TRACKING DES TRANSFERTS DES BACTERIES PORTEUSES DE RESISTANCES ENTRE ANIMAL, HOMME ET ENVIRONNEMENT

Colloque hepta-académique

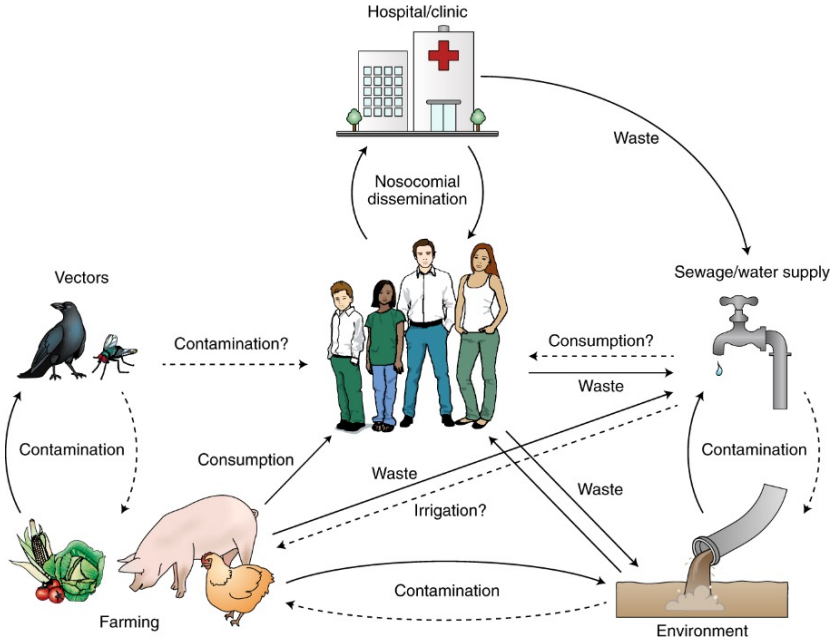
« ***Une seule santé : les microbes et l'antibiorésistance*** en partage »

Mercredi 15 juin 2022

Académie d'agriculture – Paris

Marie-Cécile PLOY
Université de Limoges – UMR Inserm 1092
CHU Limoges – Service de Bactériologie-Virologie-Hygiène

Le réseau complexe de dissémination de la résistance aux antibiotiques



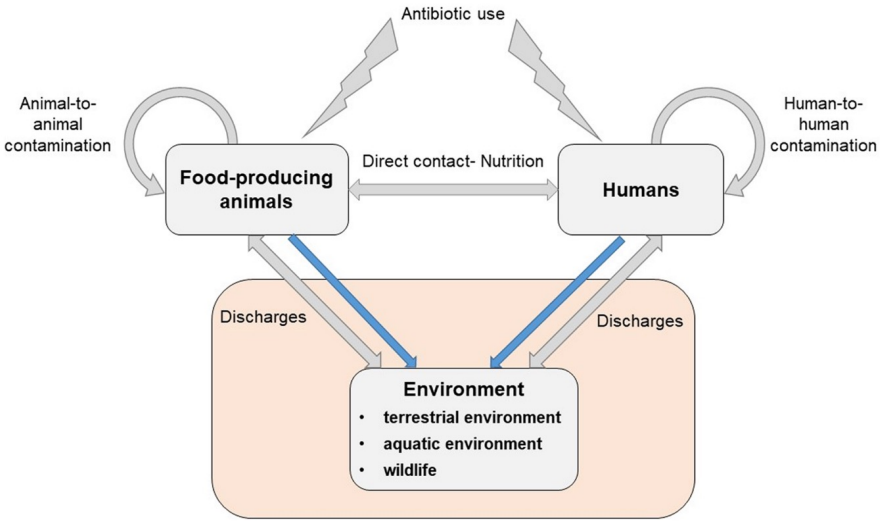


Fig. 1. The flow of antimicrobial resistance and antibiotics across the One Health continuum of food-producing animals, humans, and the environment. Grey arrows indicate flow of resistance genes and resistant bacteria; blue arrows indicate flow of antibiotic residues.

T. Walsh, 2018

Haenni et al, Environment international, 2022

L'environnement est une source de nouveaux gènes de resistance

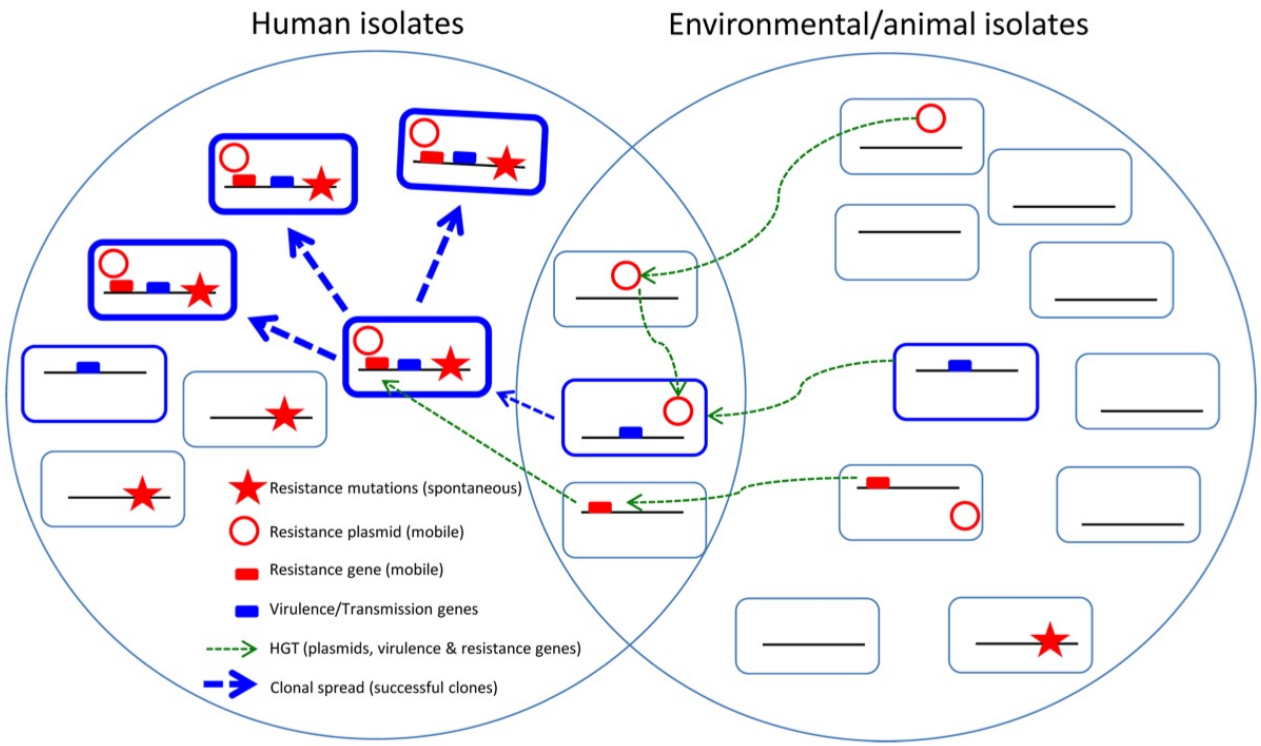


FIGURE 4 Generic scheme for the creation and spread of globally successful antibiotic-resistant clones. In all environments (human, animal, and the wider environment), there are bacterial variants with resistance plasmids, resistance mutations, resistance genes, virulence genes, genes that increase transmission, etc. The mechanisms of HGT, coupled with selection by use of antibiotics, can select for combinations of these elements in one clone. When a clone arises that combines clinical resistance with high fitness and transmissibility, such a clone can spread through the global human population and become a dominant successful clone such as ST131 or ST258.

Microbiology Spectrum
American Society for Microbiology Press

Selection and Transmission of Antibiotic-Resistant Bacteria

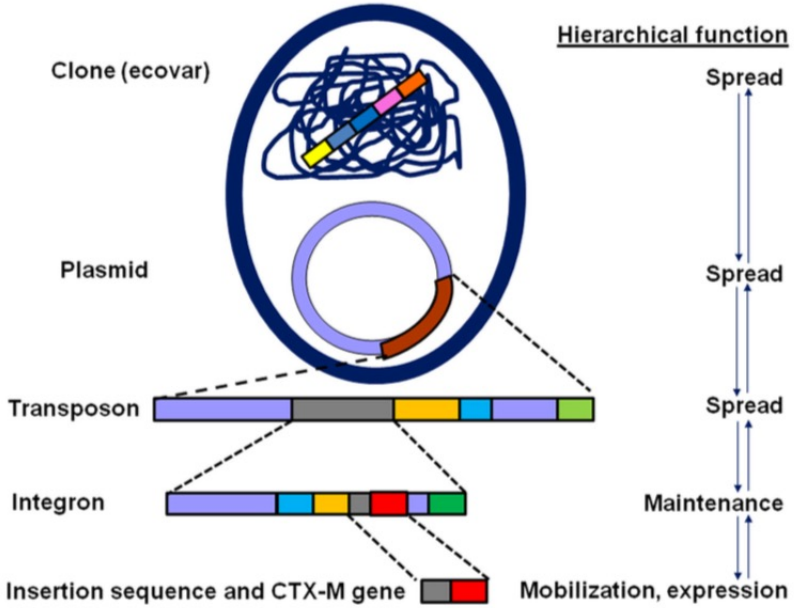
DAN I. ANDERSSON and DIARMAID HUGHES
Department of Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden

Le succès CTX-M

frontiers in
MICROBIOLOGY

CTX-M enzymes: origin and diffusion

Rafael Cantón[1,2]*, José María González-Alba[1] and Juan Carlos Galán[1,2]



ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, Apr. 2006, p. 1282–1286 Vol. 50, No. 4
0066-4804/06/$08.00+0 doi:10.1128/AAC.50.4.1282–1286.2006
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In Vitro Analysis of IS*Ecp1B*-Mediated Mobilization of Naturally Occurring β-Lactamase Gene bla_{CTX-M} of *Kluyvera ascorbata*

Marie-Frédérique Lartigue, Laurent Poirel, Daniel Aubert, and Patrice Nordmann*

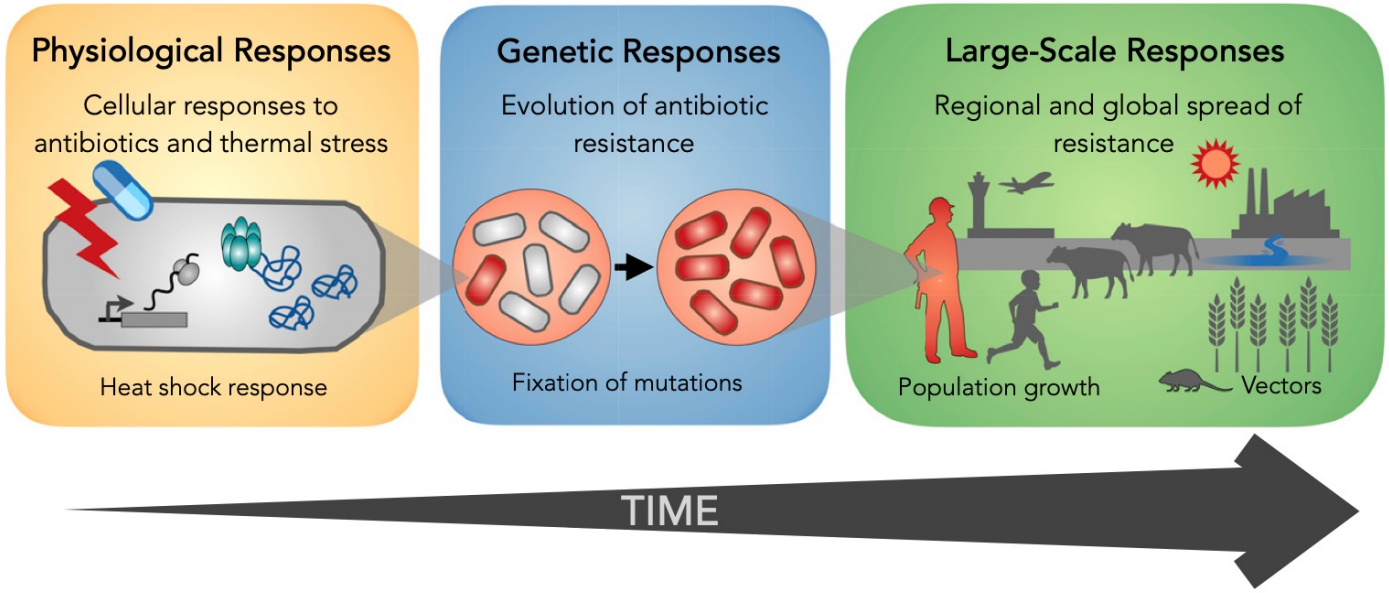
iScience

CellPress REVIEWS

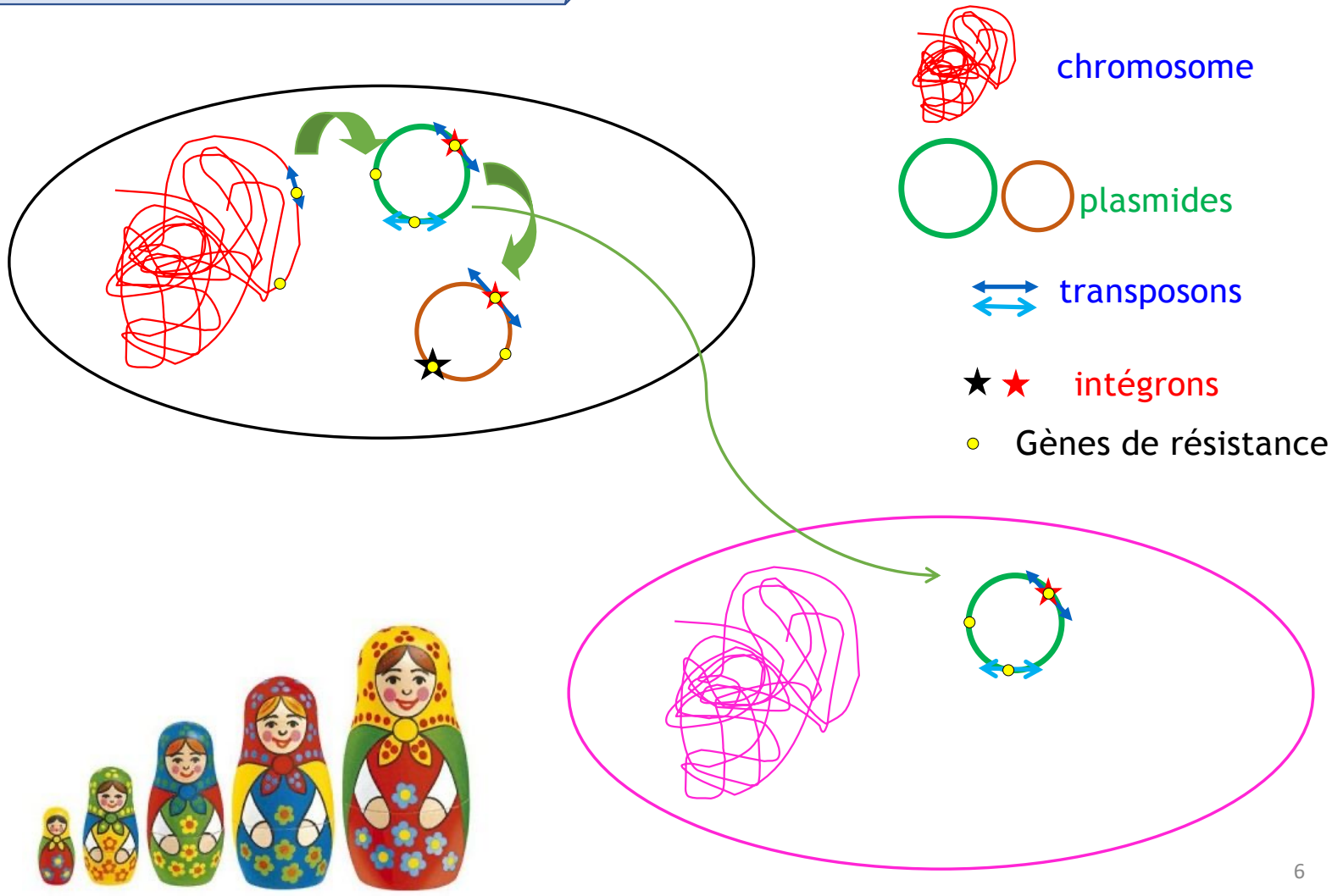
Review

Compounding Effects of Climate Warming and Antibiotic Resistance

Alejandra Rodríguez-Verdugo,[1] Natalie Lozano-Huntelman,[2] Mauricio Cruz-Loya,[3] Van Savage,[2,3,4] and Pamela Yeh[2,4,*]



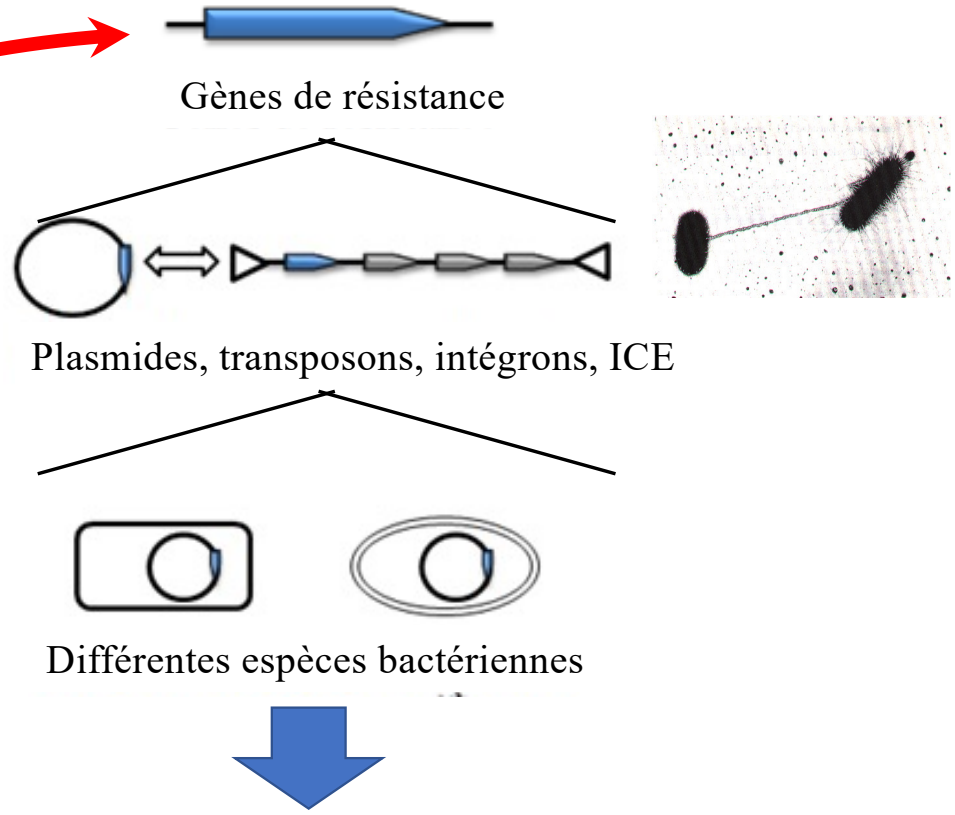
Diversité des éléments génétiques mobiles



Diversité des gènes, des éléments génétiques mobiles et des espèces bactériennes

Antibiotiques	Diversité de gènes
Aminoglycosides	**158**
β-lactamines	**1200**
Chloramphénicol	22
Quinolones	40
Tétracyclines	37
Triméthoprime	41

Diversité de gènes de résistance aux antibiotiques



- Microbiome de l'homme ≈ 400 espèces
- STEP ≈ 1000/3000 espèces
- Sol ≈ 1000/10000 espèces

Delmont *et al.*, 2011
Eckburg *et al.*, 2005
Zang *et al.*, 2012
Mullany *et al.*, 2011

MAIS …. des contraintes écologiques limitent les transferts

J Antimicrob Chemother
https://doi.org/10.1093/jac/dkac054

Journal of Antimicrobial Chemotherapy

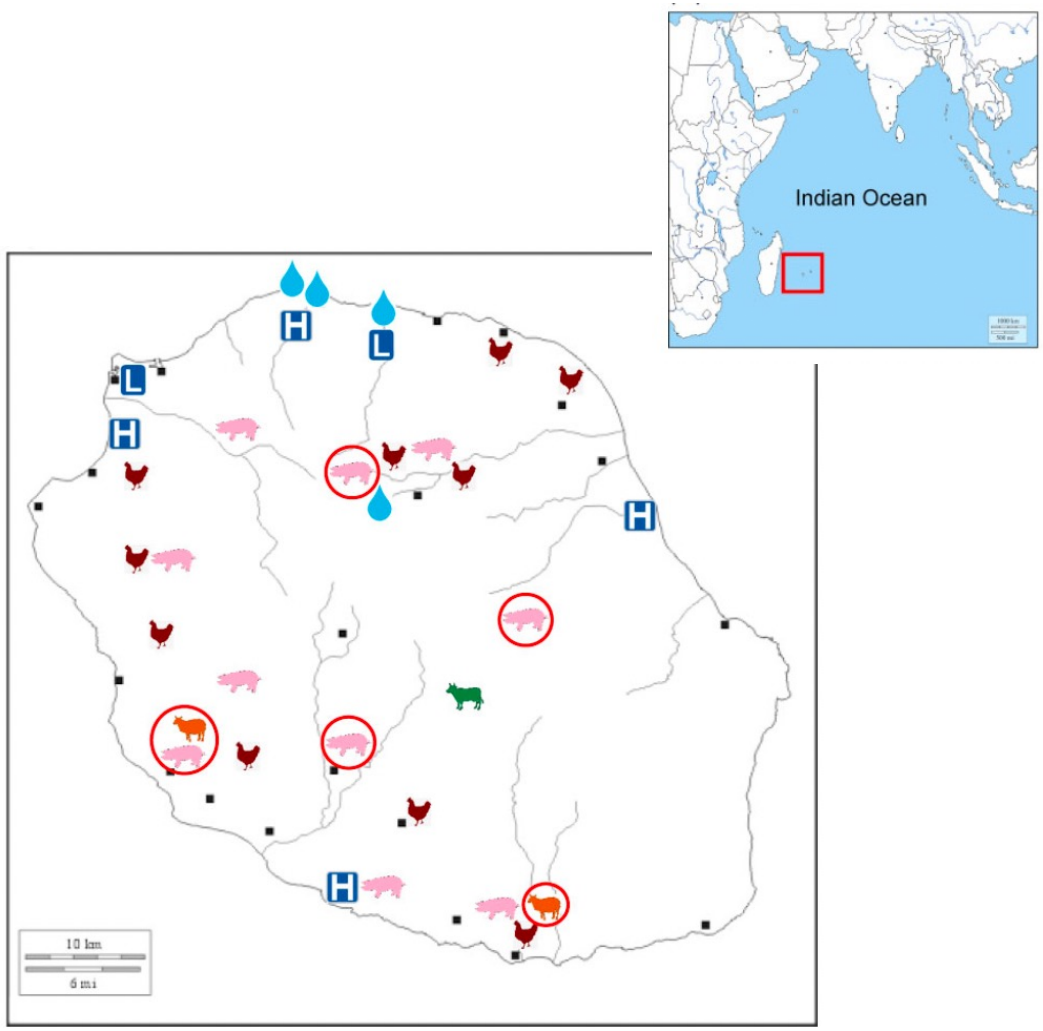
One Health compartmental analysis of ESBL-producing *Escherichia coli* on Reunion Island reveals partitioning between humans and livestock

Guillaume Miltgen[1,2]*, Daniel Martak[3,4], Benoit Valot[4], Laure Kamus[1], Thomas Garrigos[1], Guillaume Verchere[2], Houssein Gbaguidi-Haore[3,4], Céline Ben Cimon[5], Mahery Ramiandrisoa[6], Sandrine Picot[7], Anne Lignereux[8], Geoffrey Masson[9], Marie-Christine Jaffar-Bandjee[1], Olivier Belmonte[1], Eric Cardinale[10,11], Didier Hocquet[3,4], Patrick Mavingui[2] and Xavier Bertrand[3,4]

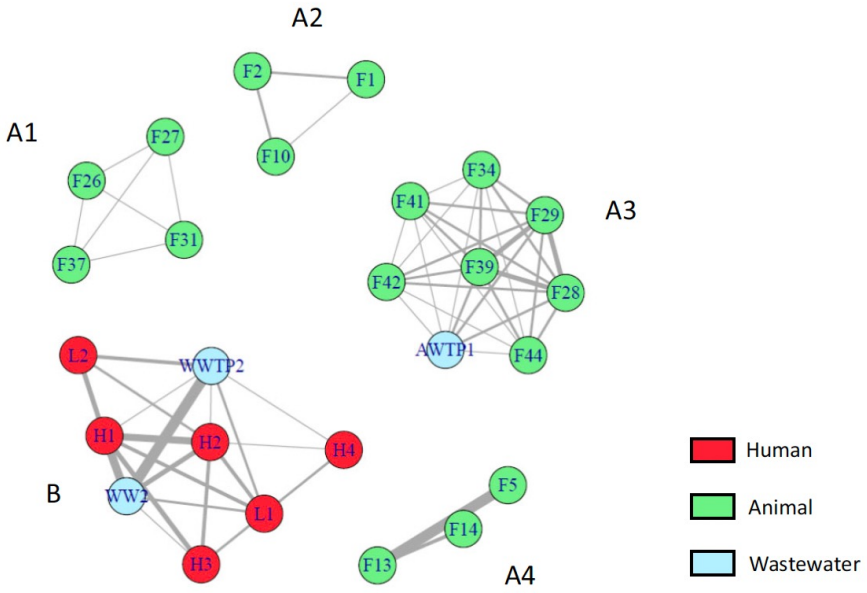
Avril 2015 – Décembre 2018

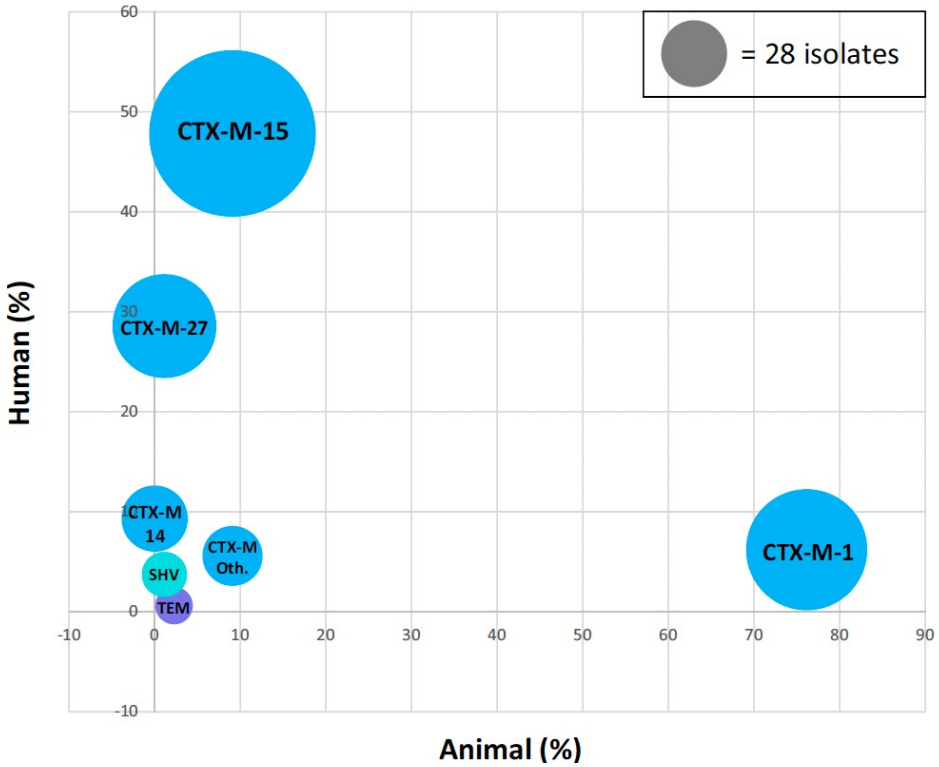
Inclusion : souches de *E. coli* BLSE
homme : 161
animaux d'élevage (veaux, porcs, volailles, lapins, moutons et chèvres) : 161
eaux usées d'origine humaine ou animale : 88

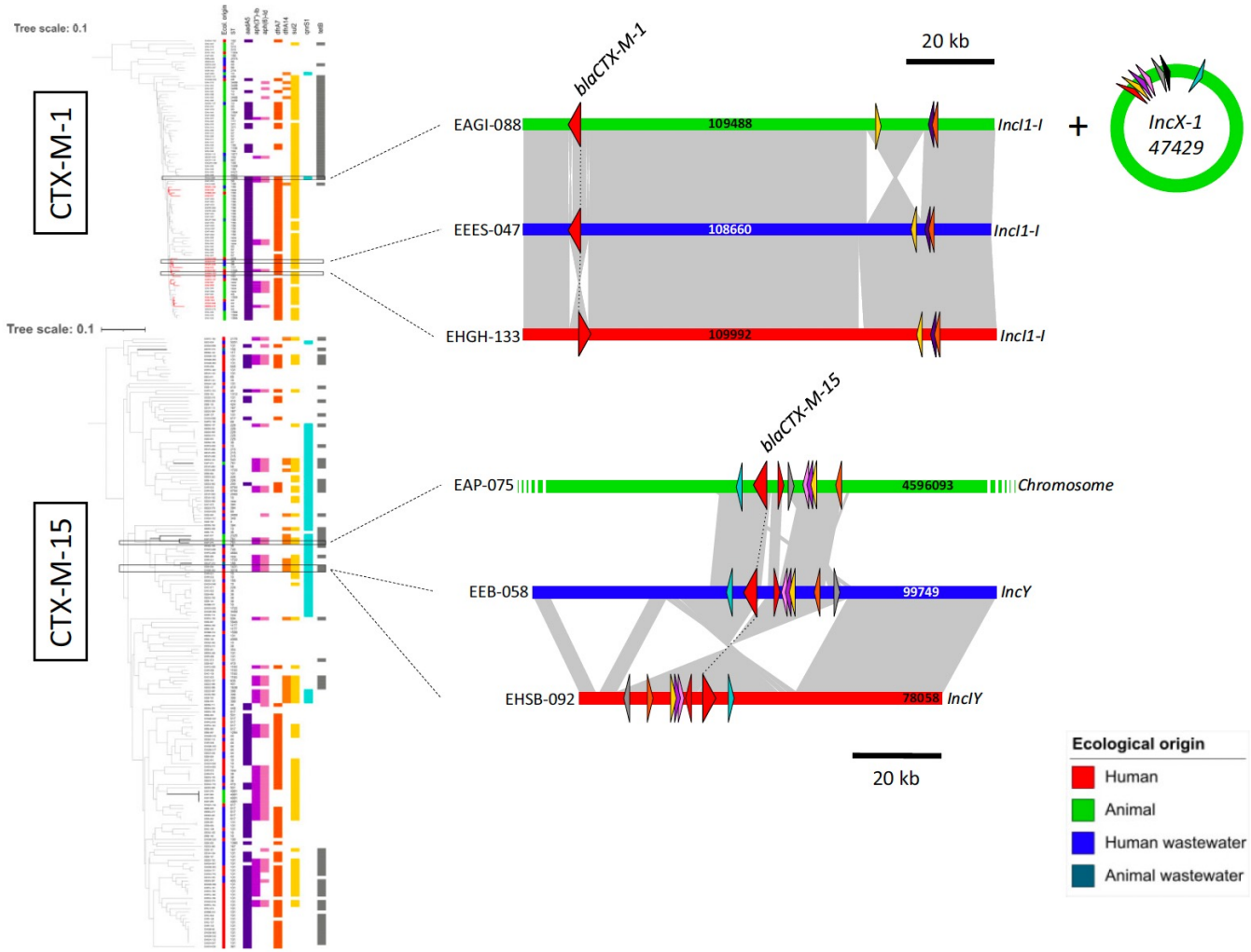
Exclusion : souches suspectes d'avoir été importées (voyages 6 mois, rapatriements sanitaires, nourriture importée)



Des niches écologiques spécifiques






Tree scale: 0.1
CTX-M-1
Tree scale: 0.1
CTX-M-15
blaCTX-M-1
20 kb
EAGI-088
109488
IncI1-I
+
IncX-1
47429
EEES-047
108660
IncI1-I
EHGH-133
109992
IncI1-I
blaCTX-M-15
EAP-075
4596093
Chromosome
EEB-058
99749
IncY
EHSB-092
78058
IncIY
20 kb
Ecological origin
Human
Animal
Human wastewater
Animal wastewater

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Contents lists available at ScienceDirect

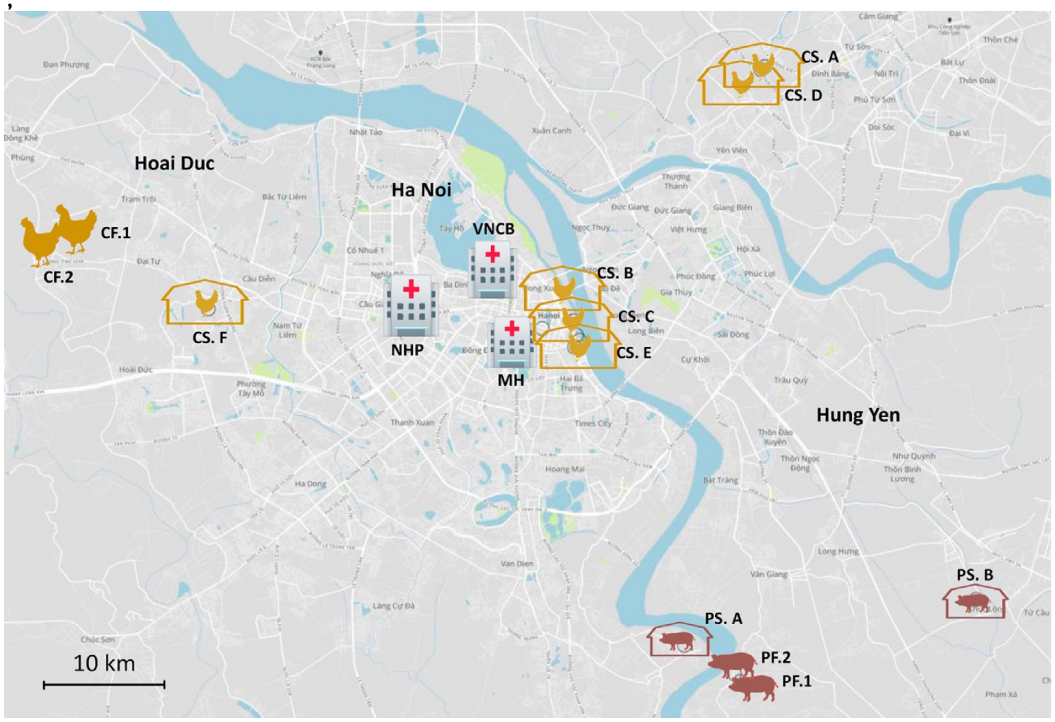
Clinical Microbiology and Infection

journal homepage: www.clinicalmicrobiologyandinfection.com

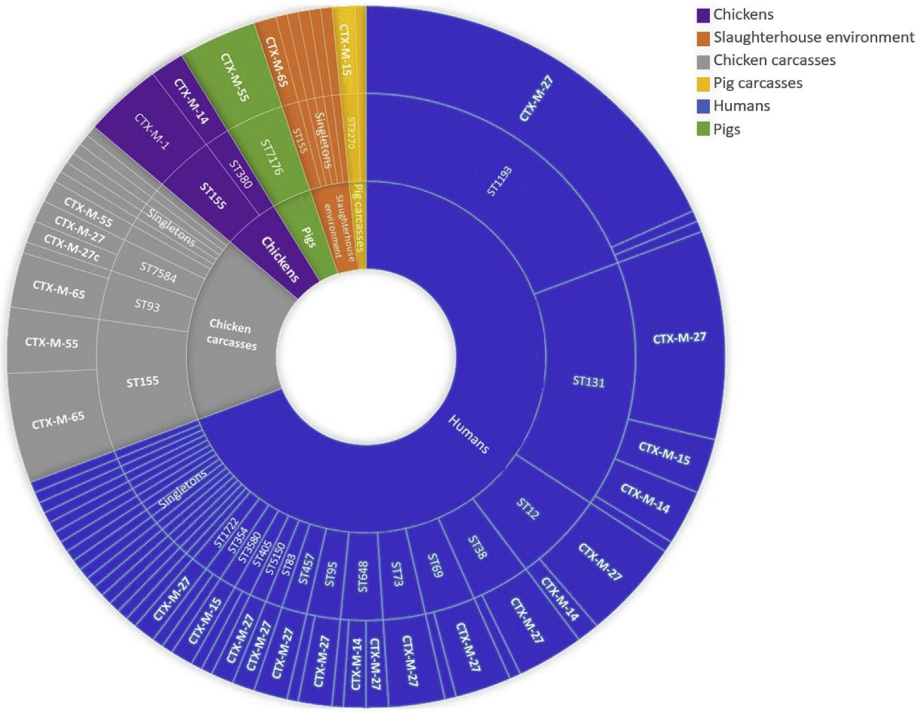
Original article

Prospective One Health genetic surveillance in Vietnam identifies distinct $bla_{CTX\text{-}M}$-harbouring *Escherichia coli* in food-chain and human-derived samples

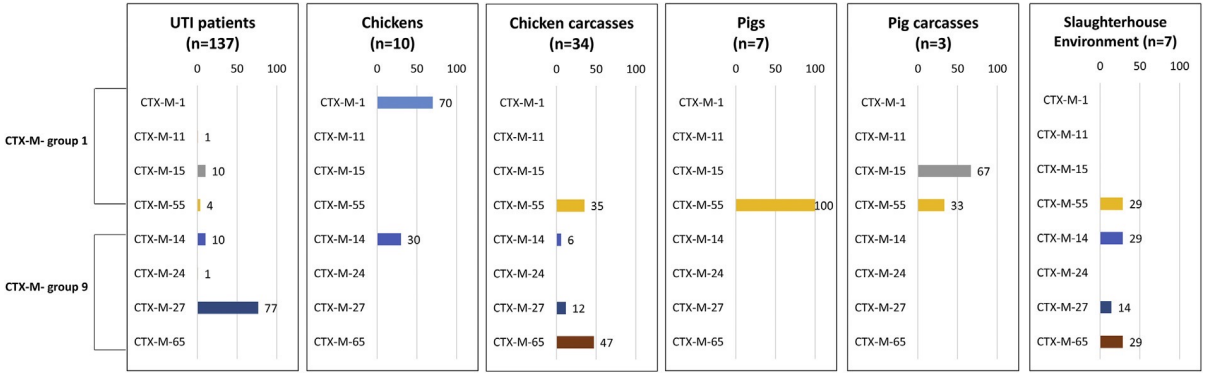
Minh Ngoc Nguyen [1,†], Ha Thi Thu Hoang [2,†], Basil Britto Xavier [1], Christine Lammens [1], Hai Thanh Le [3], Ngoc Thi Bich Hoang [3], Son Thai Nguyen [4], Ngoc Thi Pham [5], Herman Goossens [1], Anh Duc Dang [3], Surbhi Malhotra-Kumar [1,*]



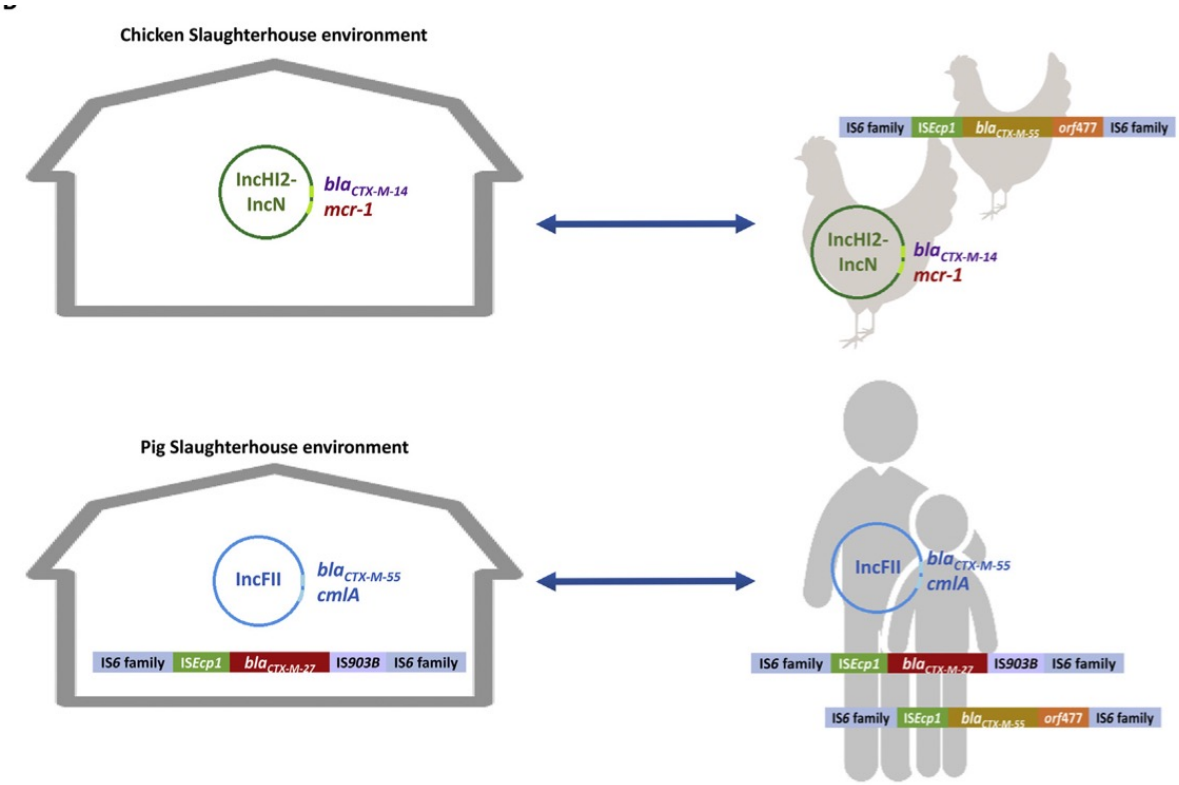
A


Chickens
Slaughterhouse environment
Chicken carcasses
Pig carcasses
Humans
Pigs
Humans
Chicken carcasses
Chickens
Pigs
Slaughterhouse environment
Pig carcasses
ST131
ST1193
ST12
ST38
ST69
ST73
ST648
ST95
ST457
ST783
ST5150
ST405
ST590
ST354
ST1722
Singletons
ST155
ST93
ST7584
ST7176
ST380
ST145
ST2270
CTX-M-27
CTX-M-15
CTX-M-14
CTX-M-65
CTX-M-55
CTX-M-27c
CTX-M-1

B


UTI patients (n=137)
Chickens (n=10)
Chicken carcasses (n=34)
Pigs (n=7)
Pig carcasses (n=3)
Slaughterhouse Environment (n=7)
0 50 100
CTX-M-1
CTX-M-11
CTX-M-15
CTX-M-55
CTX-M-14
CTX-M-24
CTX-M-27
CTX-M-65
CTX-M- group 1
CTX-M- group 9
1
10
4
10
1
77
70
30
35
6
12
47
100
67
33
29
29
14
29

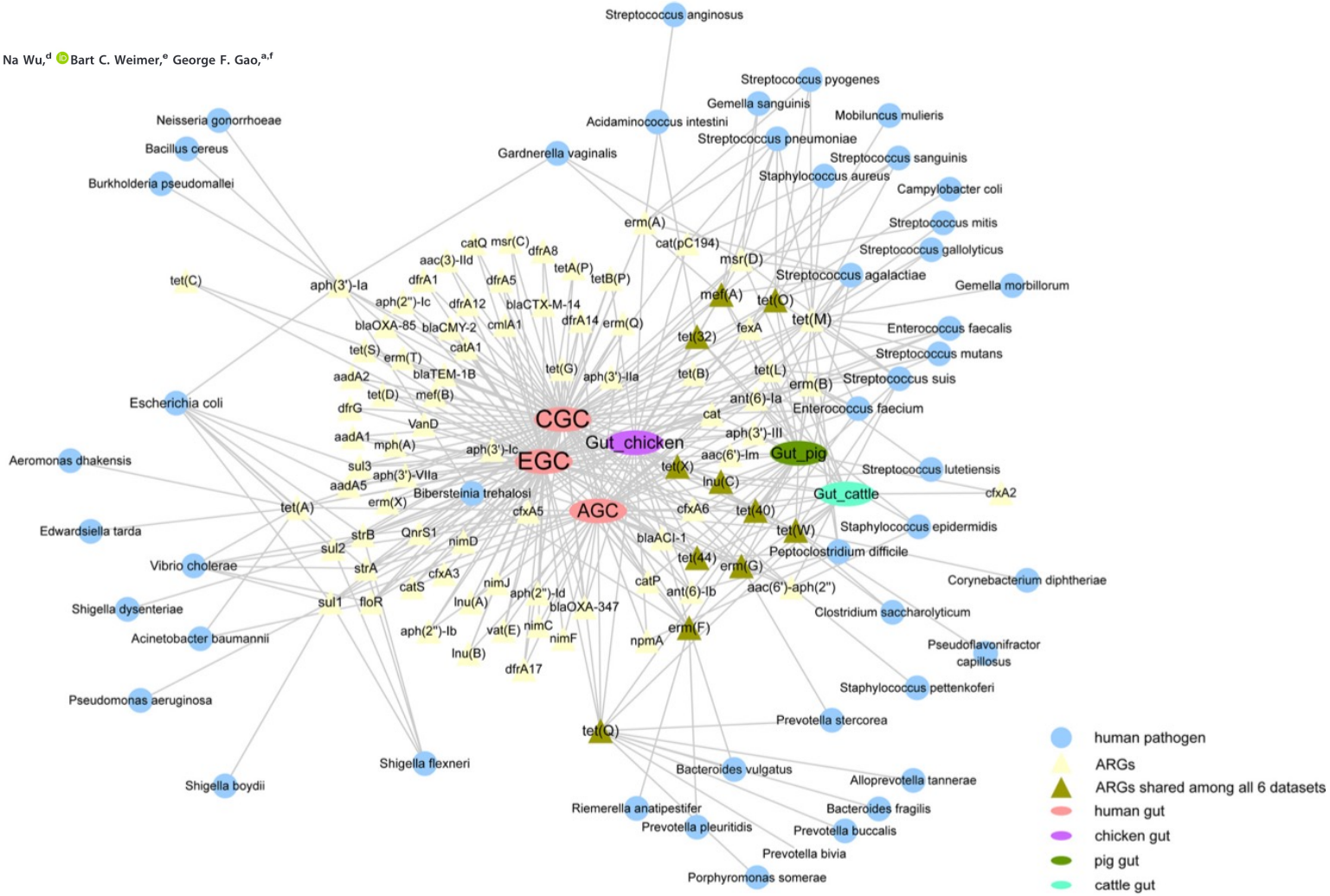
Possibilités de transfert restreintes



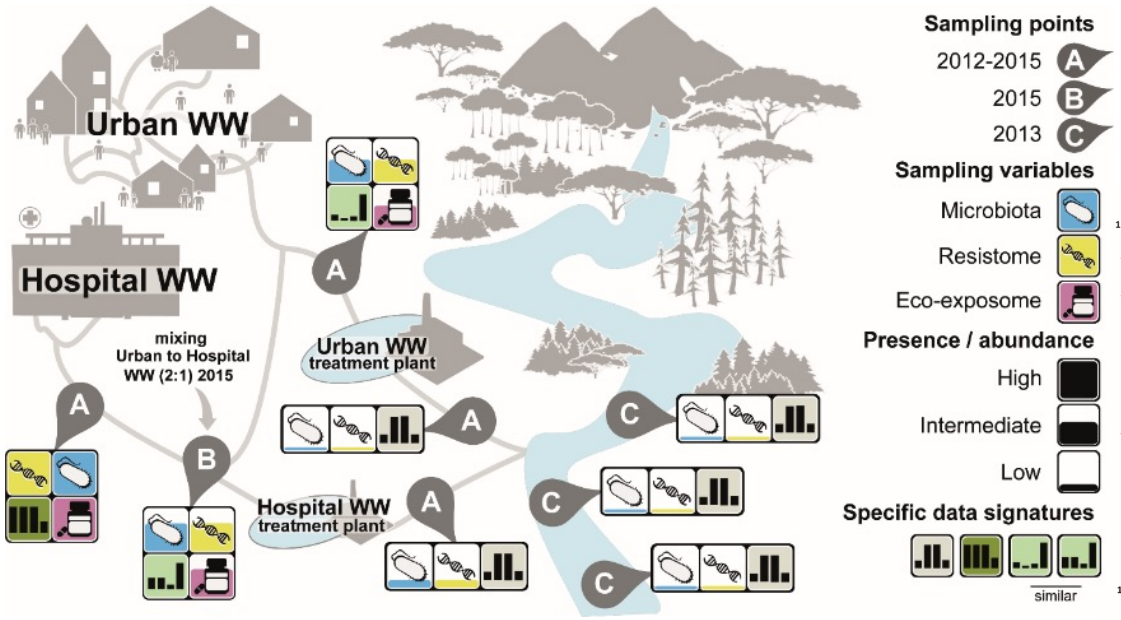
AMERICAN SOCIETY FOR MICROBIOLOGY | Applied and Environmental Microbiology

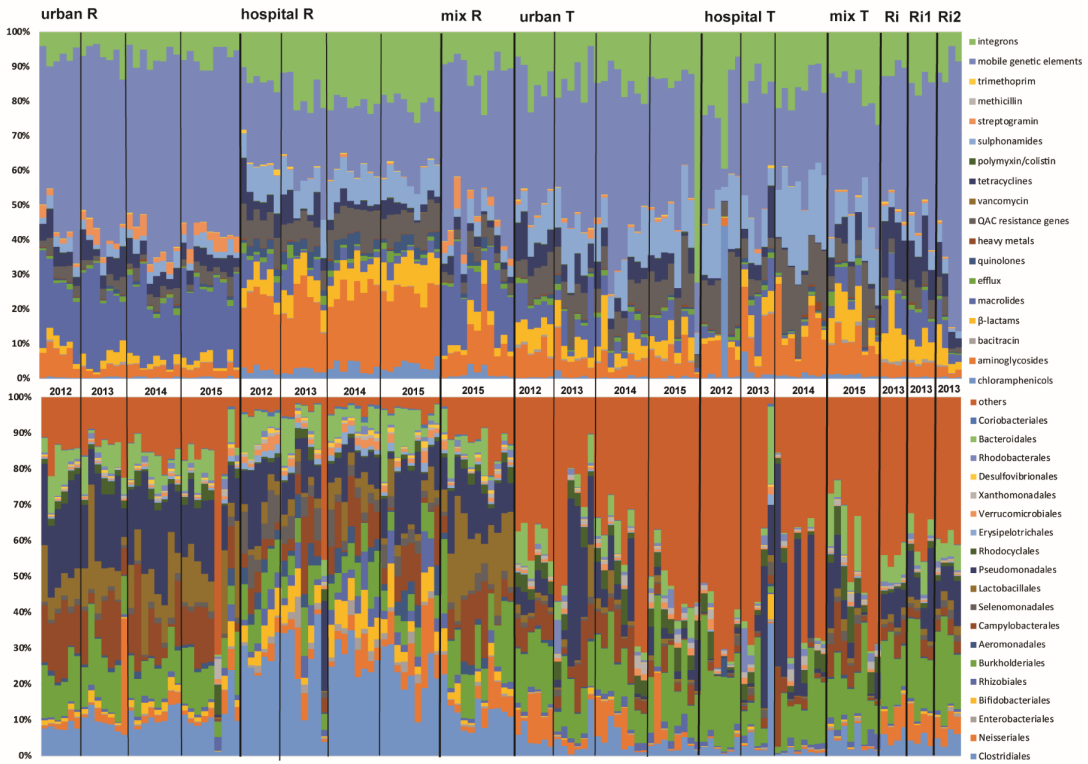
The Bacterial Mobile Resistome Transfer Network Connecting the Animal and Human Microbiomes

Yongfei Hu,[a,b,c] Xi Yang,[a] Jing Li,[a,b] Na Lv,[a,b] Fei Liu,[a,b,c] Jun Wu,[a,b] Ivan Y. C. Lin,[a,b] Na Wu,[d] Bart C. Weimer,[e] George F. Gao,[a,f] Yulan Liu,[d] Baoli Zhu[a,b,c]



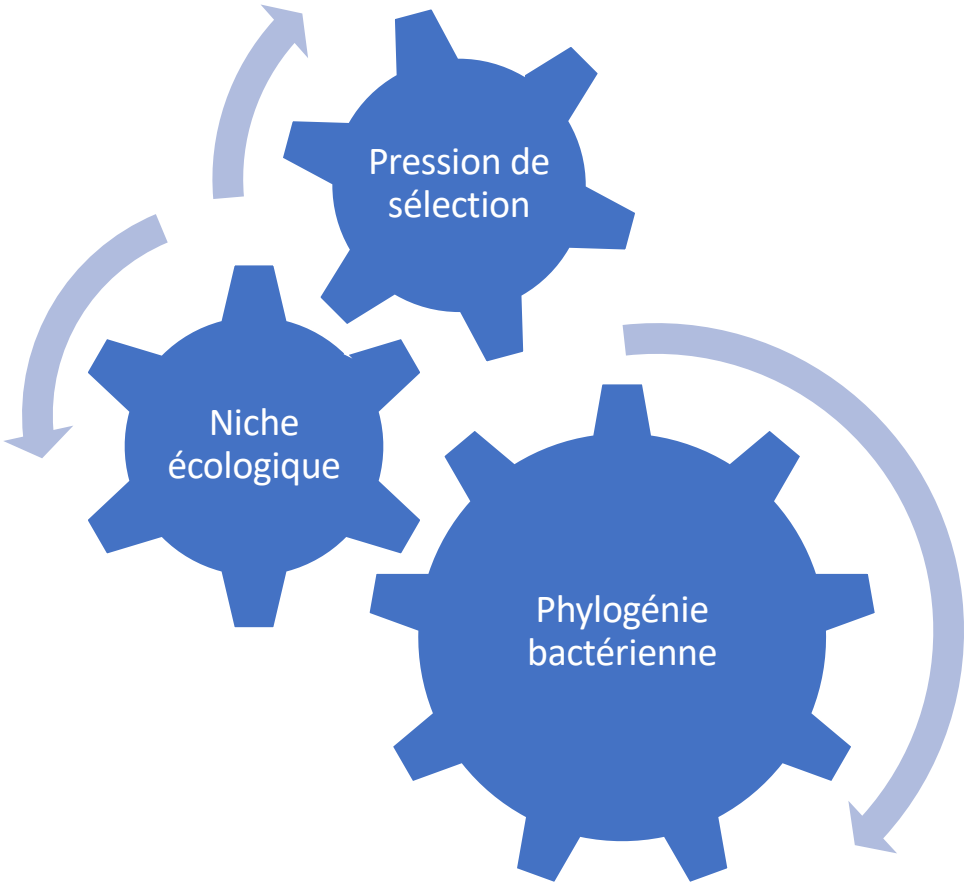
Des signatures spécifiques dans l'environnement





Buelow *et al*. Water Research X, 2020

Les conditions pour un transfert horizontal de gènes efficace entre les compartiments homme, animal, environnement



TRACKING DES TRANSFERTS DES BACTERIES PORTEUSES DE RESISTANCES ENTRE ANIMAL, HOMME ET ENVIRONNEMENT

Pas de marqueur idéal

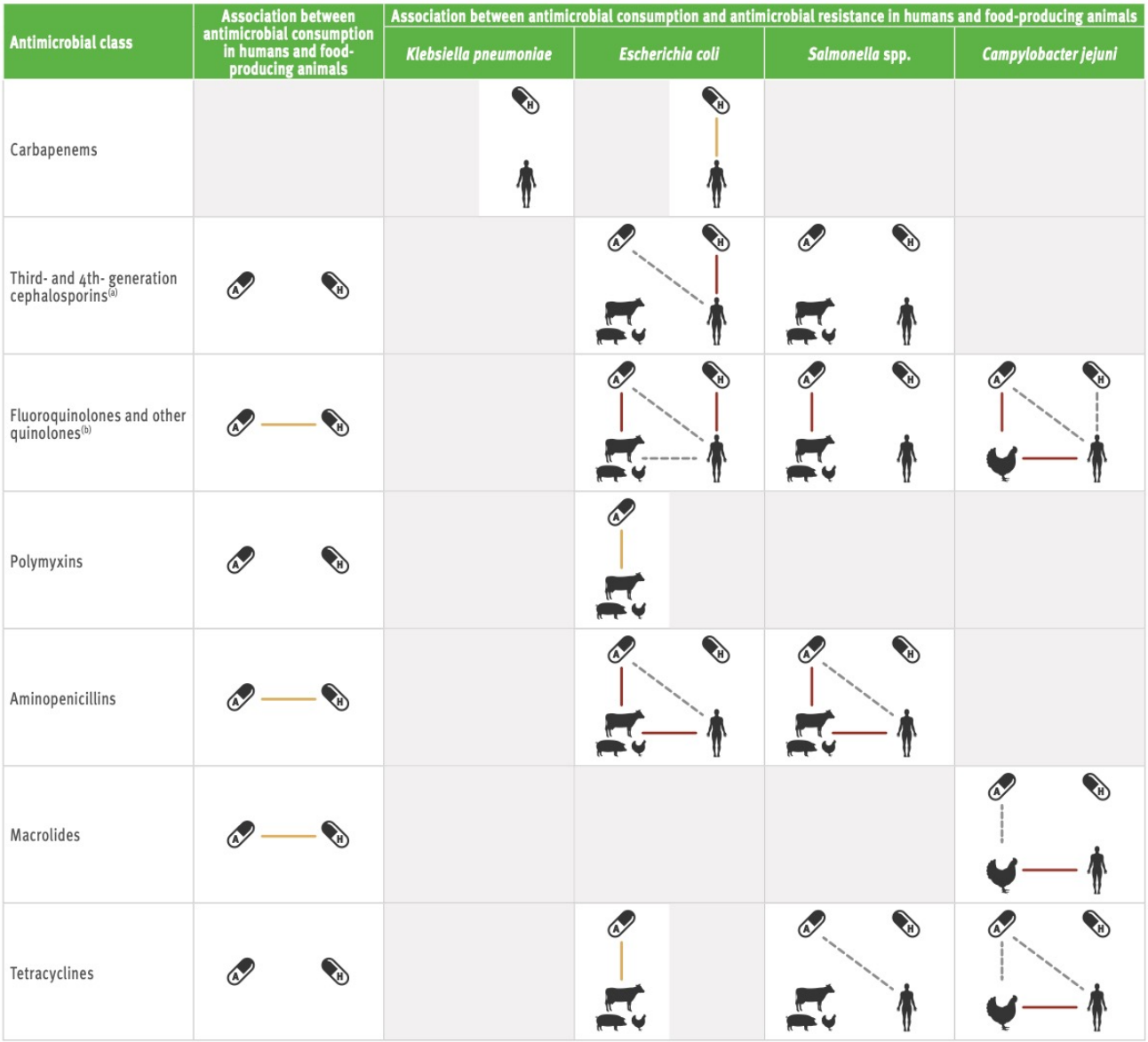
Combinaisons de méthodes génomiques et culturomiques

Intérêt majeur du séquençage de génomes entiers

Vers une surveillance intégrée

+ données environnementales : réseau AMR-Env en construction
+ données exposome
+ données omiques …..

It was on a short-cut through the hospital kitchens that Albert was first approached by a member of the Antibiotic Resistance.

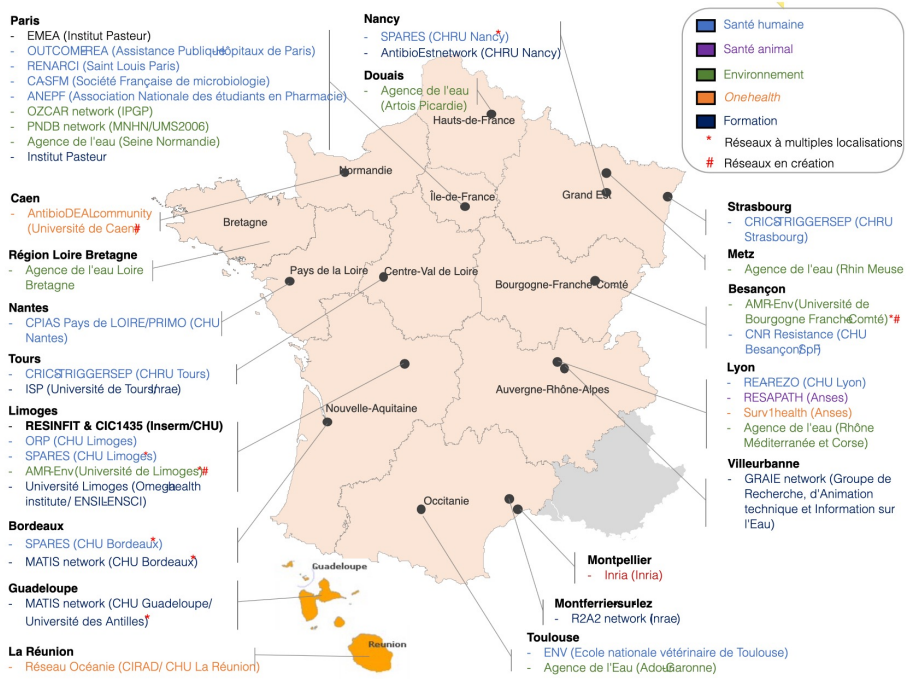


PROMISE

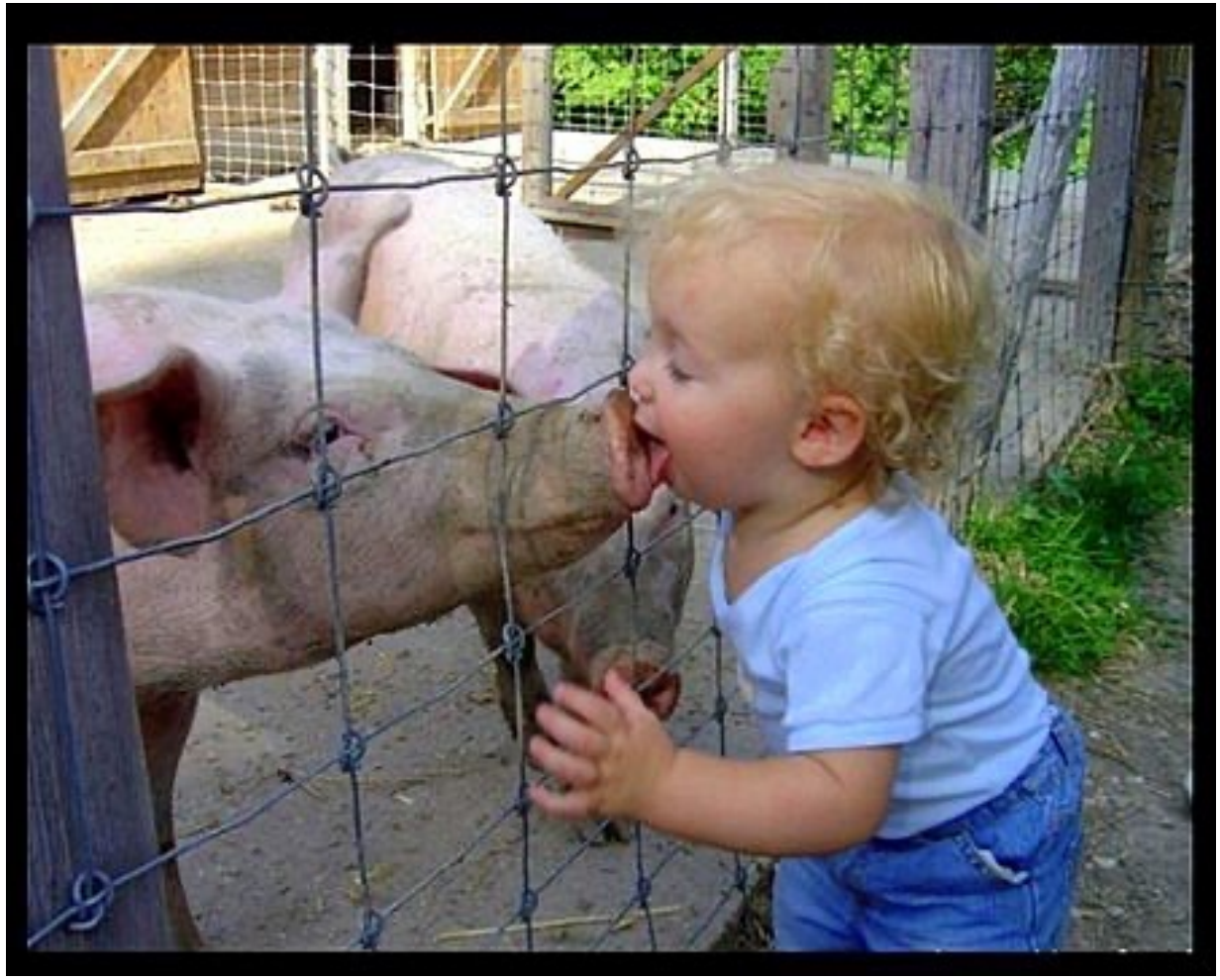
Professional community network on antimicrobial resistance

Programme prioritaire de recherche
Antibiorésistance

23 réseaux de professionnels



OZCAR
RENARCI
SFM Société Française de Microbiologie
EUCAST
Comité de l'antibiogramme de la Société Française de Microbiologie
réAZ
RéPiAS PRIMO
cirad
IRD
ANEPF
ORP Observatoires régionaux du pneumocoque
ANTIBIOEST Conseil, information, bon usage des antibiotiques
OUTCOME RÉA
RéPiAS SPARES
CNR RÉSISTANCE AUX ANTIBIOTIQUES
ONERBA France
CRICS-TRIGGERSEP Clinical Research in Intensive Care and Sepsis TRial Group for Global Evaluation and Research in SEPsis F-CRIN Network
THE WATER AGENCIES
anses alimentation, environnement, travail
RESAPATH
graie
PNDB
RéPiAS MATIS Réseau de Prévention des Infections Associées aux Soins
INRA GISA Réseau Recherche Antibiotiques Animal R2A2



Recommendation

"*Les marqueurs moléculaires sont un outil important pour la surveillance One Health de l'antibiorésistance. Ils pourraient être utilisés dans une approche globale mondiale de l'antibiorésistance en utilisant des marqueurs simples, communs à tous les écosystèmes, homme, animal et environnement, et faisables par tous les pays impliqués*".