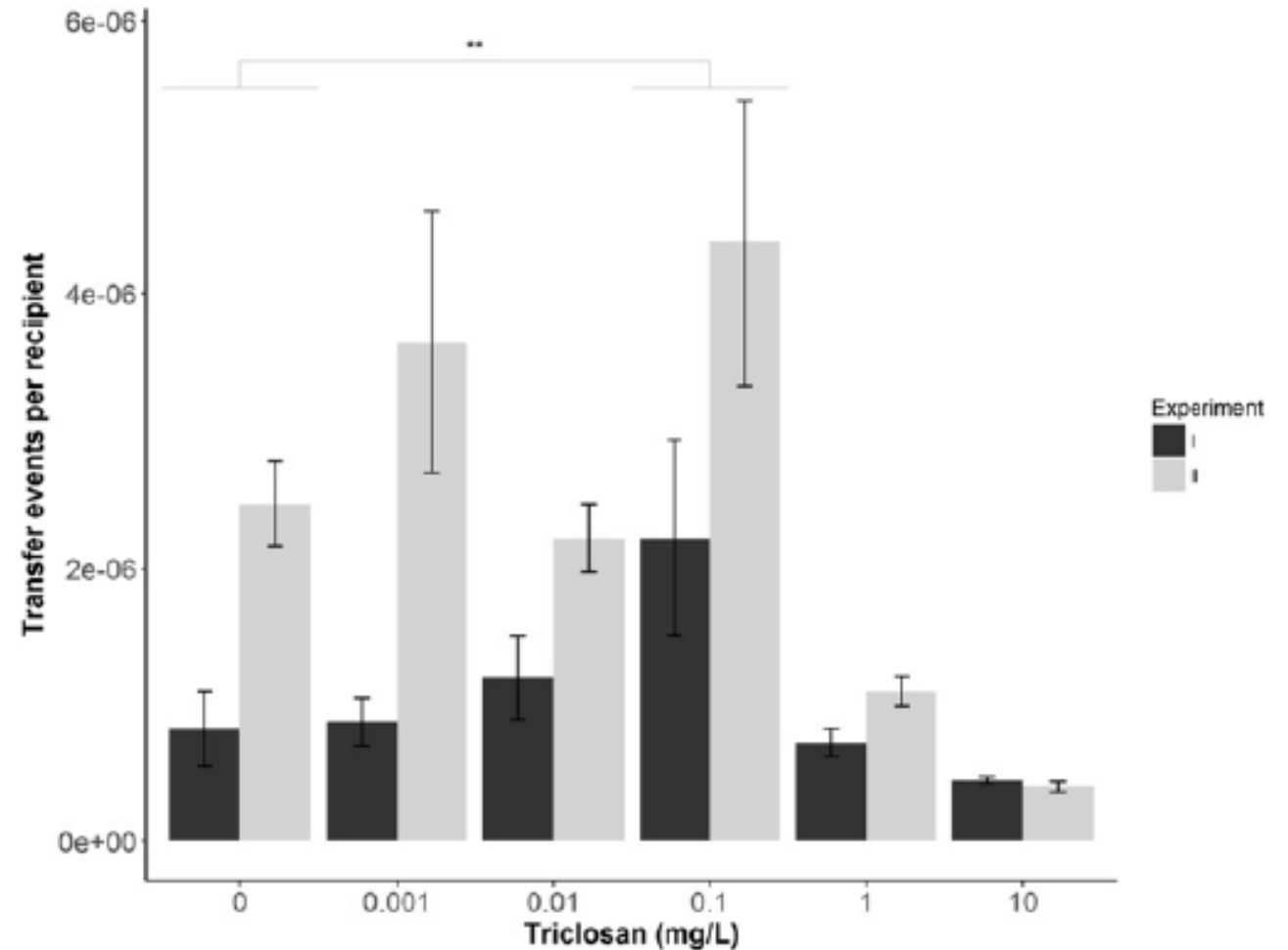
Do other chemical compounds than antibiotics select AMR ?



Pollution with pharmaceuticals

Do other chemical compounds than antibiotics select AMR ?

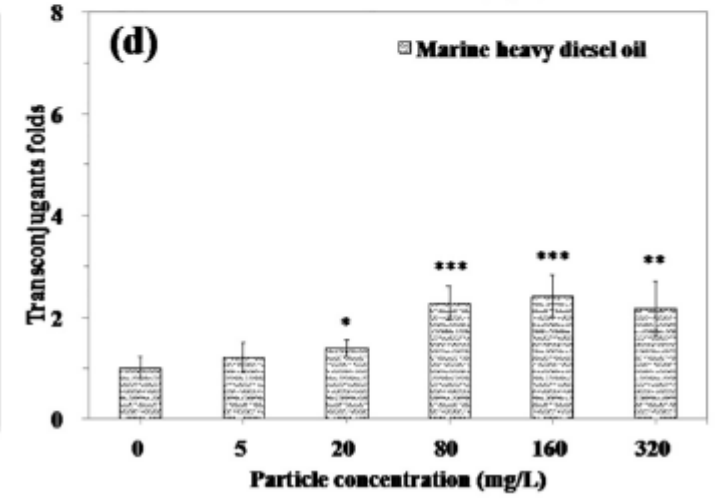
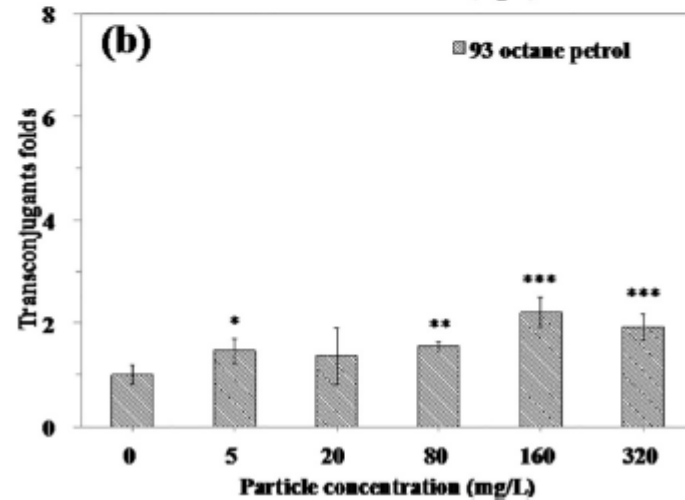
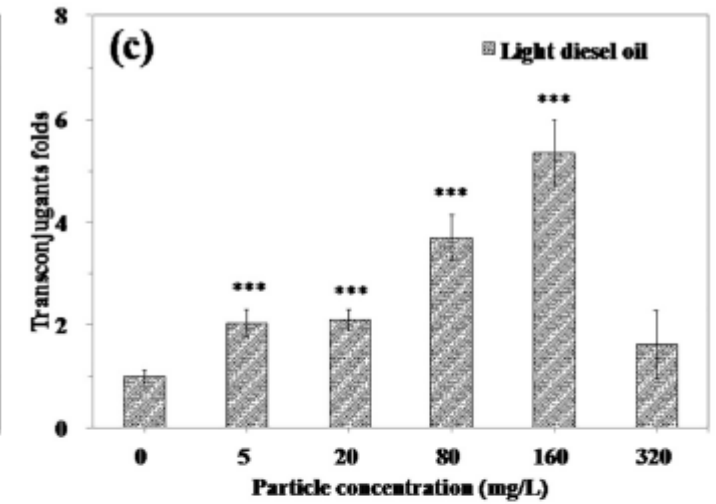
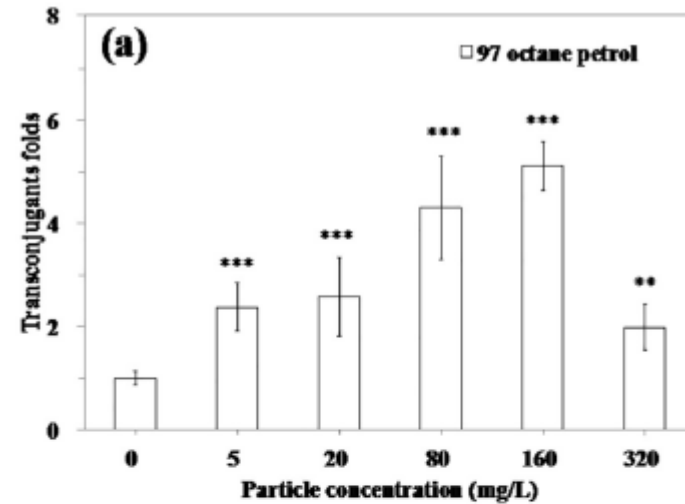
Effect of **triclosan** on conjugative transfer of **sulfonamide resistance** from a complex sewage community effluent to an *E. coli* recipient



Pollution with pharmaceuticals

Do other chemical compounds than antibiotics select AMR ?

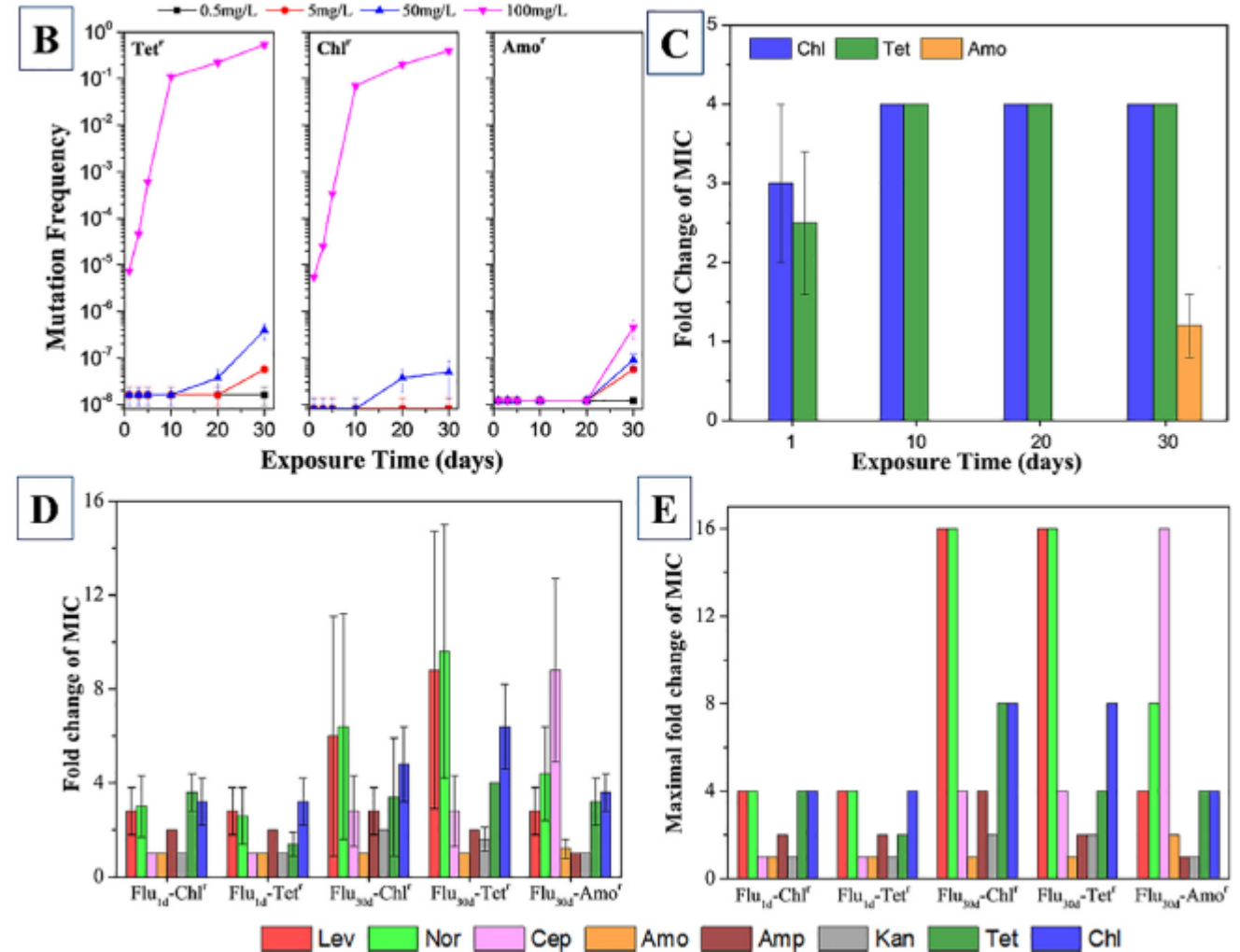
Petrol and **diesel** exhaust particles induces concentration-dependent increase in conjugative transfer rates of AMR genes



Pollution with pharmaceuticals

Do other chemical compounds than antibiotics select AMR ?

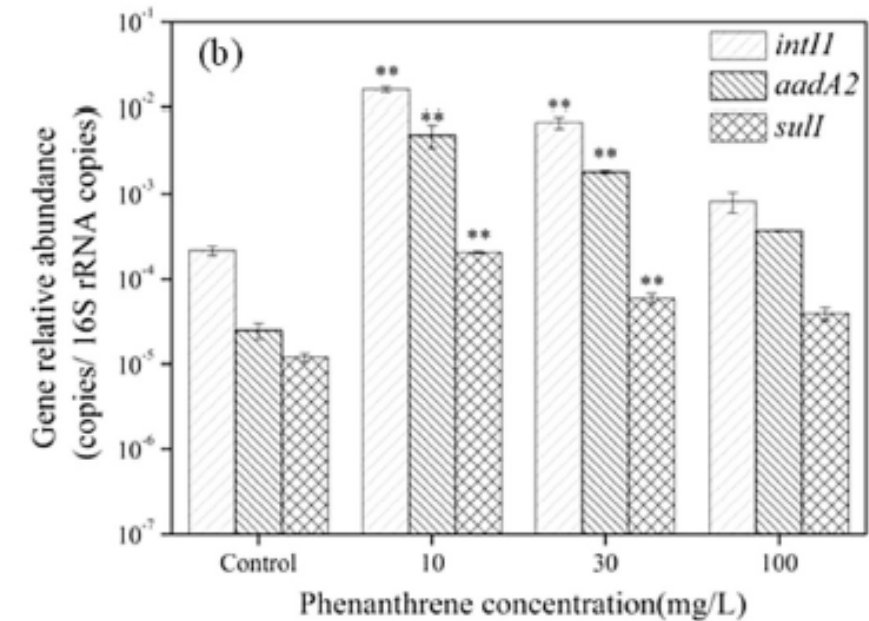
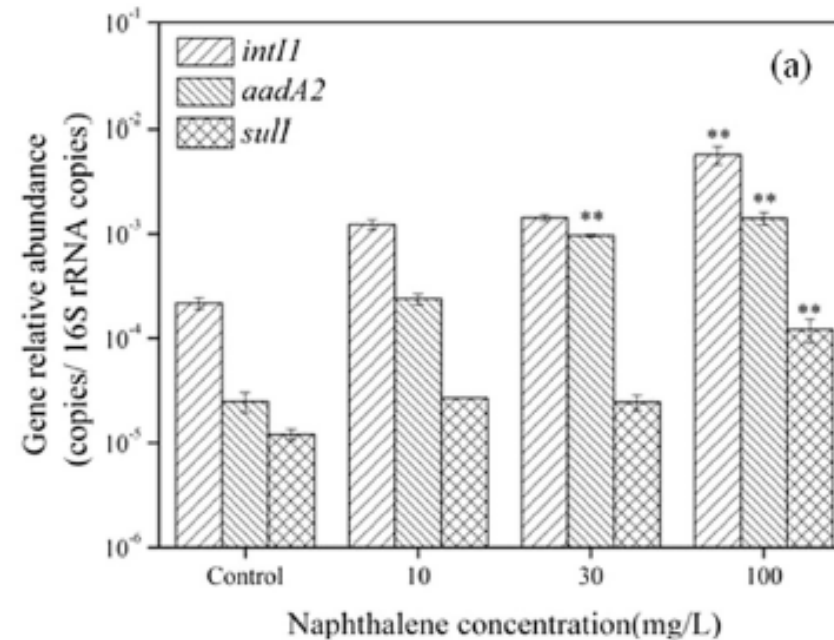
Antidepressant **fluoxetine** induces resistance to multiple antibiotics in *E. coli* through chromosome mutagenesis



Pollution with pharmaceuticals

Do other chemical compounds than antibiotics select AMR ?

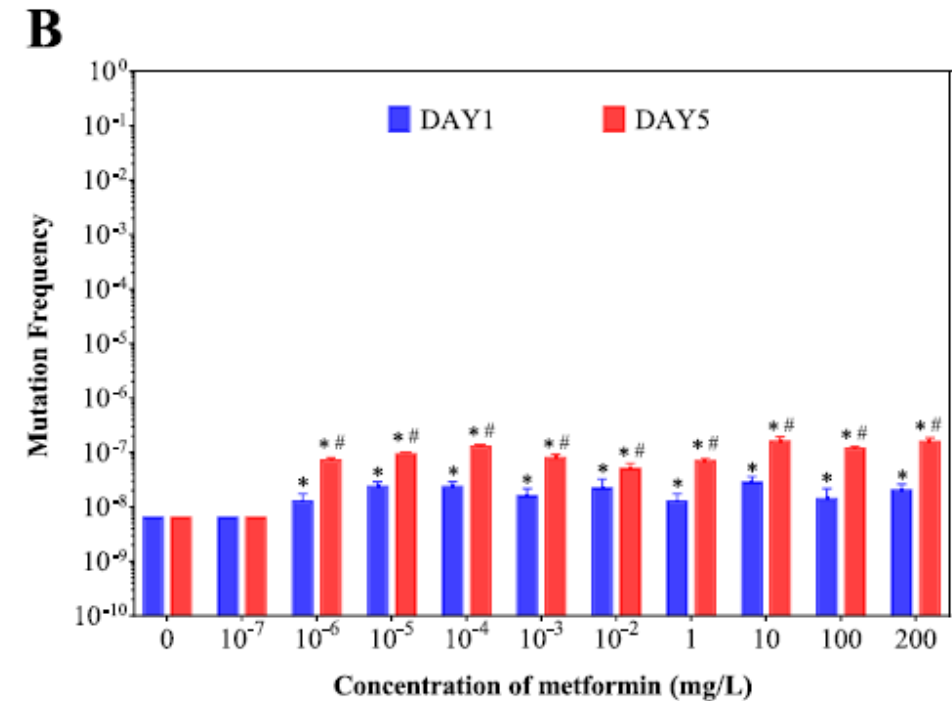
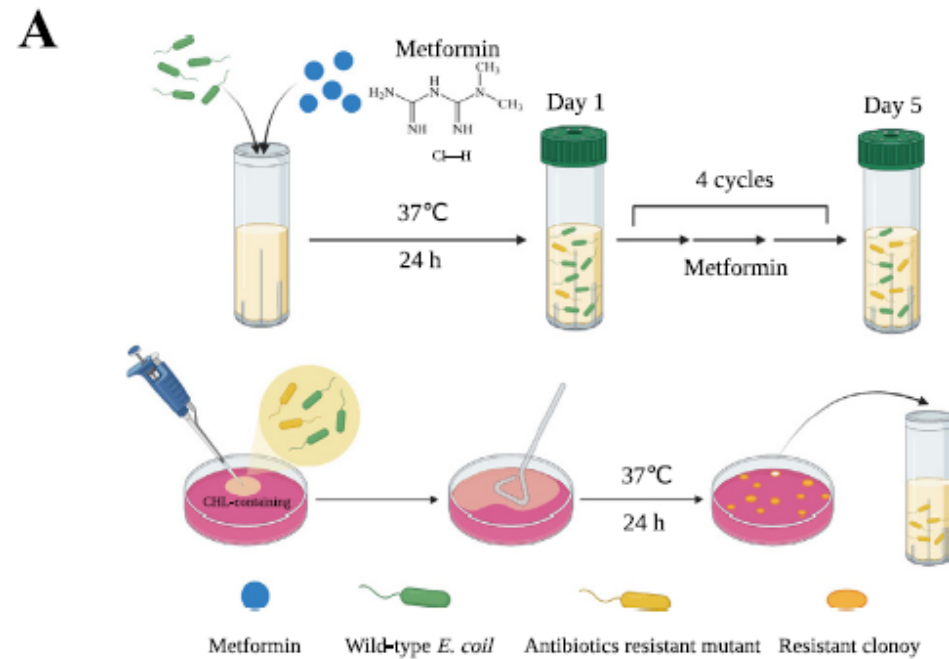
Polycyclic aromatic hydrocarbons (PAH) accelerate the propagation of AMR genes in coastal water microbial communities



Pollution with pharmaceuticals

Do other chemical compounds than antibiotics select AMR ?

Metformin promotes AMR development in *E. coli* through chromosome mutagenesis



What about risk assessment
related to AMR in the
environment ?

Arguments for immediate human exposure ?



Table 3

The number (%) of surfers and controls colonised by antibiotic-resistant *E. coli*.

	Surfers (N = 143)	Controls (N = 130)	Risk ratio (95% CI)	<i>p</i> value
Carriage of cefotaxime-resistant <i>E. coli</i>	13 (9.1%)	4 (3.1%)	2.95 (1.05 to 8.32)	0.040
Carriage of <i>bla</i> _{CTX-M} -bearing <i>E. coli</i>	9 (6.3%)	2 (1.5%)	4.09 (1.02 to 16.4)	0.046

Immediate human exposure ?



Critical Review

pubs.acs.org/est

Role of the Environment in the Transmission of Antimicrobial Resistance to Humans: A Review

Patricia M. C. Huijbers,^{†,‡} Hetty Blaak,^{*,‡} Mart C. M. de Jong,[†] Elisabeth A. M. Graat,[†]
Christina M. J. E. Vandenbroucke-Grauls,[§] and Ana Maria de Roda Husman^{‡,||}

Huijbers et al, Environmental Sci Technol 2015

Mughini-Gras et al, Lancet Planet Health 2019

Attributable sources of community-acquired carriage of *Escherichia coli* containing β -lactam antibiotic resistance genes: a population-based modelling study

Lapo Mughini-Gras, Alejandro Dorado-García, Engeline van Duijkeren, Gerrita van den Bunt, Cindy M Dierikx, Marc J M Bonten, Martin C J Bootsma, Heike Schmitt, Tine Hald, Eric G Evers, Aline de Koeijer, Wilfrid van Pelt, Eelco Franz, Dik J Mevius*, Dick J J Heederik*, on behalf of the ESBL Attribution Consortium

	Mean (95% CrI)	Median	SD
Hood consumption and preparation	18.9% (7.4–30.3)	17.0%	8.1
Seafood	6.6% (0.3–21.6)	5.1%	5.8
Chicken meat	4.5% (0.2–13.1)	3.7%	3.5
Bovine meat	3.6% (0.1–12.5)	2.7%	3.3
Turkey meat	1.8% (0–6.1)	1.3%	1.6
Raw vegetables	1.1% (0–3.9)	0.8%	1.1
Pork	0.9% (0–3.3)	0.6%	0.9
Sheep or goat meat	0.4% (0–1.6)	0.3%	0.4
Animals			
Contact with companion animals	7.9% (1.4–19.9)	7.0%	4.9
Dogs	5.1% (0.2–16.3)	3.9%	4.4
Cats	2.4% (0.1–8.0)	1.9%	2.2
Horses	0.5% (0–1.7)	0.3%	0.5
Non-occupational contact with farm animals	3.6% (0.6–9.9)	3.0%	2.5
Chickens	2.8% (0.1–9.0)	2.1%	2.4
Cattle	0.4% (0–1.4)	0.3%	0.4
Sheep or goats	0.3% (0–1.1)	0.2%	0.3
Pigs	0.1% (0–0.5)	0.1%	0.1
Environment	2.6% (0.2–8.7)	1.9%	2.3
Swimming in surface freshwater	2.3% (0.1–8.4)	1.6%	2.3
Contact with wild birds	0.3% (0–1.1)	0.2%	0.3

The percentage attributions of intestinal carriage of ESBL or pAmpC gene detections in *E. coli* isolates from individuals of the open community (n=454) to the different human and non-human sources. ESBL=extended-spectrum β -lactamase. pAmpC=plasmid-mediated AmpC. CrI=credible interval.

Table: Estimated attributions of each considered source of intestinal carriage of ESBL or pAmpC gene-carrying *Escherichia coli* detected in the open community in the Netherlands, 2005–17

Arguments for immediate human exposure ?

Increased use of reclaimed wastewater as an alternative for crop irrigation

ENVIRONMENTAL
Science & Technology

Article

pubs.acs.org/est

Human Exposure to Wastewater-Derived Pharmaceuticals in Fresh Produce: A Randomized Controlled Trial Focusing on Carbamazepine

Ora Paltiel,^{*,†,‡,§} Ganna Fedorova,^{§,||} Galit Tadmor,^{†,§,||} Geffen Kleinstem,^{†,§} Yehoshua Maor,[§]
and Benny Chefetz^{§,||}



Is manure application at risk to spread AMR ?

Tetracycline resistance genes abundance in soils after 6 years with manure
tet genes were present in all soil layers (0-5 cm, 5-10 cm, 10-20 cm)
tetO was introduced by manure, and *tetG*, *tetL* abundance increased after fertilization

Science of the Total Environment 506–507 (2015) 279–286



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Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Long-term application of fresh and composted manure increase tetracycline resistance in the arable soil of eastern China

Shuang Peng^{a,b}, Yiming Wang^a, Beibei Zhou^{a,b}, Xiangui Lin^{a,*}

Is manure application at risk to spread AMR ?

Macrolide exposure of soils for 8 years at a dose from 0.1 to 10 mg/kg soil
Several AMR genes were enriched at the 10 but not the 0.1 mg/kg soil
Exposure at realistic concentrations did not increase AMR genes abundance



Minimal environmental targets for antibiotic manufacturers ?

UN High-Level Meeting on AMR (2016)

13 pharmaceutical companies

Roadmap with 4 key commitments to reduce AMR

Science-based Targets for Antibiotics in Receiving Waters from Pharmaceutical Manufacturing Operations

Joan Tell,† Daniel J Caldwell,‡ Andreas Häner,§ Jutta Hellstern,|| Birgit Hoeger,|| Romain Journal,# Frank Mastrocco,††** Jim J Ryan,‡‡ Jason Snape,§§ Jürg Oliver Straub,§ and Jessica Vestel†*

†Merck & Co, Kenilworth, New Jersey, USA

‡Johnson & Johnson, New Brunswick, New Jersey, USA

§F Hoffmann-La Roche, Basel, Switzerland

||Novartis Pharma AG, Basel, Switzerland

#Sanofi, Gentilly, France

††Pfizer Inc, New York, New York, USA

‡‡GlaxoSmithKline, Ware, United Kingdom

§§AstraZeneca, Cheshire, United Kingdom

Tell et al, Integrated Environmental Assessment and Management, 2019

Is the environmental risk assessment (ERA) appropriate to protect against AMR ?

Environment International 109 (2017) 155–169



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Review article

Integrating human and environmental health in antibiotic risk assessment: A critical analysis of protection goals, species sensitivity and antimicrobial resistance

Gareth Le Page^a, Lina Gunnarsson^a, Jason Snape^{b,c}, Charles R. Tyler^{a,*}

Water Research 200 (2021) 117233



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Contents lists available at ScienceDirect

Water Research

journal homepage: www.elsevier.com/locate/watres

Dawning of a new ERA: Environmental Risk Assessment of antibiotics and their potential to select for antimicrobial resistance

Aimee K. Murray^{a,*}, Isobel Stanton^a, William H. Gaze^a, Jason Snape^b

In Europe, an ERA is required for a medicine if the predicted environmental concentration exceeds 10 ng/L

It leads to the calculation of a Predictable No Effect Concentration (PNEC)

There is a concern that ERA is biased for antibiotics

Modelling approaches to estimate the risks of AMR development in the environment

Environmental Toxicology and Chemistry—Volume 41, Number 3—pp. 648–662, 2022

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Hazard/Risk Assessment

Ecological Risk Assessment of Pharmaceuticals in the Transboundary Vecht River (Germany and The Netherlands)

Daniel J. Duarte,^{a,*1} Gunnar Niebaum,^{b,1} Volker Lämmchen,^{b,1} Eri van Heijnsbergen,^c Rik Oldenkamp,^d Lucia Hernández-Leal,^c Heike Schmitt,^{c,e,f} Ad M. J. Ragas,^{a,g} and Jörg Klasmeier^b

OPEN

The ISME Journal (2015) 9, 1467–1476

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www.nature.com/ismej

ORIGINAL ARTICLE

Validated predictive modelling of the environmental resistome

Gregory CA Amos^{1,7}, Emma Gozzard², Charlotte E Carter¹, Andrew Mead^{1,3}, Mike J Bowes², Peter M Hawkey^{4,5}, Lihong Zhang^{1,8}, Andrew C Singer², William H Gaze^{6,9,10} and Elizabeth MH Wellington^{1,9}

United Nations Environment Programme (UNEP)

**United Nations Environment
Programme's work on AMR**



Tackling Environmental Antimicrobial Resistance

United Nations Environment Programme (UNEP)

an authoritative advocate for the global environment



United Nations Environment Assembly (UNEA):

- World's highest-level decision-making body on the environment.

The Assembly is the governing body of the United Nations Environment Programme (UNEP).

- UNEP sets the global environmental agenda

UNEP's mission is to provide leadership and encourage partnership in caring for the environment by inspiring, informing, and enabling nations and peoples to improve their quality of life without compromising that of future generations.

Final remarks

Environment International 117 (2018) 132–138

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Environment International

journal homepage: www.elsevier.com/locate/envint

Critical knowledge gaps and research needs related to the environmental dimensions of antibiotic resistance

D.G. Joakim Larsson^{a,b,*}, Antoine Andreumont^{c,d}, Johan Bengtsson-Palme^{a,b}, Kristian Koefoed Brandt^e, Ana Maria de Roda Husman^{f,g}, Patriq Fagerstedt^h, Jerker Fickⁱ, Carl-Fredrik Flach^{a,b}, William H. Gaze^j, Makoto Kuroda^k, Kristian Kvint^{a,b}, Ramanan Laxminarayan^l, Celia M. Manaia^m, Kaare Magne Nielsenⁿ, Laura Plant^h, Marie-Cécile Ploy^o, Carlos Segovia^p, Pascal Simonet^q, Kornelia Smalla^r, Jason Snape^{s,t}, Edward Topp^u, Arjon J. van Hengel^v, David W. Verner-Jeffreys^w, Marko P.J. Virta^x, Elizabeth M. Wellington^t, Ann-Sofie Wernersson^y

1. What are the **relative contributions** of different sources of antibiotics and AMR into the environment ?
2. What is the role of the environment (as affected by anthropogenic inputs) **on the evolution of AMR** ?
3. How significant is the exposure of humans to AMR via different environmental routes, and **what is the impact on human health** ?
4. What technological, social, economic, behavioral interventions are effective **to mitigate the spread of AMR** via the environment ?

'In India'

EN INDE :

'Of course ! It's full of antibiotics !'

'Are you sure water is safe ?'

