



CATÓLICA PORTO
BIOTECNOLOGIA

Antibiotic resistance in urban wastewater: environmental contamination and risks of water reuse

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Summary

- 1. Five adjectives to characterize antibiotic resistance**
- 2. Evidences of antibiotic resistance in wastewater systems**
- 3. Wastewater: a bioreactor for antibiotic resistance enrichment?**
- 4. Wastewater and environmental contamination**

Five adjectives to characterize antibiotic resistance

Natural

Widespread

Unknown

Plastic

Pollutant

Natural and ancient

Multi-resistant spore-forming bacteria (actinomyces-like) in urban, agricultural and forest soils

D' Costa et al., Science, 2006

Resistance genes in 30,000-year-old permafrost sediments (beta-lactam, tetracycline and glycopeptides)

D' Costa et al., Nature, 2011

Soil bacteria able to use natural and synthetic antibiotics as sole carbon source

Dantas et al., Science, 2008

Widespread

Habitats	References (examples)
Soils	Riesenfeld et al. 2004; D'Costa et al., 2006; Dantas et al., 2008
Surface water	Hamelin et al., 2007; Dolejská et al., 2009; Figueira et al., 2011 a; b.
Drinking water	Faria et al., 2009; Figueira et al., 2011c; Vaz-Moreira et al., 2011; Falcone-Dias et al., 2012; Gomez-Alvarez et a., 2012
Food products	Johnston & Jaykus, 2004; Wang et al., 2006
Wild life	Poeta et al., 2008; Dolejská et al., 2009; Literak et al., 2010; Allen et al., 2011; Gonçalves et al., 2011
Remote Earth zones	D' Costa et al., 2011; Hernández et al., 2012

Unknown

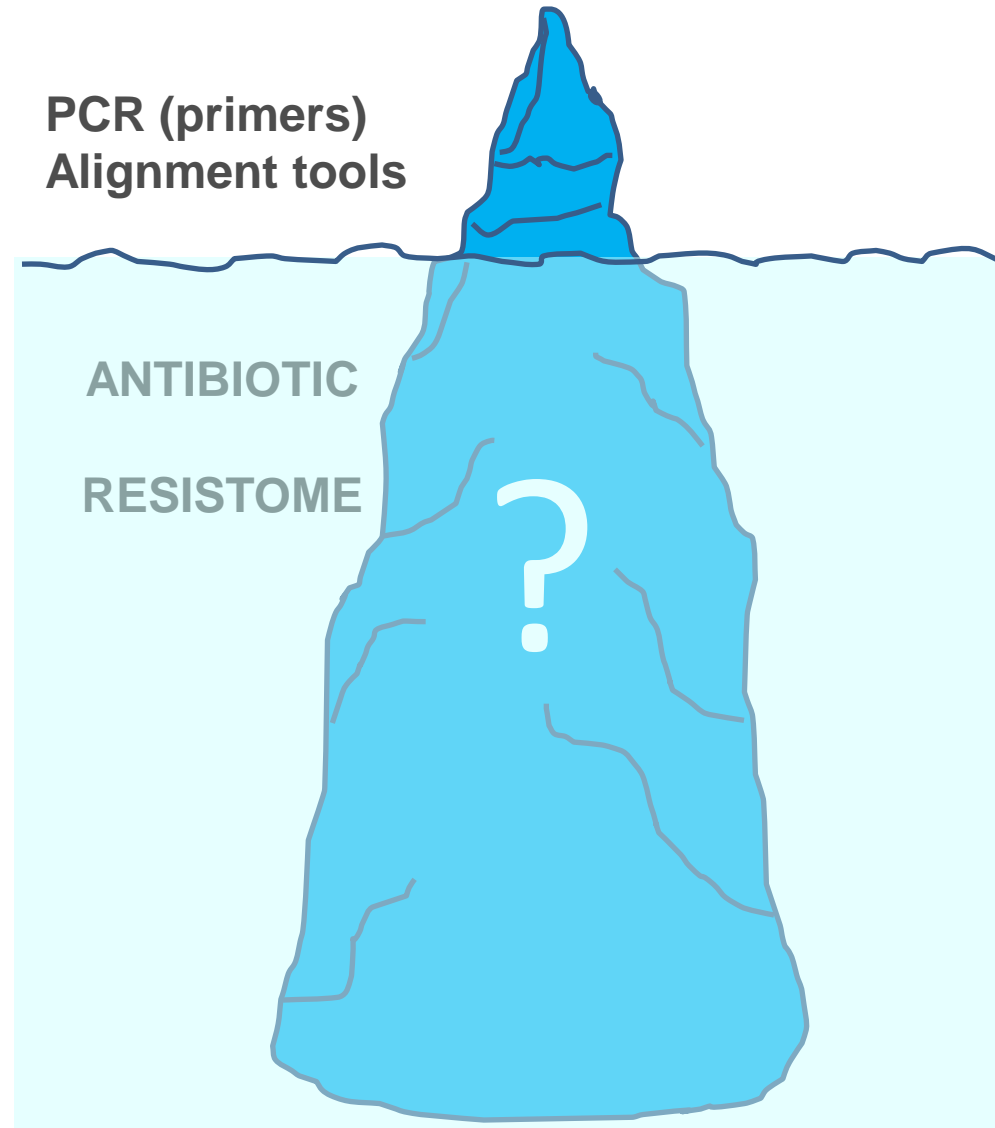
SOIL

“...resistance proteins ...deduced amino acid sequences with < 60% identity to previously published sequences...”

Riesenfeld et al., 2004

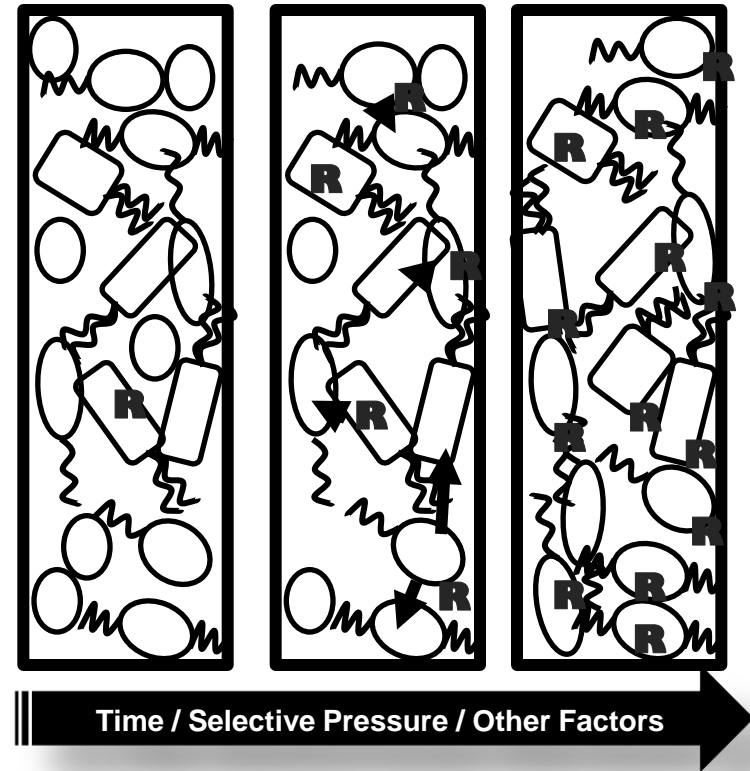
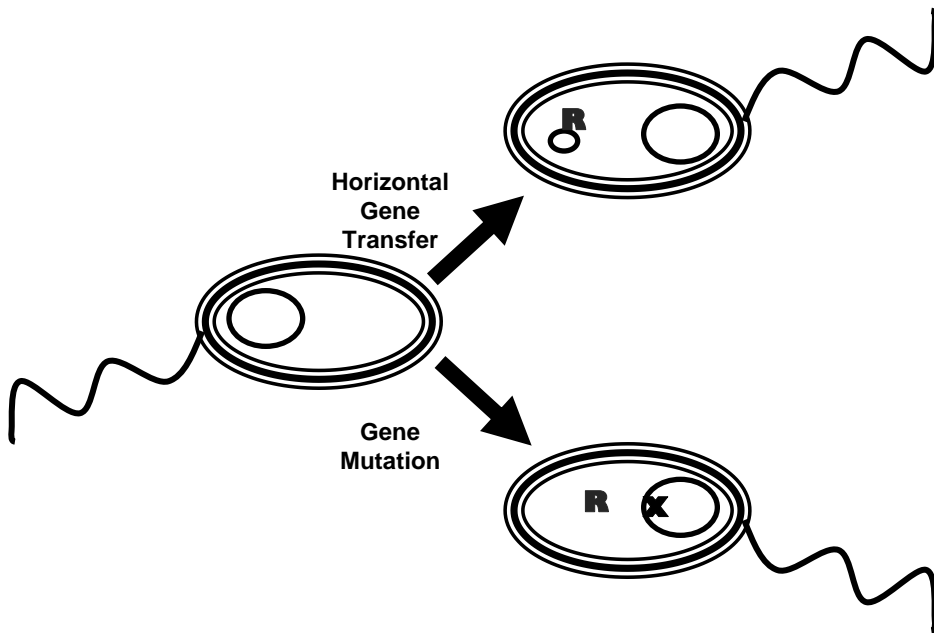
GUT HUMAN MICROBIOME

“...most of the resistance genes we identified with culture independent metagenomic sampling ... were novel when compared to all known genes in public databases. “ Sommer et al., 2010



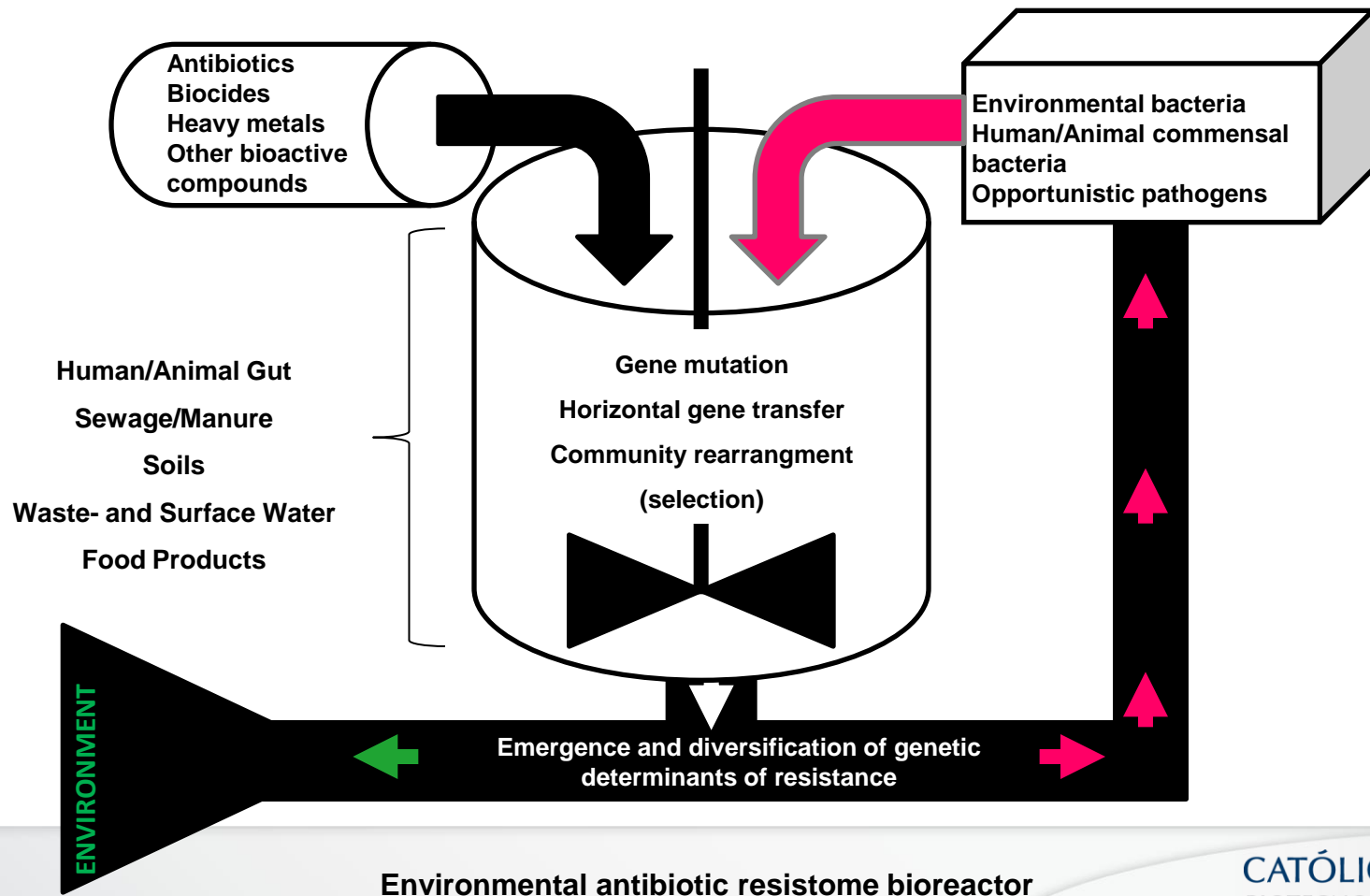
Plastic

Bacterial genomes and bacterial communities are dynamic



Plastic

**Dynamics (genomes + communities) =
reaction to environmental conditions**



Pollutant

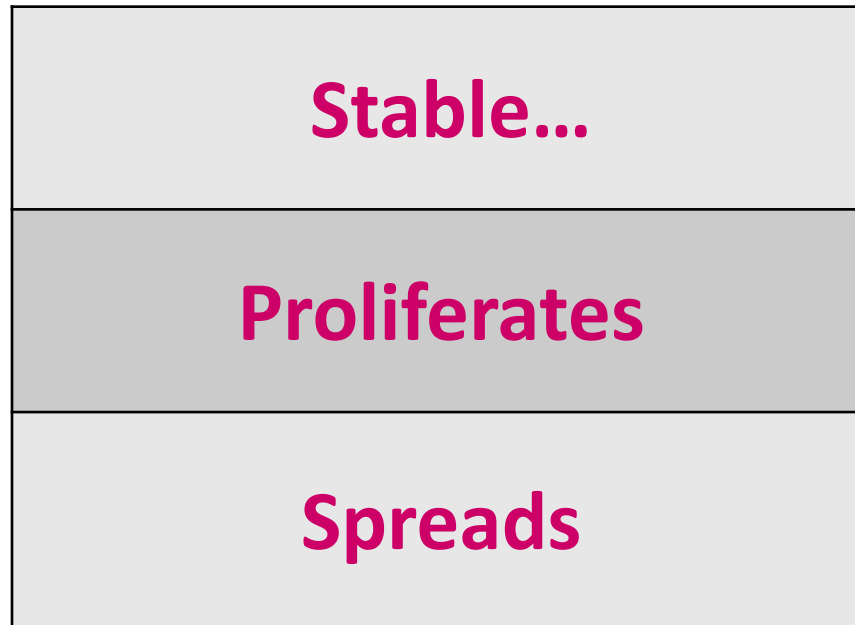
“A pollutant is a substance that is present in concentrations that may harm organisms (humans, plants and animals) or exceed an environmental quality standard. The term is frequently used synonymously with contaminant.” Organisation for Economic Co-operation and Development

70 Years antibiotics
Heavy metals
Other pollutants (biocides, pharmaceuticals)
???

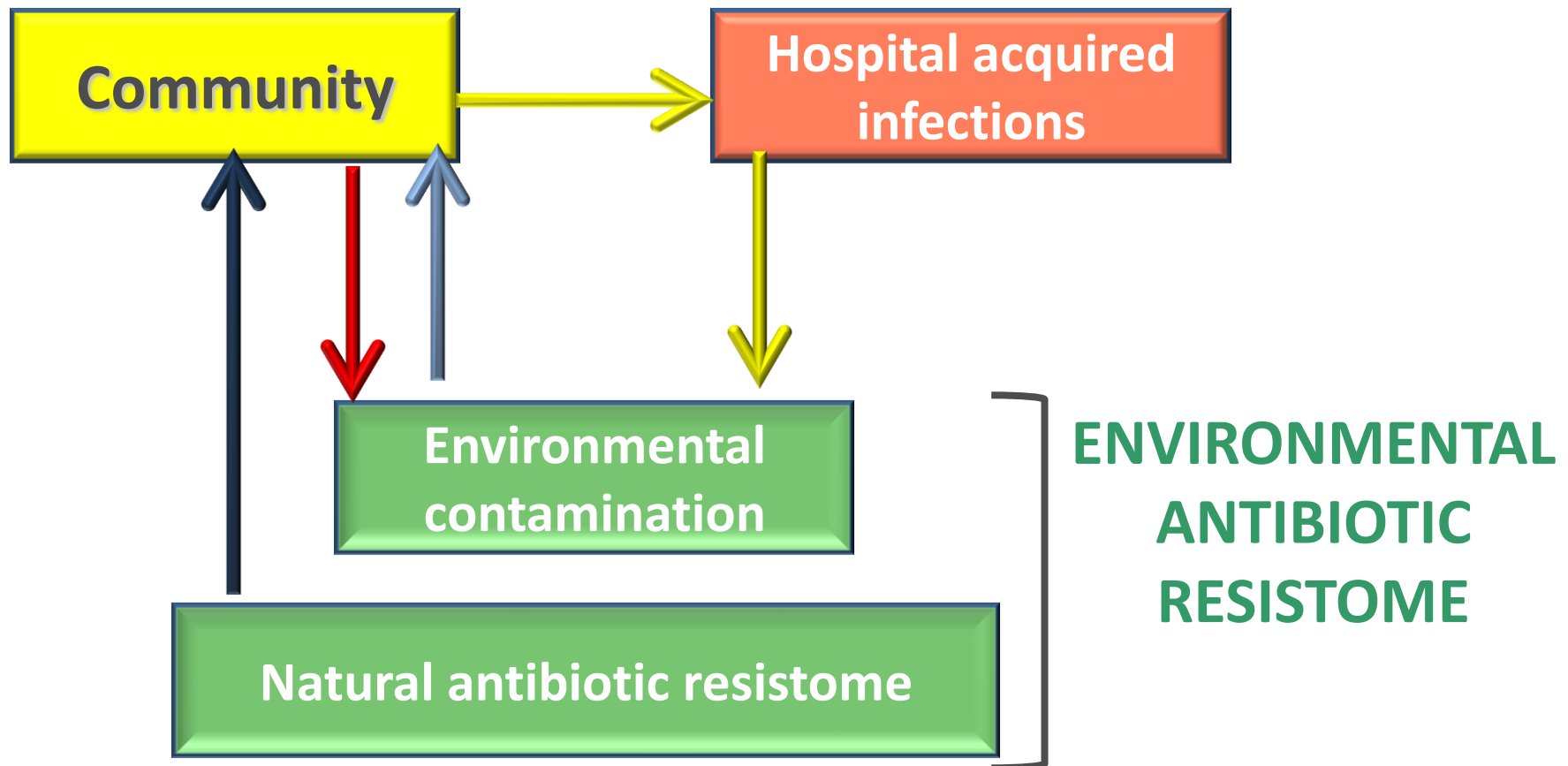
Human activities disturbed the natural equilibrium

Biological Pollutant

Unlike chemical pollution...



Antibiotic resistance sources



Urban wastewater treatment plants

a bioreactor for antibiotic resistance enrichment?



Antibiotics and wastewaters

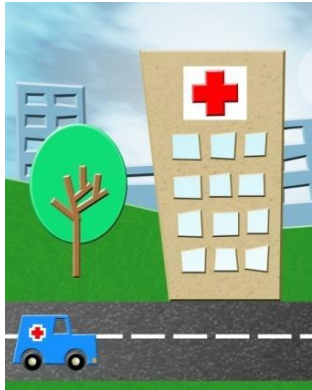
Germany



0.5 g *per capita per year*



25 % used in the Hospital



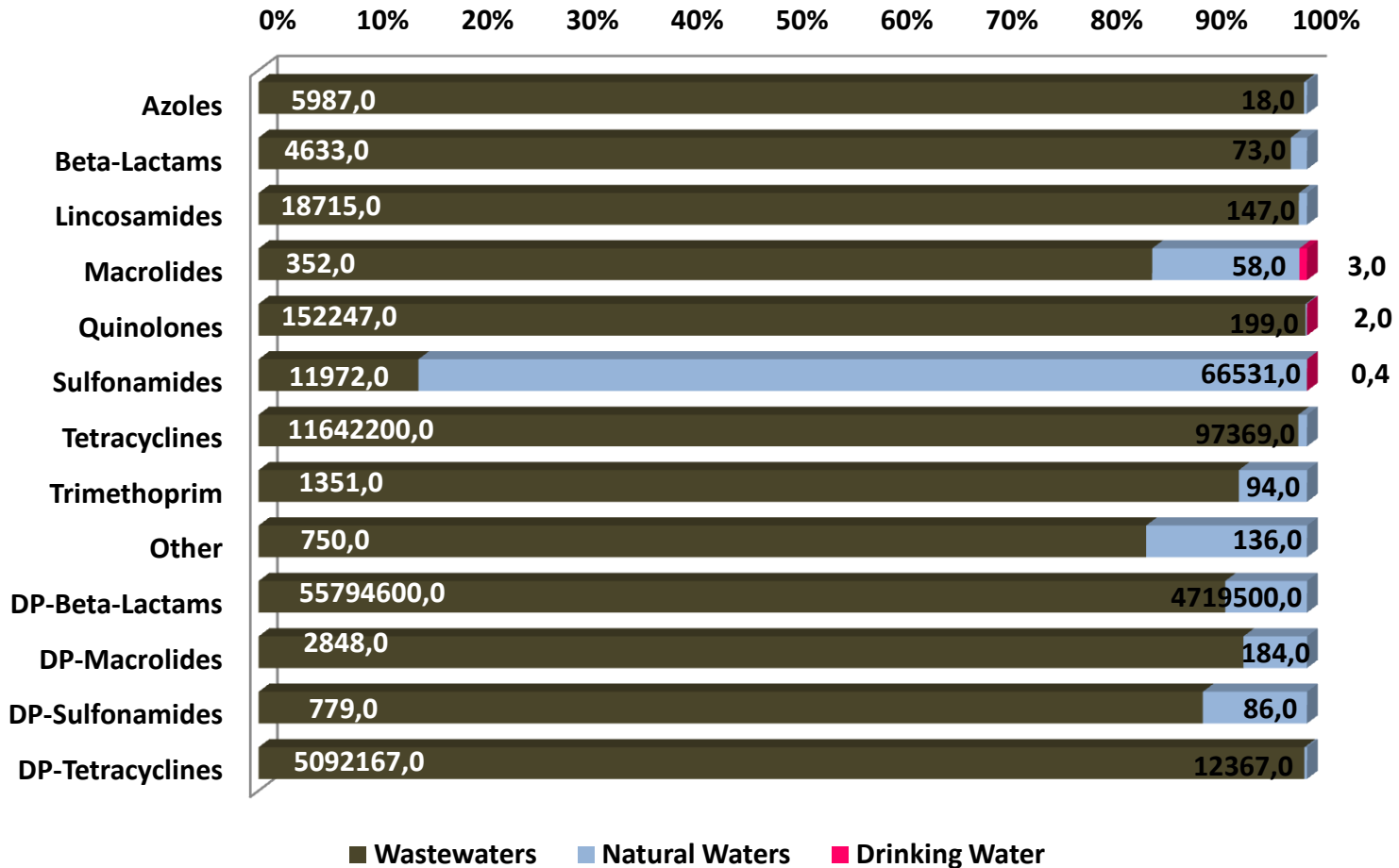
~75 % EXCRETED TO UWWTP

ANTIBIOTICS IN WASTEWATERS

Web of Science and Google Scholar search for articles published in peer-reviewed journals written in the English language since 1984

Up to 1 g/L

ng L⁻¹



Evidences of antibiotic resistance in urban wastewaters

VRE
MRSA

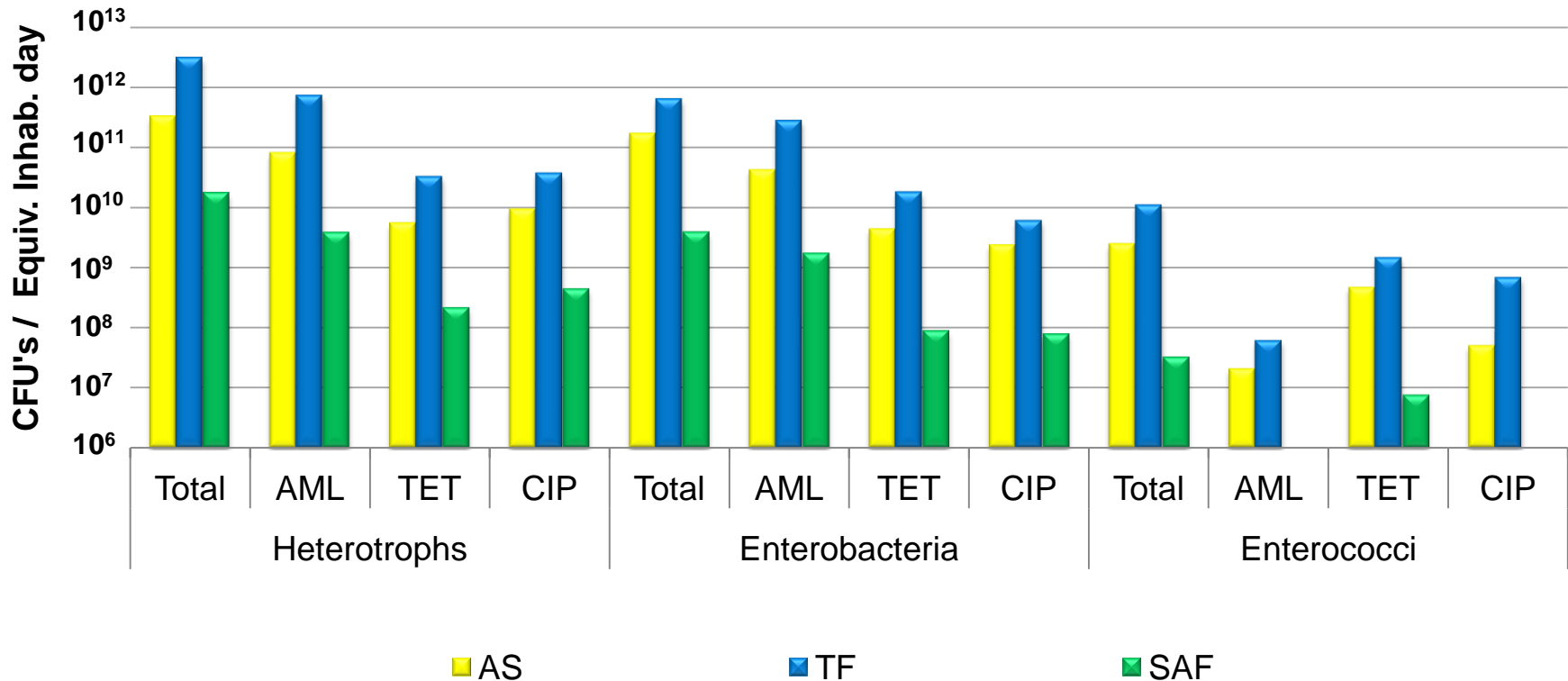
Percentage of resistance (concentration of antibiotic, µg or µ/mL)											
	Total heterotrophs	<i>Acinetobacter</i>		<i>E. coli</i>					<i>Enterococcus</i>		
Aminopenicillins Ampicillin (AP) Amoxicillin (AX)	22.4-26.1 (32) ^{AX}	0.0-0.6 (10) ^{AP}	19.5 (30) ^{AX1}	30.9 (25) ^{AX}	15 (10) ^{AP}	36.0- 41.0 (32) ^{AP}	16.5- 23.5 (32) ^{AP}	34 (2-16) ^{AP}	7.0 (0.5- 32.0) ^{AP}	0.4-0.9 (32) ^{AX}	2.0 (25) ^{AX}
Tetracycline	1.1-1.8 (16)	5.5- 10.4 (30)	n.a.	34.1 (30)	10.0 (30)	19-23 (16)	6.8 (4)	23.5 (1-8)	20.0 (0.5-8.0)	14.5- 22.8 (10)	32.0 (30)
Sulfamethoxazole (+trimethoprim, T)	n.a.	0.6-2.4 (25)	11.2 (250) ²	22.3 (25) ^T	17.0 (300) ³	34-37 (350)	17.5 (256)	11.1 (10-40) ^T	n.a.	n.a.	1.0 (25) ^T
Quinolones Nalidixic acid (NA) Ciprofloxacin (C)	1.7-2.8 (4) ^C	0.0-5.5 (5) ^C	7.5 (5) ^C	5.5 (5) ^C	5.0 (30) ^{NA}	5.0-7.0 (4) ^C	0.7-0.9 (4) ^C	10.5 (0.5-2) ^C	28.6 (0.5- 4.0) ^C	2.4-5.0 (4) ^C	18.0 (5) ^C
Gentamycin	n.a.	0.0-0.6 (10)	0.8 (10)	4.4 (10)	0.0 (10)	n.a.	n.a.	2.0 (1-8)	3.2 (synergy) (500)	n.a.	50.0 (10)
Method (antibiotic concentration)	AIA (µg/mL)	DDM (µg)	DDM (µg)	DDM (µg)	DDM (µg)	AIA (µg/mL)	MMPN (µg/mL)	MD (µg/mL)	MD (µg/mL)	AIA (µg/mL)	DDM (µg)
Region (Observations)	Portugal FE, RV3	Danmark RV2, TT	USA TT	Portugal	Australia AV5	Australia FE, RV2	Ireland FE, RV2	Poland	Poland	Portugal FE, RV3	Portugal
Reference	Novo and Manaia, 2010	Guardab assi et al., 2002	Zhang et al., 2009	Ferreira da Silva et al., 2007	Watkinso n et al., 2007a	Watkinson et al., 2007 b	Galvin et al., 2010	Łuczkiewic z et al., 2010	Łuczkiewic z et al., 2010	Novo and Manaia, 2010	Ferreira da Silva et al., 2006

n.a. not /available; -, not applicable; 1, with clavulanic acid; 2, Sulfisoxazole; 3, Sulfafurazole; AIA, Antibiotic impregnated agar; DDM, Disk diffusion method; MMPN, Modified Most Probable Number; MD, Microdilution method; FE, Final effluent; RVn, Range values of n plants; AVn, Average values of n plants; TT, tertiary treatment implemented.

Urban wastewater treatment

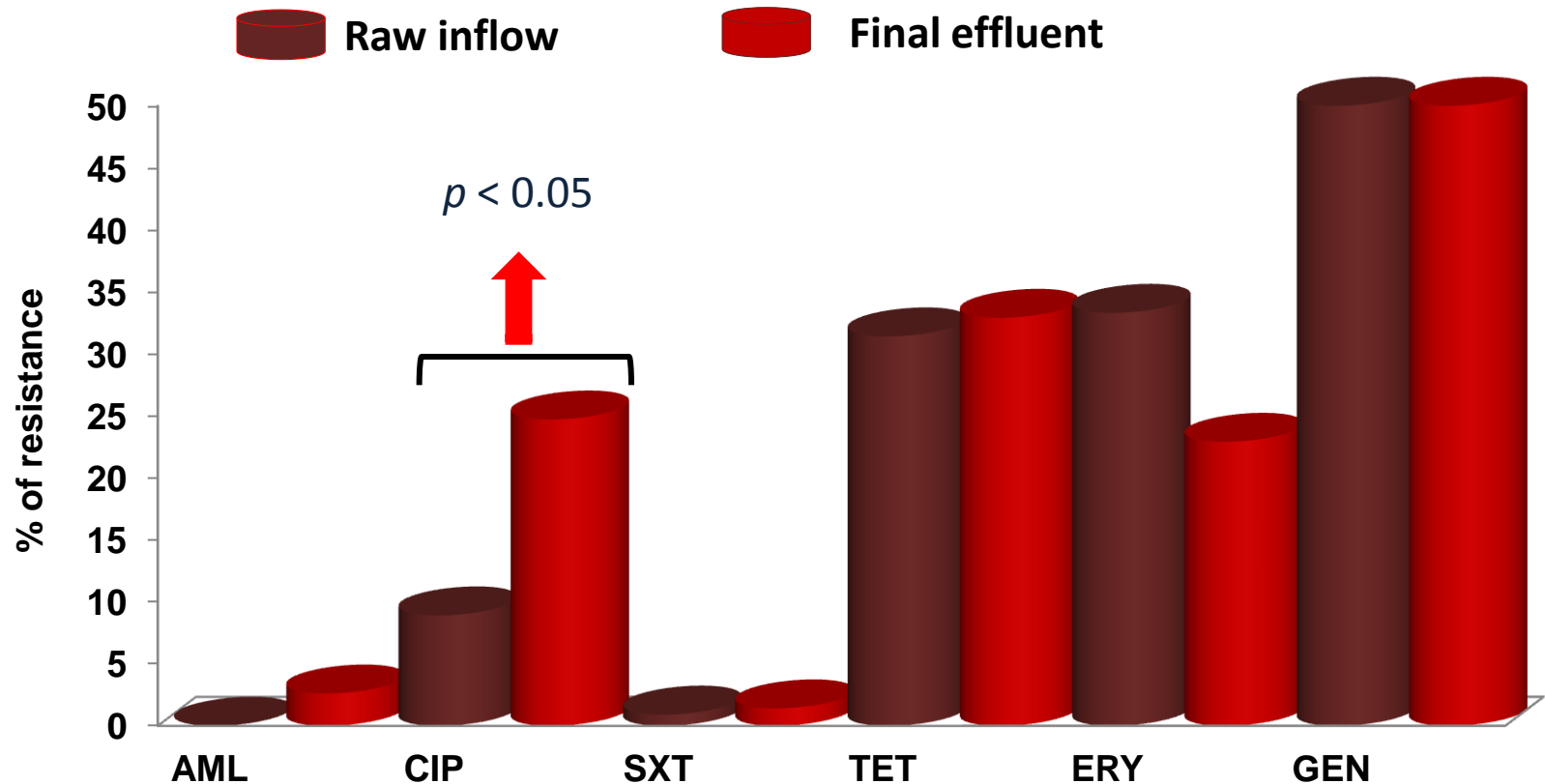
~ 10^7 - 10^{11} CFU/E.DAY OF ANTIBIOTIC RESISTANT BACTERIA

IN THE FINAL EFFLUENT



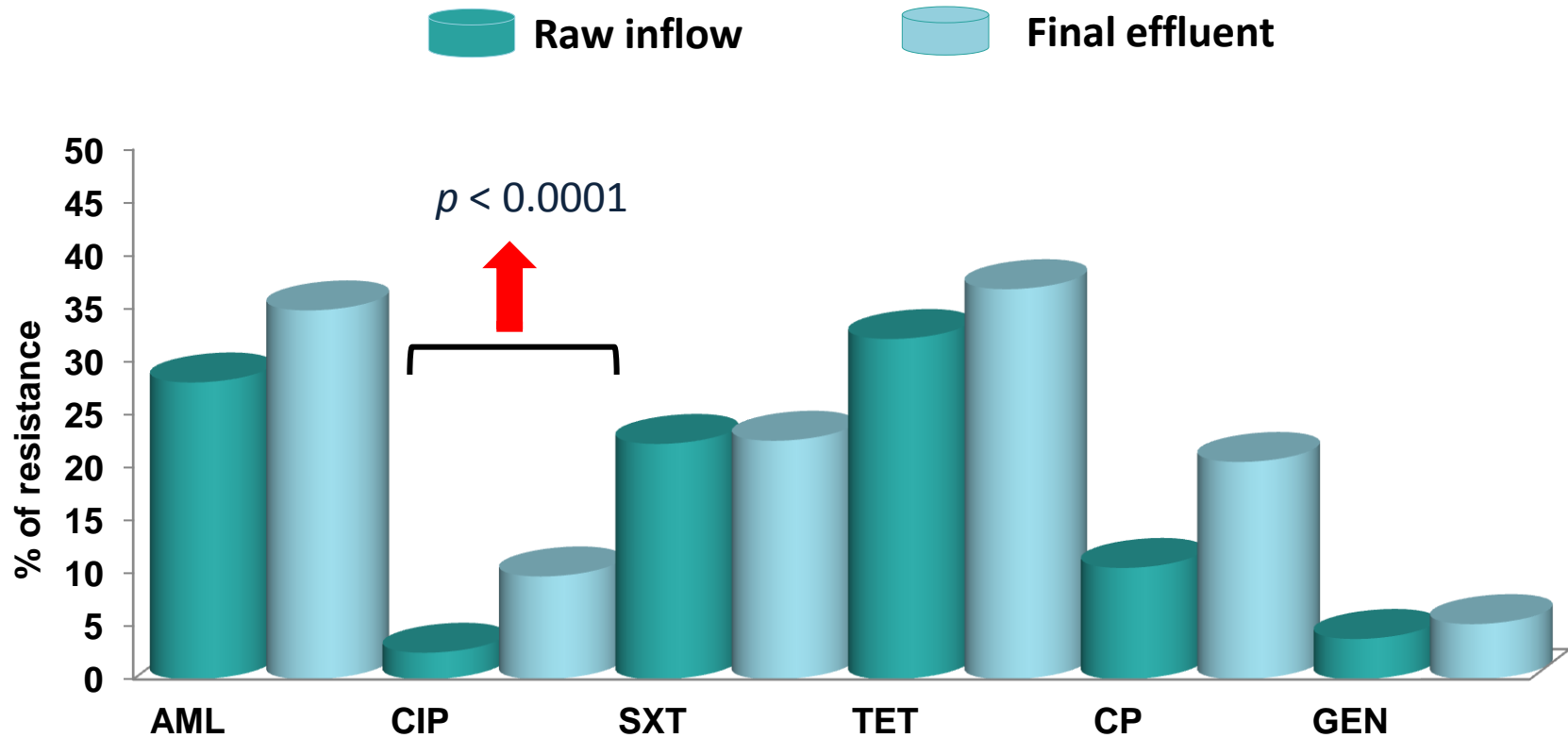
AS =activated sludge ;TF = trickling filter; SAF = submerged aerated filter

Wastewater treatment Enterococci



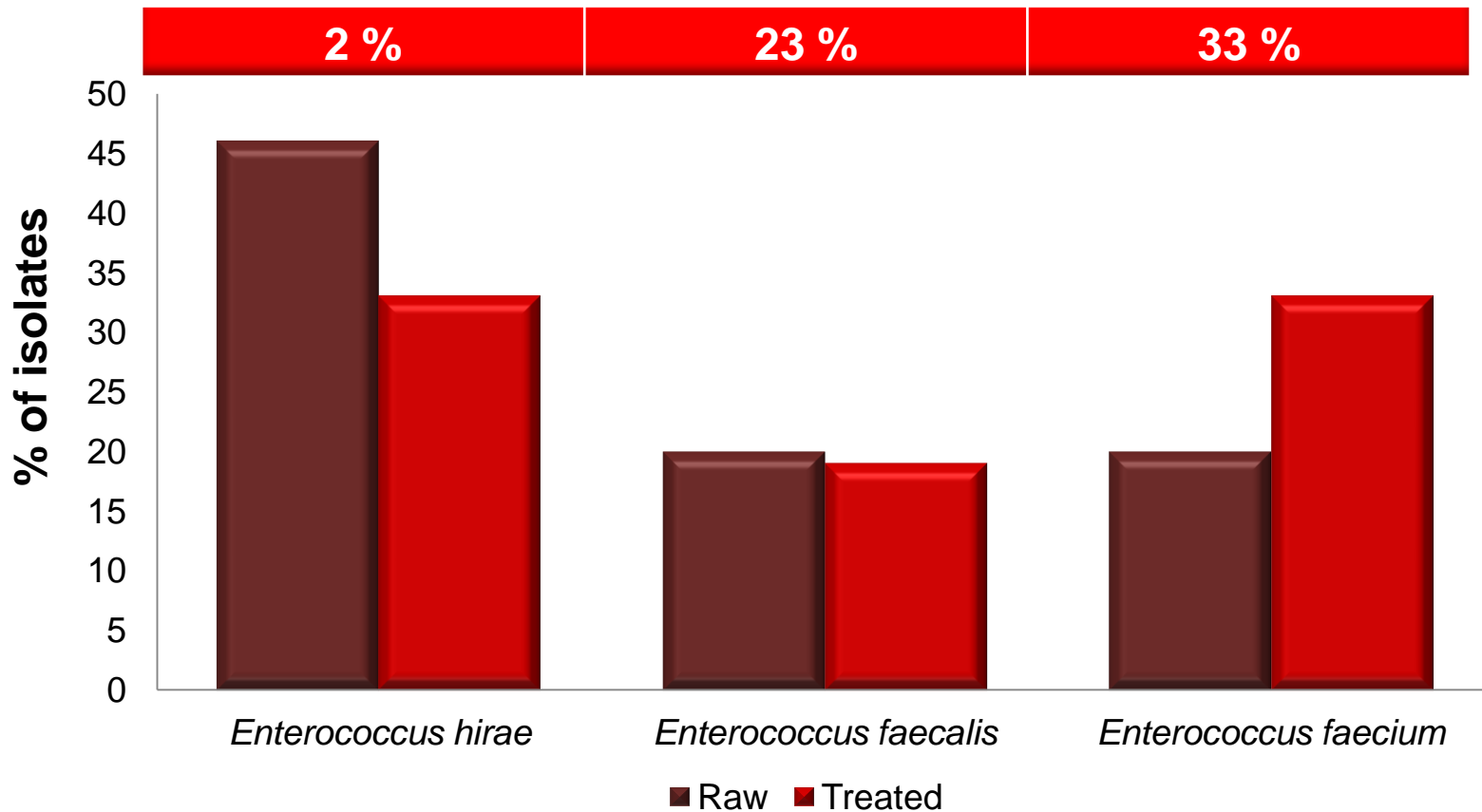
Wastewater treatment

Escherichia coli



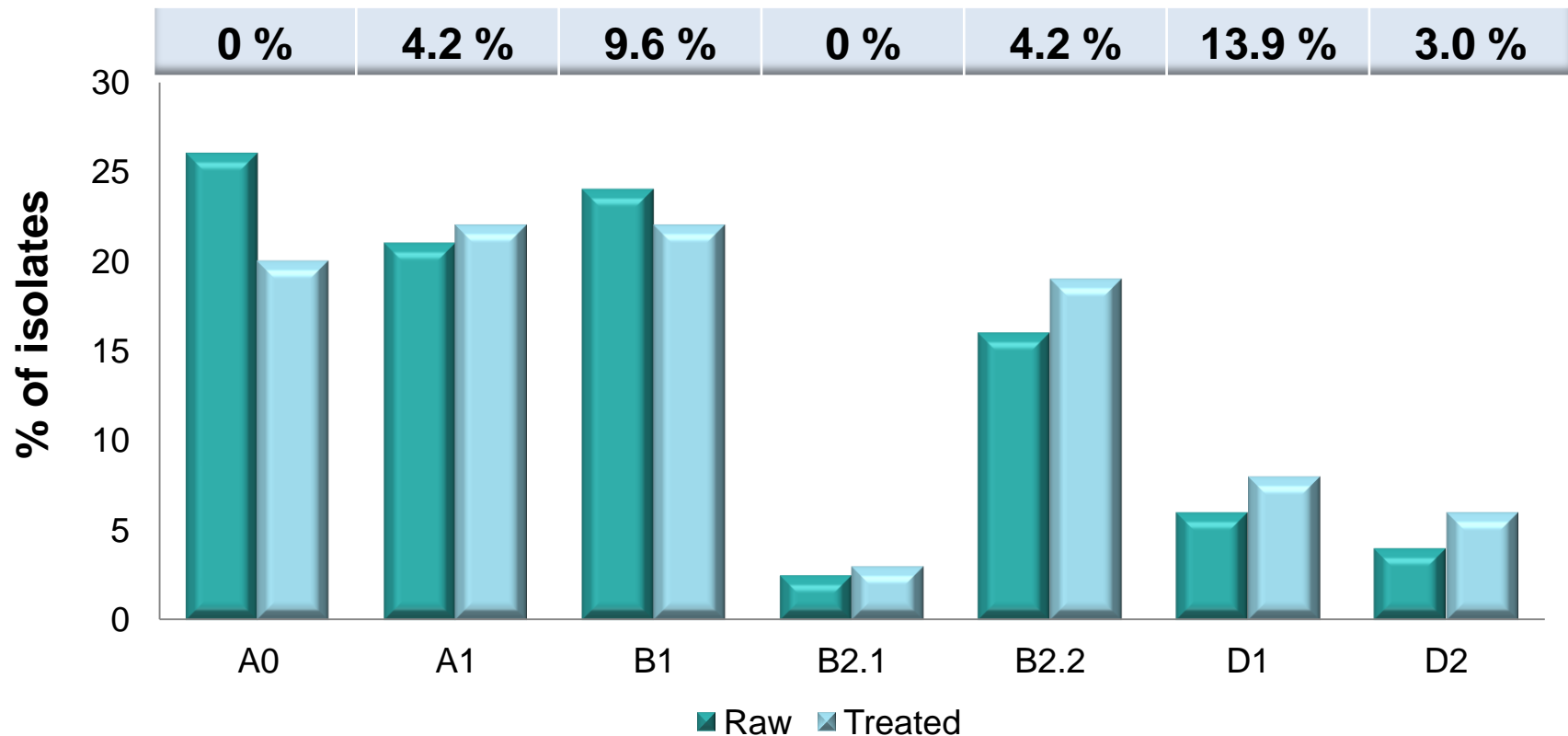
Quinolone resistance and enterococci species distribution

Quinolone resistance

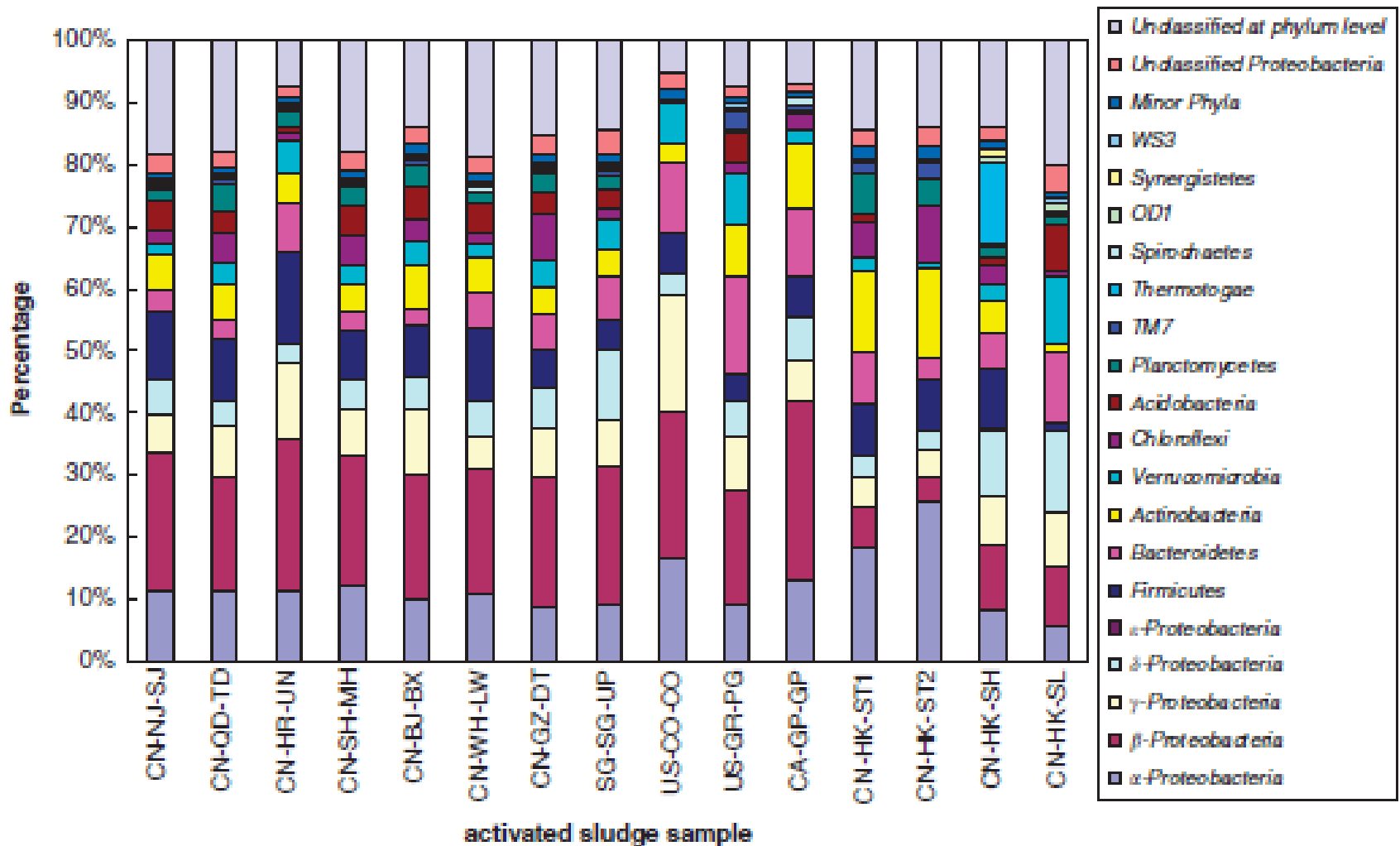


Quinolone resistance and *Escherichia coli* genotypic groups distribution

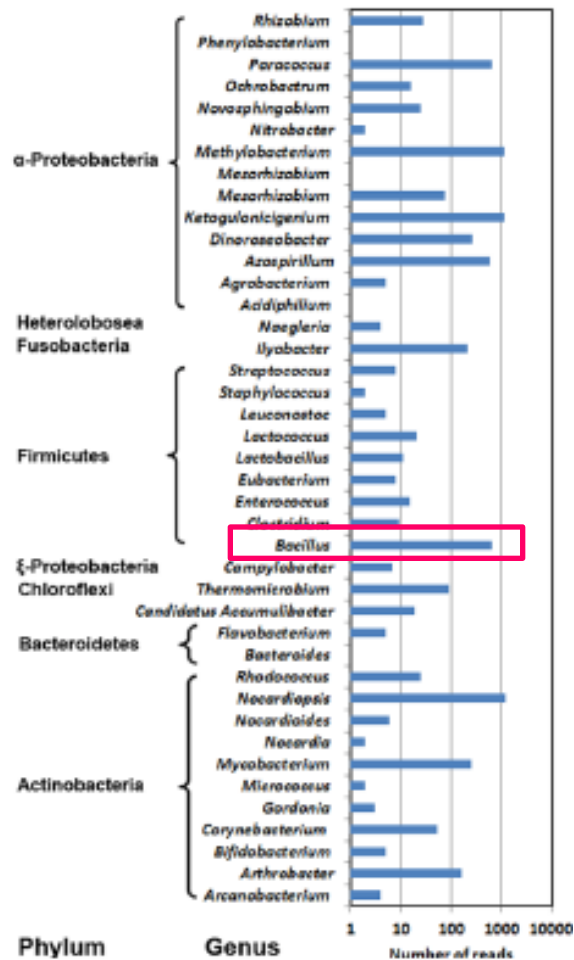
Quinolone resistance (100 % chromosome encoded)



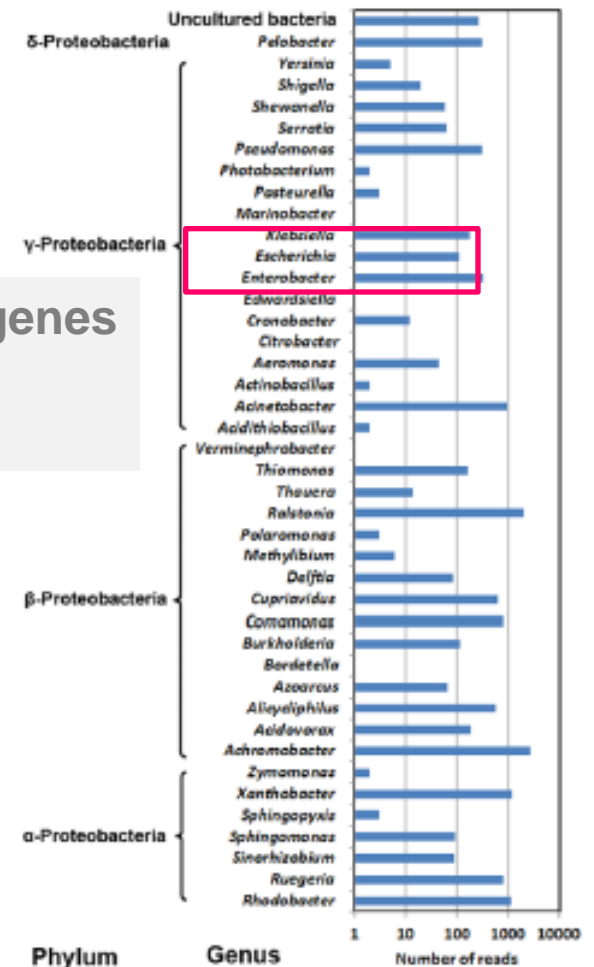
Wastewater systems: hidden microbial worlds



Plasmid hosts in activated sludge



Antibiotic resistance genes
Integrans
Transposons



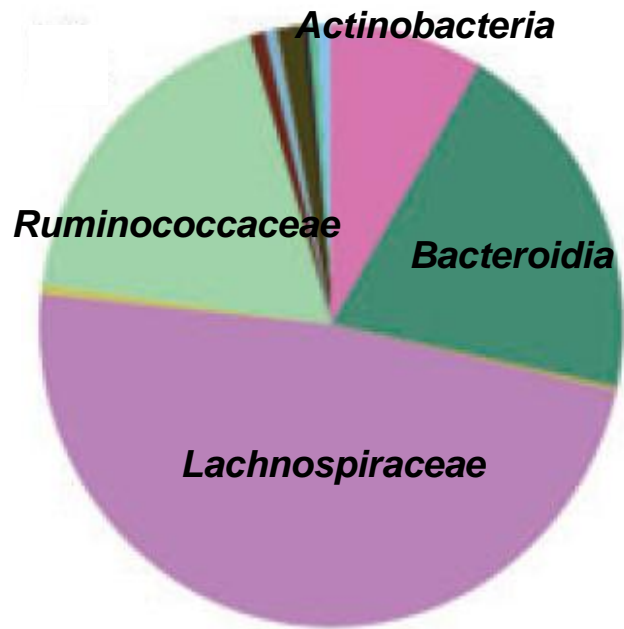
AFTER WASTE WATER TREATMENT? Environmental contamination

**Fate of antibiotic resistant
bacteria and genetic determinants**

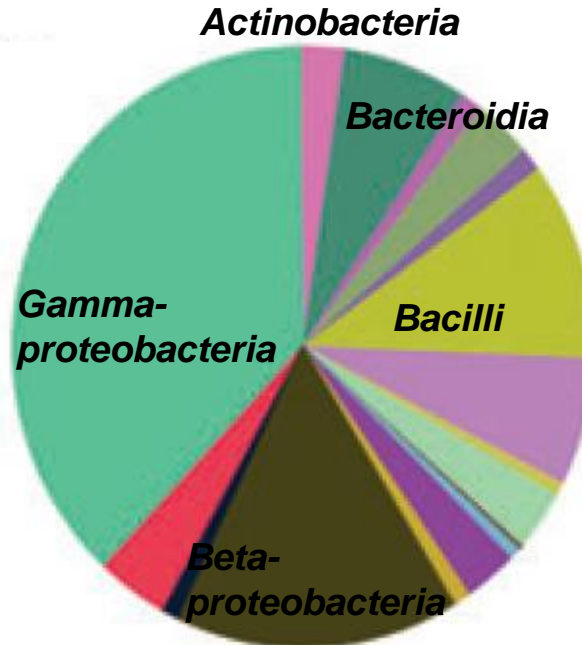
?

Bacterial communities are dynamic

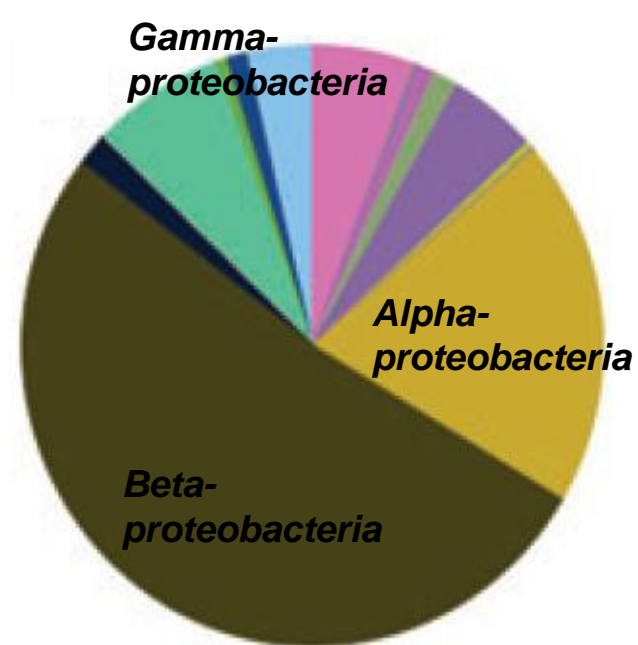
Human



Sewage



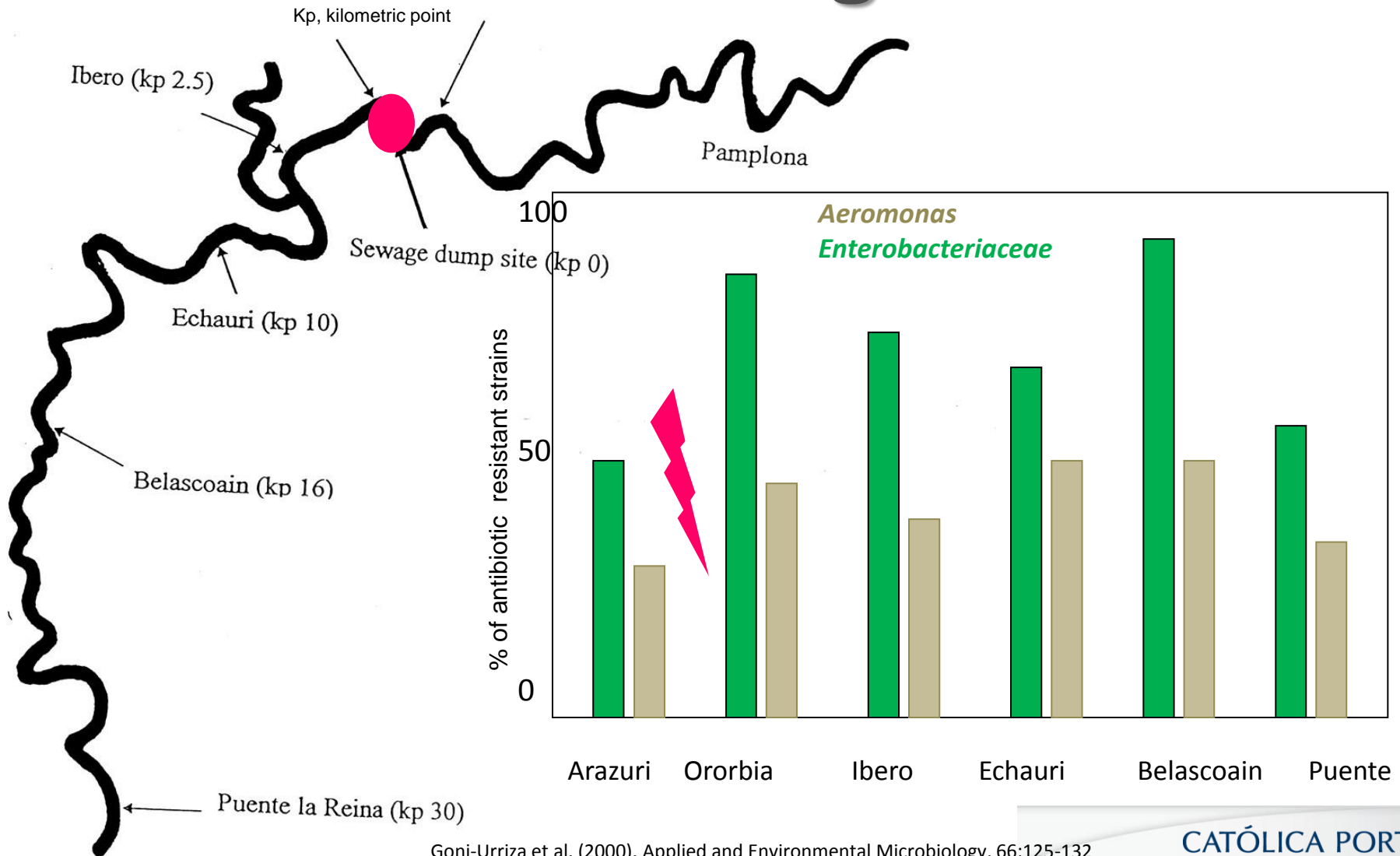
Surface water



Examples of antibiotic resistance genes detected in wastewater of UWWTP

Class	Mechanism (Type) ^a	Examples of genes ^b	Approach ^c	Reference ^d
Aminoglycosides	Modification by adenylation (DM)	aad(A1, A2, A13, B)	CD	4; 8
	Modification by phosphorylation (DM)	aph(A, A-3, A-6, 2); str(A, B) strB	CI CD	11 9
Beta-lactams	Beta-lactam ring cleavage (beta-lactamase production) (DM)	Class A: CTX, GES, NPS,PER, SHV, TEM,TLA, VEB	CI	3; 6; 11; 12
		Class B: IMP, VIM	CI	11
		Class C: ampC, CMY	CI	11
		Class D: OXA	CI	11
	Class D: OXA	CD	8	
	Penicillin binding protein (TP)	mecA	CI	2; 3; 10
Glycopeptides	Modified peptidoglycan pentapeptide (TM)	vanA	CD	1
			CI	10
Macrolides	Macrolide-efflux protein (DE)	mel	CI	11
	Erythromycin inactivation (DM)	ereA2	CI	11
	Modification by 23S rRNA methylation (TP)	ermB	CD	1
		erm(B, F)	CI	11
Macrolide phosphotransferase (DM)	mph(A, B)	CI	11	
Quinolones	Modification by acetylation (DM)	aacA6-ib-cr	CD	5
	DNA gyrase protection (TP)	qnr(A3, B1, B2, B4, B5, S2)	CI	11
		qnrVC; qnrS	CD	5; 12
Sulfonamides	Modified dihydropteroate synthase (TM)	sul2	CD	9
		sul(1, 2, 3)	CI	11
Tetracyclines	Other	tetU	CI	11
	Tetracycline efflux pump (DE)	tetA	CD	9
		tet(A, B, D, G, H, Y, 31, 35, 36, 39)	CI	2; 7; 11
	Ribosomal protection protein (TP)	tetM	CD	1
		tet(M, S)	CI	7; 11
Tetracycline modification (DM)	tetX	CI	7; 11	
Trimethoprim	Dihydrofolate reductase (DM)	dfr(A1, A12, 18)	CD	4; 8; 9
		dfr (II, V, VII, XII, 13, 16, 17, A19, B2, D); dhfr (I, VIII, XV)	CI	11
Multidrug	Multidrug resistance efflux pump (DE)	acr(B, D), mex(B, D, F, I, Y)	CI	11

Effect of UWWTP effluent discharge



Selectors for antibiotic resistance genes in a river

Antibiotic resistance gene abundances associated with waste discharges to the Almendares River near Havana, Cuba

TABLE 3. Antibiotic Resistance Genes (ARG) Correlated with Sediment Heavy–Metal and Water–Column Antibiotic Levels^a

parameter	number of correlated ARG	specific ARG significantly correlated with indicated parameter
Cu	7	<i>tet(M)</i> , <i>tet(O)</i> , <i>tet(Q)</i> , <i>tet(W)</i> , <i>erm(B)</i> , <i>erm(E)</i> , <i>bla_{OXA}</i>
Cd	0	–
Cr	0	–
Pb	2	<i>tet(M)</i> , <i>bla_{OXA}</i>
Co	2	<i>tet(Q)</i> , <i>erm(B)</i>
Zn	3	<i>tet(M)</i> , <i>tet(Q)</i> , <i>tet(W)</i>
tetracyclines	2	<i>tet(M)</i> , <i>bla_{TEM}</i>
ampicillin	5	<i>tet(M)</i> , <i>tet(O)</i> , <i>tet(Q)</i> , <i>tet(W)</i> , <i>bla_{OXA}</i>
benzyl–penicillin	0	–

^a $\alpha = 0.05$ significance level.

FAQS vs. NYAQS

FAQS

(Frequently Asked Questions)

Which bacteria?
Which genes?
Which habitats?

NYAQS

(not yet answered questions)

Clues about the unknown resistome?

How important is the environment?

Factors triggering gene transfer?

What makes a resistance gene a case of success?

In summary...

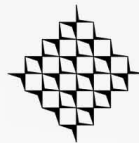
The question is not where we can find antibiotic resistant bacteria, but which are “relevant resistance types” and the conditions which favour their selective development and/or horizontal gene transfer

Partnership

CBOQF

Centro de Biotecnologia
e Química Fina

LABORATÓRIO ASSOCIADO DO ESTADO



Lepae

Laboratory for Process, Environmental and Energy Engineering



AGÊNCIA PORTUGUESA DO AMBIENTE

Ministério do Ambiente e do Ordenamento do Território

cost

EUROPEAN COOPERATION
IN SCIENCE AND TECHNOLOGY

People

Célia M. Manaia

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Vânia Figueira

Ana Rita Varela

Carlos Narciso da Rocha

Olga Nunes

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Cátia Faria

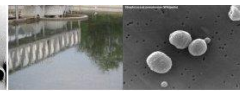
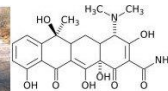
Maria Fernanda Falcone-Dias

Paula Viana

Sandra André

Edward Moore

DARE



Detecting evolutionary hot spots of Antibiotic Resistance in Europe

Samples

A special thanks for sample
suppliers

WWTP/DWTP/Hospital

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“Dynamics of antimicrobial resistance between the hospital and the environment” (PTDC/ AAC-AMB/113840/2009)



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