La transmission des résistances bactériennes par les aliments

Sanders P

Laboratoire de Fougères

- Bactéries zoonotiques
  - *Salmonella*
  - *Campylobacter* sp.
- Bactéries indicatrices et gènes de résistance
  - *E. Coli*
  - *Enterococcus* sp.

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PLOS | ONE

Risk Factors for Human Salmonellosis Originating from Pigs, Cattle, Broiler Chickens and Egg Laying Hens: A Combined Case-Control and Source Attribution Analysis

Lapo Mughini-Gras*, Remko Enserink, Ingrid Friesema, Max Heck, Yvonne van Duynhoven, Wilfrid van Pelt

National Institute for Public Health and the Environment (RIVM), Centre for Infe

Viande crue

Œuf cru ou mal cuit

Hygiène cuisine

Animal de compagnie

Médicament sur risque

Inter-humain

Table 3. Adjusted odds ratios and 95% confidence intervals of the significant risk factors for human salmonellosis attributable to specific animal reservoirs and overall.

Risk factor (% of imputed missing values)	Overall	Pigs	Cattle	Layers/eggs	Broilers
Eating raw/undercooked meat (3.9)	**2.1 (1.4–3.1)**	**2.8 (1.7–4.6)**	**3.4 (1.7–6.6)**		**2.9 (1.1–7.2)**
Eating chicken (0.9)				0.7 (0.5–1.0)	
Eating pork (0.8)				0.6 (0.5–0.9)	0.5 (0.3–0.8)
Eating meat in pastry (5.0)	0.7 (0.5–0.9)	0.6 (0.4–0.8)	0.5 (0.3–0.9)		
Eating raw/undercooked eggs (0.3)	**2.6 (1.5–5.5)**			**2.6 (1.2–5.8)**	
Eating products containing raw/undercooked eggs (1.0)				**1.8 (1.1–3.1)**	
Eating fish (2.9)	0.7 (0.5–1.0)	0.6 (0.4–0.9)	0.4 (0.3–0.7)		
Drinking pasteurized milk (1.6)			0.6 (0.4–0.9)		
Eating pasteurized dairy products other than milk and cheese (1.8)	0.6 (0.4–0.8)	0.5 (0.4–0.8)	0.5 (0.3–0.8)	0.5 (0.4–0.8)	
Eating raw vegetables (2.0)	0.7 (0.6–0.9)	0.6 (0.5–0.9)			
Eating cooked vegetables (3.2)	0.6 (0.5–0.8)	0.6 (0.4–1.0)		0.5 (0.3–0.7)	0.4 (0.3–0.7)
Eating salad (1.5)					0.6 (0.4–0.9)
Eating fruit (2.3)	0.7 (0.5–0.9)		0.6 (0.4–0.8)	0.5 (0.4–0.7)	0.5 (0.4–0.8)
Eating chocolate (2.1)	0.6 (0.5–0.8)	0.7 (0.5–1.0)		0.5 (0.4–0.7)	0.5 (0.4–0.8)
Eating nuts (3.1)	0.7 (0.5–0.9)	0.7 (0.5–1.0)	0.6 (0.4–0.9)		0.7 (0.4–1.0)
Not cleaning chopping board when using it for raw meat and other foods (1.7)	**1.4 (1.1–1.7)**	**1.5 (1.1–2.1)**	**1.7 (1.1–2.6)**		
Changing kitchen rags less than once a week (1.3)					**1.5 (1.0–2.3)**
Owning a puppy (0.0)		**2.5 (1.2–5.1)**			
Owning more than one dog, at least one puppy (1.5)				**1.7 (1.1–2.5)**	**1.8 (1.1–2.7)**
Occupation with animals and/or raw meat (1.0)			**6.7 (3.0–22.2)**	0.1 (0.0–0.3)	
Using antibiotics (0.0)	**1.9 (1.2–3.1)**	**2.5 (1.5–4.4)**	**2.8 (1.4–5.4)**		
Using proton-pump inhibitors (0.0)	**5.1 (3.1–8.2)**	**6.5 (3.6–11.6)**	**5.6 (2.9–10.5)**	**4.7 (2.7–8.3)**	**8.2 (3.6–18.4)**
Using H2-receptor antagonists (0.0)	**3.5 (1.4–8.6)**			**4.8 (1.9–12.2)**	**6.8 (2.6–17.9)**
Playing in a sandbox (1.1)		**1.8 (1.2–2.7)**	**2.2 (1.3–3.5)**		
Contacting people with gastroenteritis outside the household (7.9)	**1.8 (1.2–2.5)**	**2.3 (1.5–3.6)**	**2.2 (1.3–3.6)**		**2.0 (1.2–3.5)**
Contacting people with gastroenteritis within the household (1.3)				**1.9 (1.2–3.0)**	

Odds ratios presented are also adjusted for age, sex, degree of urbanization, season, and level of education. Risk factors are in bold, protective factors in normal font. Estimates are based on 414 cases (168 and 197 of which caused by *S.* Enteritidis and *S.* Typhimurium, respectively) and 3165 controls.

doi:10.1371/journal.pone.0087933.t003

Ceftiofur Resistance in *Salmonella enterica* Serovar Heidelberg from Chicken Meat and Humans, Canada

Lucie Dutil, Rebecca Irwin, Rita Finley, Lai King Ng, Brent Avery, Patrick Boerlin, Anne-Marie Bourgault, Linda Cole, Danielle Daignault, Andrea Desruisseau, Walter Demczuk, Linda Hoang, Greg B. Horsman, Johanne Ismail, Frances Jamieson, Anne Maki, Ana Pacagnella, and Dylan R. Pillai

- Programme Canadien de surveillance de la résistance (CIPARS)
  - *Salmonella* heidelberg
    - Viande
    - Cas humain
- Dynamique de l'exposition

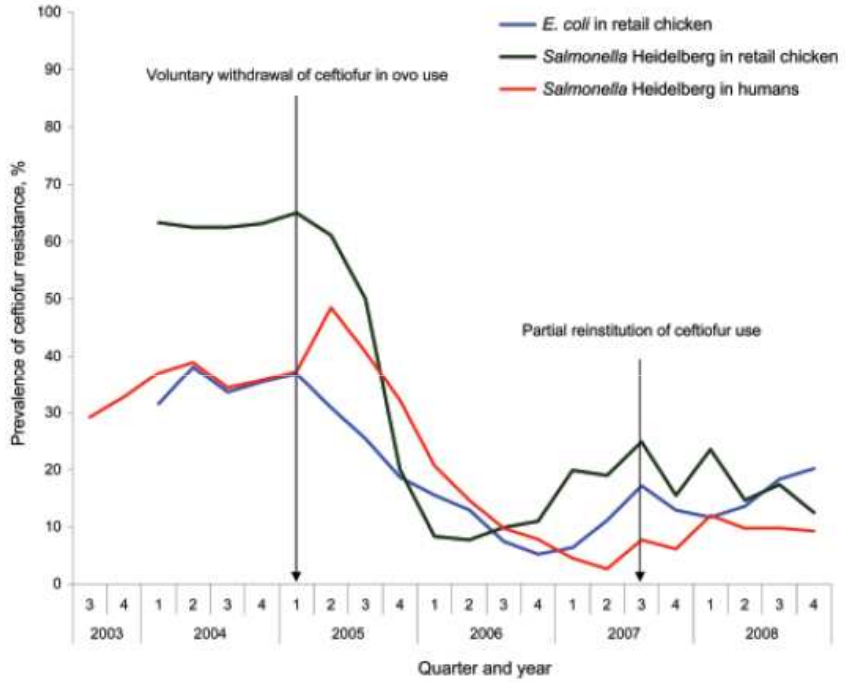

Figure 2. Prevalence of ceftiofur resistance (moving average of the current quarter and the previous 2 quarters) among retail chicken *Escherichia coli*, and retail chicken and human clinical *Salmonella enterica* serovar Heidelberg isolates during 2003–2008 in Québec, Canada.

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 16, No. 1, January 2010

anses

Sciencexpress

Distinguishable Epidemics of Multidrug-Resistant *Salmonella* Typhimurium DT104 in Different Hosts

A. E. Mather,[1] S. W. J. Reid,[2]‡ D. J. Maskell,[3] J. Parkhill,[1] M. C. Fookes,[1] S. R. Harris,[1] D. J. Brown,[4] J. E. Coia,[4] M. R. Mulvey,[5] M. W. Gilmour,[5]* L. Petrovska,[6] E. de Pinna,[7] M. Kuroda,[8] M. Akiba,[9] H. Izumiya,[10] T. R. Connor,[1]† M. A. Suchard,[11] P. Lemey,[12] D. J. Mellor,[13] D. T. Haydon,[13] N. R. Thomson[1]‡

PROCEEDINGS OF THE ROYAL SOCIETY B BIOLOGICAL SCIENCES

An ecological approach to assessing the epidemiology of antimicrobial resistance in animal and human populations

Alison E. Mather, Louise Matthews, Dominic J. Mellor, Richard Reeve, Matthew J. Denwood, Patrick Boerlin, Richard J. Reid-Smith, Derek J. Brown, John E. Coia, Lynda M. Browning, Daniel T. Haydon and Stuart W. J. Reid

Proc. R. Soc. B 2012 **279**, doi: 10.1098/rspb.2011.1975 first published online 16 November 2011

Processus épidémiologique réétudié et révisé avec les nouveaux outils moléculaires et d'analyse de données

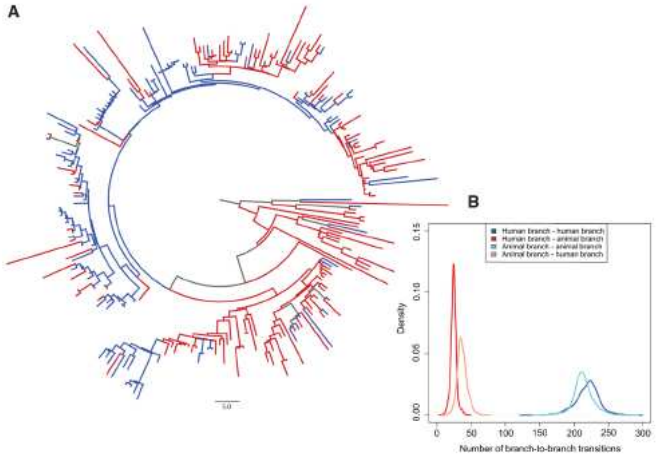

Fig. 2. Bayesian maximum clade credibility phylogenetic tree and most probable ancestral state reconstruction of host population for *S.* Typhimurium DT104 in Scotland. (**A**) Branches with a reconstructed state (host population) posterior probability of >0.75 are colored red for human, blue for animal; branches with a state probability of <0.75 are colored gray. The same tree is shown in fig. S6 with branch width scaled by the posterior probabilities. (**B**) Posterior density plot of the numbers of human branches ancestral to human branches, human branches ancestral to animal branches, animal branches ancestral to human branches, and animal branches ancestral to animal branches integrated over the subsample of 3600 phylogenetic trees with reconstructed host population states along branches obtained by using BEAST. These results suggest (i) circulation of DT104 predominantly within animals and humans separately, with only a low frequency of spillover in both directions, and/or (ii) animals and humans were each sinks for different and separate sources of infection, with only a low frequency of spillover in both directions.

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PLoS one

Risk Factors for Campylobacteriosis of Chicken, Ruminant, and Environmental Origin: A Combined Case-Control and Source Attribution Analysis

Lapo Mughini Gras[1,2,3*9], Joost H. Smid[2,9], Jaap A. Wagenaar[4,5,6], Albert G. de Boer[4], Arie H. Havelaar[2,7], Ingrid H. M. Friesema[2], Nigel P. French[8], Luca Busani[1], Wilfrid van Pelt[2]

Table 3. Multivariable odds ratios and percent PAR or PPR (and 95% confidence intervals) for food-related risk factors for human campylobacteriosis according to the attributed origin of the *Campylobacter* strain (chicken, ruminant, and the environment).

Risk factor (% imputed missing values[a])	Overall[a]	Chicken[b]	Ruminants[c]	Environment[d]
Food consumption				
Chicken (1)	**1.5 (1.2–1.9)**	**1.9 (1.2–2.9)**	ns	ns
	28% (13–41%)	**42% (14–60%)**		
Beef (1)	ns	0.6 (0.4–0.9)	ns	ns
		30% (7–44%)		
Pork (2)	ns	0.7 (0.5–0.9)	ns	ns
		16% (5–26%)		
Tripe (1)	ns	ns	**4.0 (1.1–14.2)**	ns
			12% (1–37%)	
Game (0)	ns	ns	ns	**3.3 (1.4–7.8)**
				37% (10–64%)
Undercooked meat (5)	**2.1 (1.6–2.7)**	ns	ns	ns
	16% (10–23%)			
Barbecued, grilled, or microwaved meat (5)	**18% (10–25%)**	ns	**63% (41–78%)**	ns
in urban areas	**1.2 (0.7–2.2)**[**]	ns	0.8 (0.1–7.3)[**]	ns
in urbanized areas	**1.7 (1.3–2.2)**	ns	**7.1 (3.2–15.6)**	ns
in rural areas	**3.0 (1.8–4.9)**	ns	**4.1 (1.3–14.2)**	ns

Poulet

Cuisson

Anl de compagnie

Homme

Table 4. Multivariable odds ratios and percent PAR or PPR (and 95% confidence intervals) for non-food related risk factors fc human campylobacteriosis according to the attributed origin of the *Campylobacter* strain (chicken, ruminant, and the environment).

Risk factor (% imputed missing values*)	Overall[a]	Chicken[b]	Ruminants[c]	Environment[d]
Contact with animals				
Contact with dog(s) owned by other people (3)	0.6 (0.5–0.8)	ns	ns	ns
	8% (4–10%)			
Contact with pets and/or farm animals outside the household (1)	ns	ns	ns	0.4 (0.2–1.0)
				17% (1–22%)
Ownership of several dogs, at least one dog <1 year-old (0)	**2.5 (1.1–5.8)**	ns	ns	ns
	2% (1–7%)			
Ownership of several dogs, all dogs >1 year-old (0)	ns	ns	ns	**3.5 (1.0–12.0)**
				33% (1–54%)
Ownership of cat(s) (1)	**1.4 (1.2–1.8)**	ns	ns	ns
	10% (5–17%)			
Recent use of medication				
Antibiotics (0)	0.4 (0.2–0.8)	ns	ns	ns
	1% (0–2%)			
Proton-pump inhibitors (0)	**3.7 (2.5–5.5)**	**4.7 (2.4–9.1)**	**5.7 (2.2–16.15.3)**	ns
	22% (14–33%)	**34% (11–53%)**	**34% (11–58%)**	
Other				
Swimming in a domestic swimming pool (0)	ns	ns	ns	**28% (2–64%)**
in the spring season	ns	ns	ns	**16.8 (2.6–107.6)**
in the summer, winter or autumn seasons	ns	ns	ns	**2.5 (0.4–14.4)[ns]**
Contact with people with gastroenteritis symptoms outside the household (3)	**1.5 (1.1–2.1)**	**1.8 (1.1–3.0)**	ns	**3.4 (1.3–8.7)**
	6% (1–12%)	**10% (1–23%)**		**35% (6–63%)**
Having a chronic gastrointestinal disease (0)§	**2.4 (1.8–3.2)**	**1.8 (1.1–3.1)**	ns	**5.0 (2.1–12.1)**
	20% (13–28%)	**12% (2–27%)**		**50% (22–74%)**
Occupational exposure to animals (0)	ns	ns	**3.2 (1.2–9.0)**	ns
			17% (2–41%)	

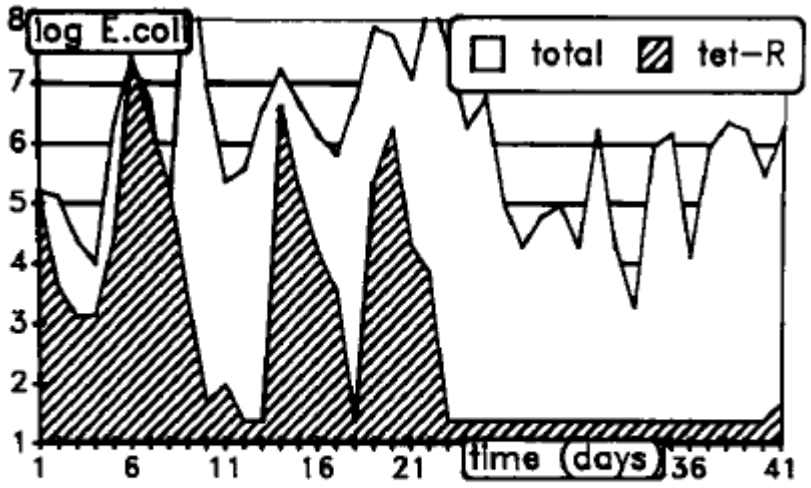
E.coli

The New England Journal Medicine, 1988, 318 (18) 1206-1207 Author's Version
May 5, **1988 – Denis E. Corpet**

ANTIBIOTIC RESISTANCE FROM FOOD

Veterinary Microbiology, 35 (1993) 199–212
Elsevier Science Publishers B.V., Amsterdam

An evaluation of methods to assess the effect of antimicrobial residues on the human gut flora



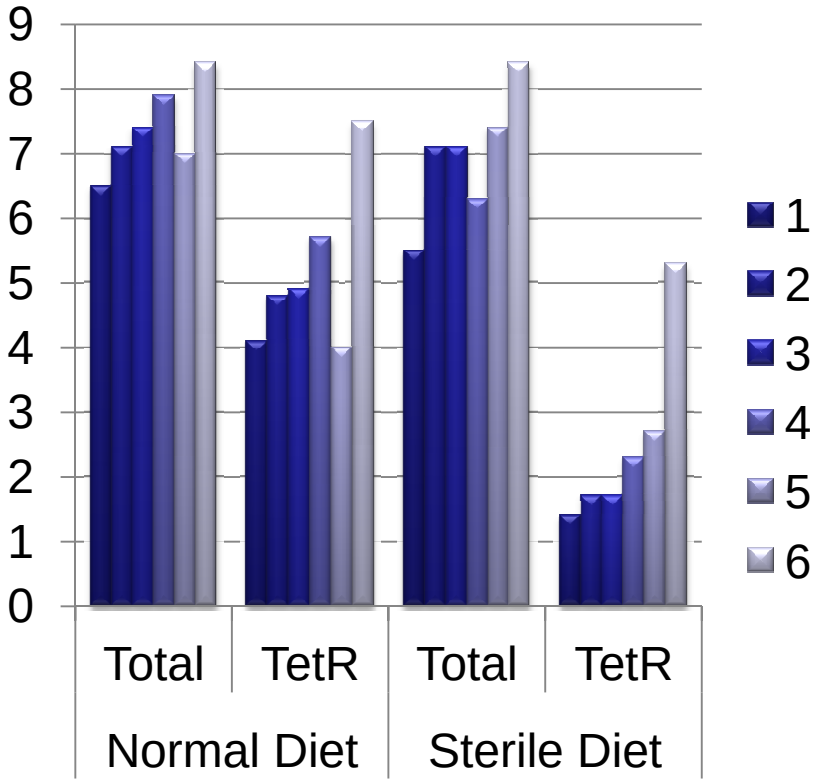


Fig. 3. Log No. of lactose-fermenting enteric organisms in the stools of a volunteer given a sterile diet from days 21 to 40.

Beta-lactamase à spectre étendu - Viande

Contents lists available at ScienceDirect

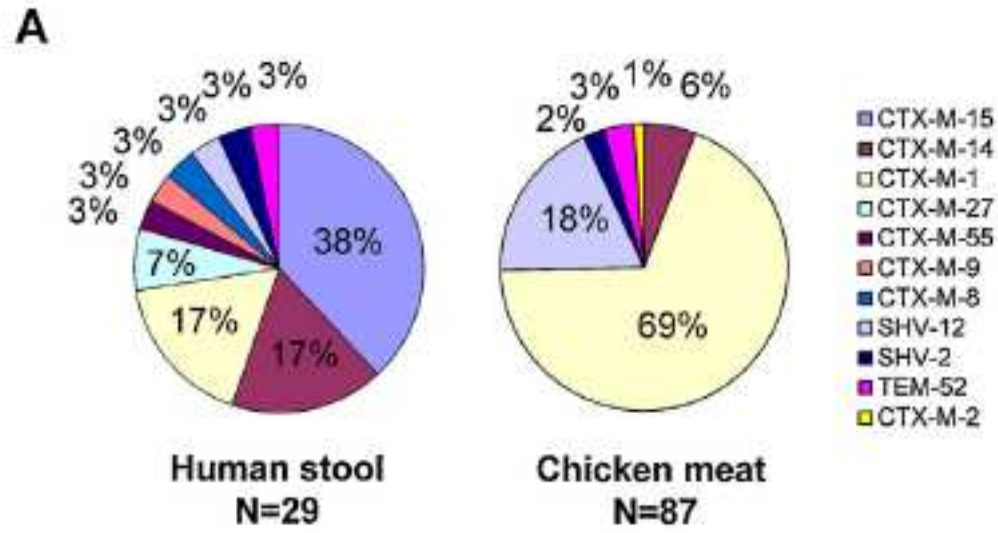
International Journal of Medical Microbiology

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

Prevalence and genotypes of extended spectrum beta-lactamases in *Enterobacteriaceae* isolated from human stool and chicken meat in Hamburg, Germany

Cristina Belmar Campos[a,*], Ines Fenner[b], Nicole Wiese[b], Carmen Lensing[b], Martin Christner[a], Holger Rohde[a], Martin Aepfelbacher[a], Thomas Fenner[b], Moritz Hentschke[a]

29/707 **72/120**



Contents lists available at SciVerse ScienceDirect
International Journal of Food Microbiology
journal homepage: www.elsevier.com/locate/ijfoodmicro

Assessment of human exposure to 3rd generation cephalosporin resistant *E. coli* (CREC) through consumption of broiler meat in Belgium

P. Depoorter [a,*], D. Persoons [b], M. Uyttendaele [c,s], P. Butaye [d], L. De Zutter [b,s], K. Dierick [e,s], L. Herman [f,s], H. Imberechts [d,s], X. Van Huffel [a], J. Dewulf [b,s]

Calcul exposition
≥1000 cfu CR E coli
1,5 %
Contamination croisée

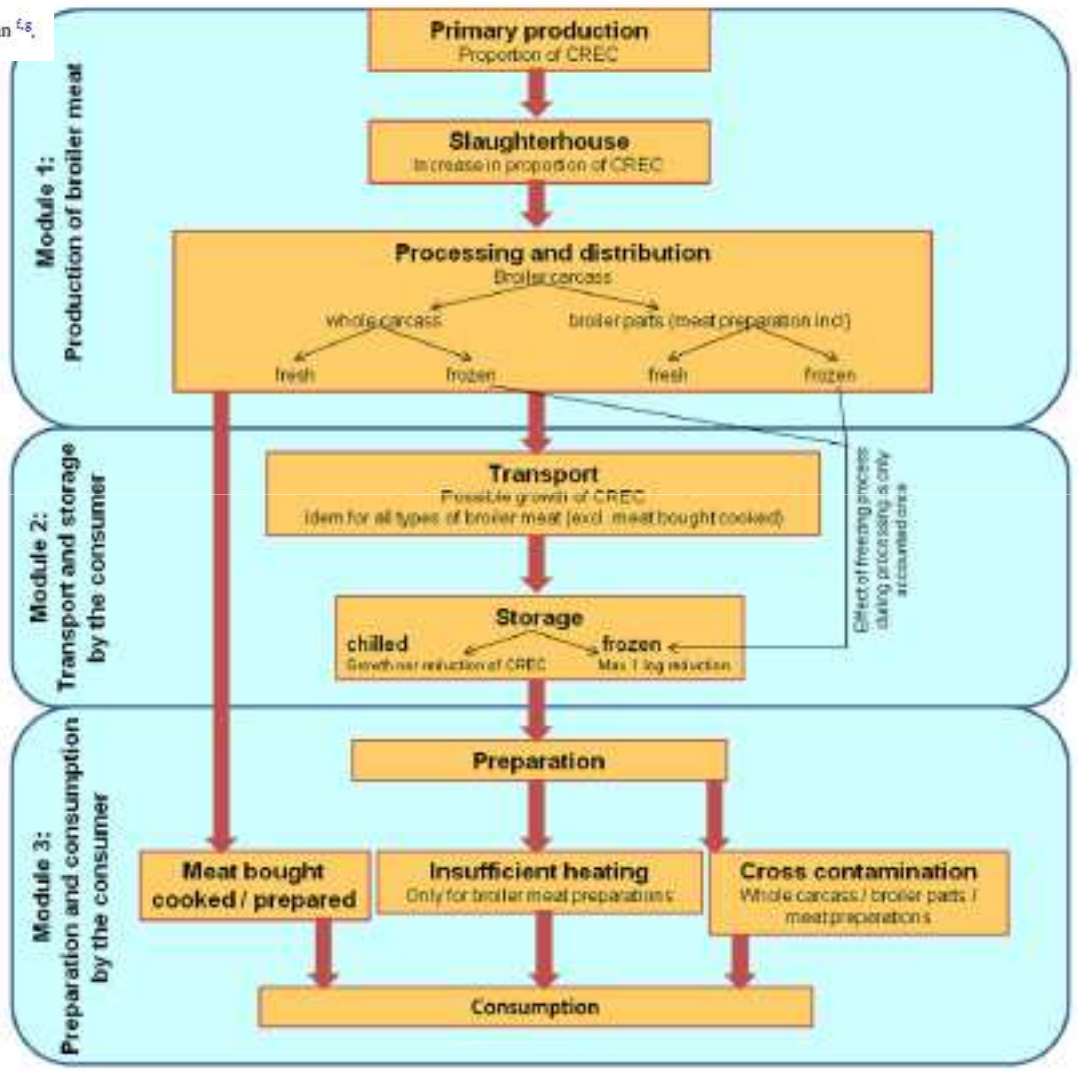


Fig. 1. Flowchart of the model.

COACTION PUBLISHING

Exposure assessment of extended-spectrum beta-lactamases/AmpC beta-lactamases-producing *Escherichia coli* in meat in Denmark

Luís P. Carmo, DVM, MSc[1,2]*, Liza R. Nielsen, DVM, PhD, DrVetSci, DipECVPH[2], Paulo M. da Costa, DVM, PhD[1,3] and Lis Alban, DVM, PhD, DipECVPH, DipECPHM[4]

Danmap

Table 1. Relative contribution (RC) of each type of meat for human exposure considering the origin and the genotypes found in DANMAP surveillance from 2009 to 2011

	RC for human exposure (%)					RC for human exposure (%)					RC for human exposure (%)			
Meat type	2009	2010	2011	2009–2011	Origin	2009	2010	2011	2009–2011	Genotype	2009	2010	2011	2009–2011
										CTX-M-1	0.0	6.2	2.5	3.1
					Danish	18.9	6.2	2.5	6.2	CTX-M-2	12.9	0.0	0.0	2.1
										Others[1]	6.0	0.0	0.0	1.0
Pork	24.2	13.8	8.4	12.5										
										CTX-M-1	2.7	7.6	4.5	5.1
					Imported	5.3	7.6	6.0	6.3	CMY-2	0.0	0.0	1.5	0.8
										CTX-M-14	2.7	0.0	0.0	0.4
					Danish	3.2	2.4	0.00	1.8	CMY-2	0.0	2.4	0.0	0.7
Beef	8.8	5.4	1.4	3.7						Others[2]	3.2	0.0	0.0	0.5
					Imported	5.7	3.1	1.4	2.5	CTX-M-1	5.7	3.1	1.4	2.5
					Danish	9.3	14.5	56.5	37.0	CMY-2	4.7	11.8	53.5	33.8
Broiler meat	67.0	80.8	90.2	83.8						CTX-M-1	4.7	2.7	3.0	3.2
					Imported	57.6	66.3	33.7	46.8	CMY-2	27.6	24.7	20.8	23.0
										CTX-M-1	14.2	29.3	7.9	15.0
										SHV-12	9.2	6.5	4.1	5.6
										Others[3]	5.0	4.1	1.0	2.5
										CTX-M-2	1.6	1.7	0.0	0.8

[1]Unknown genotypes (i.e. when it was impossible to determine a specific genotype).
[2]TEM-52 and unknown genotypes.
[3]TEM-20, TEM-52, up-regulated AmpC and unknown genotypes.

Results and discussion: Broiler meat represented the largest part (83.8%) of the estimated ESBL/AmpC-contaminated pool of meat compared to pork (12.5%) and beef (3.7%). CMY-2 was the genotype with the highest RC to human exposure (58.3%). However, this genotype is rarely found in human infections in Denmark.

Conclusion: The overlap between ESBL/AmpC genotypes in meat and human *E. coli* infections was limited. This suggests that meat might constitute a less important source of ESBL/AmpC exposure to humans in Denmark than previously thought – maybe because the use of cephalosporins is restricted in cattle and banned in poultry and pigs. Nonetheless, more detailed surveillance data are required to determine the contribution of meat compared to other sources, such as travelling, pets, water resources, community and hospitals in the pursuit of a full source attribution model.

Homme

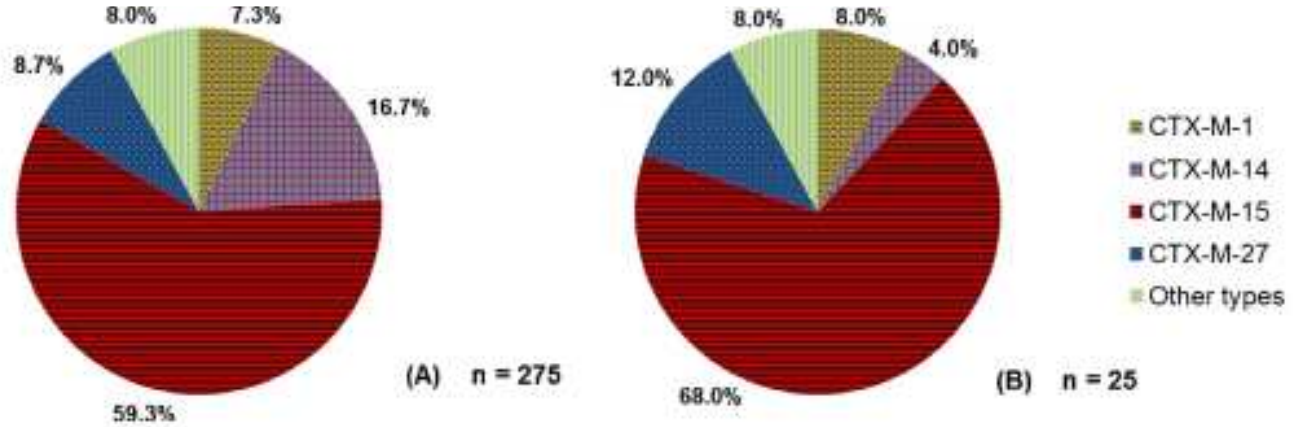


Fig. 3. (A) Proportion of various genotypes detected in ESBL-producing *E. coli* urinary tract infections in humans in Denmark in 2011. (B) Proportion of various genotypes detected in ESBL-producing *E. coli* bloodstream infections in humans in Denmark in 2011. Source: DANMAP 2011.

Vancomycin-resistant enterococci: why are they here, and where do they come from?

Marc J M Bonten, Rob Willems, and Robert A Weinstein

Avant / Après l'arrêt de l'avoparcine

Prévalence résistance à la vancomycine dans les fèces

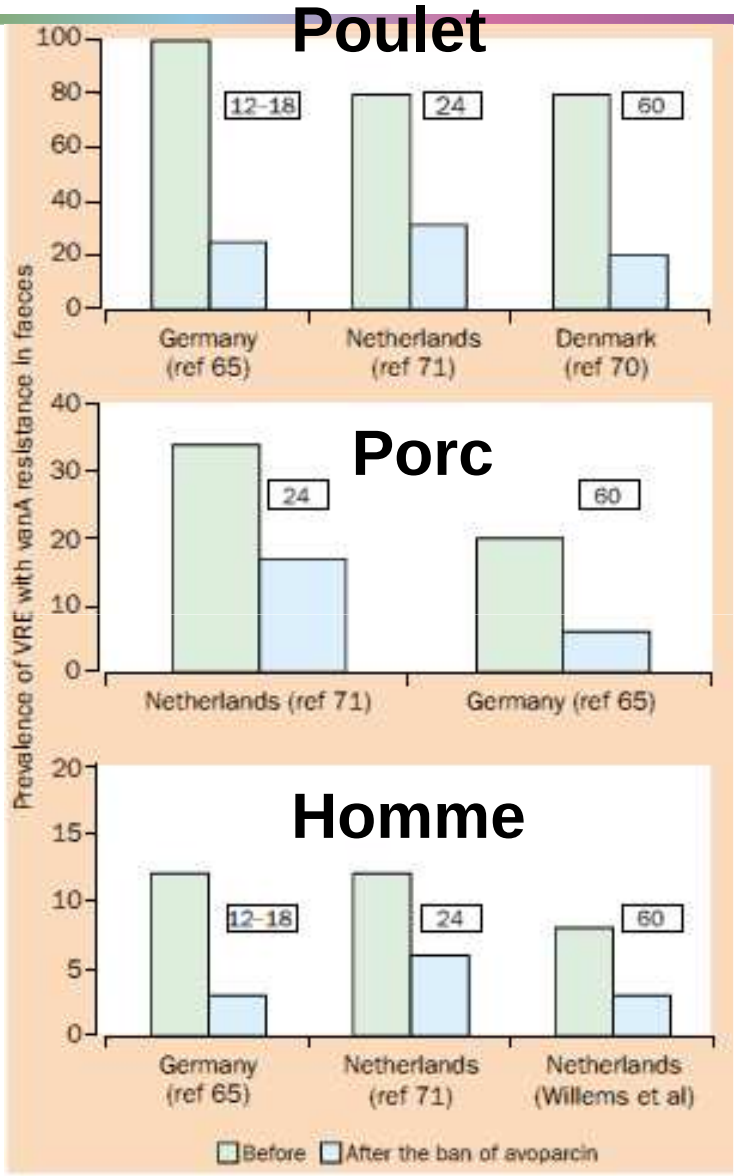


Figure 6. Effect of the European ban on avoparcin in poultry (top), pigs (middle), and human beings (bottom).

ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, Feb. 2006, p. 596–599
0066-4804/06/$08.00+0 doi:10.1128/AAC.50.2.596–599.2006

Vol. 50, No. 2

In Vivo Transfer of the *vanA* Resistance Gene from an *Enterococcus faecium* Isolate of Animal Origin to an *E. faecium* Isolate of Human Origin in the Intestines of Human Volunteers

Camilla H. Lester,[1]* Niels Frimodt-Møller,[1] Thomas Lund Sørensen,[2] Dominique L. Monnet,[1] and Anette M. Hammerum[1]

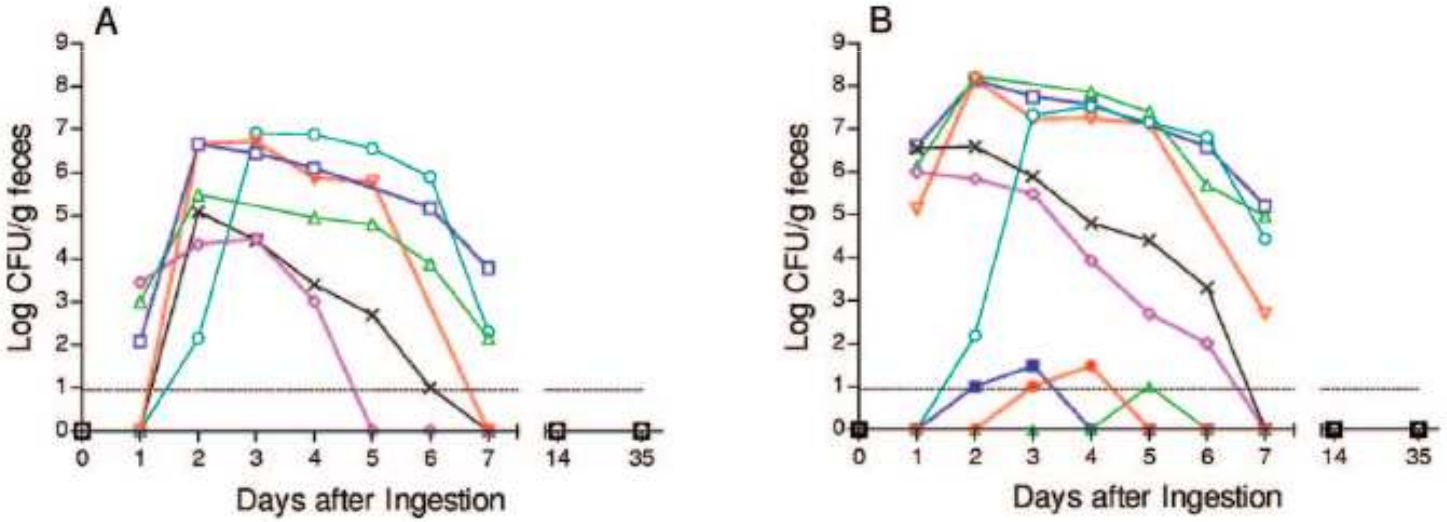


FIG. 1. Fecal excretion of strains by the six volunteers. (A) Donor strain (open symbols). (B) Recipient strain (open symbols) and transconjugants (solid symbols). Each curve shows the results for one volunteer. Each volunteer is represented by one color. Transconjugants were excreted by only three volunteers. Results from stool samples obtained within 48 h before ingestion of the bacteria are plotted as day zero. The minimal detectable level is shown by the dashed line. The solid black squares with open centers (days 0, 14, and 35) represent the superposition of results from all six volunteers.

International Journal of Medical Microbiology 303 (2013) 360–379

Contents lists available at SciVerse ScienceDirect

International Journal of Medical Microbiology

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

Mini review

Antibiotic resistant enterococci—Tales of a drug resistance gene trafficker

Guido Werner[a,*], Teresa M. Coque[b], Charles M.A.P. Franz[c], Elisabeth Grohmann[d], Kristin Hegstad[e,f], Lars Jensen[g], Willem van Schaik[h], Keith Weaver[i]

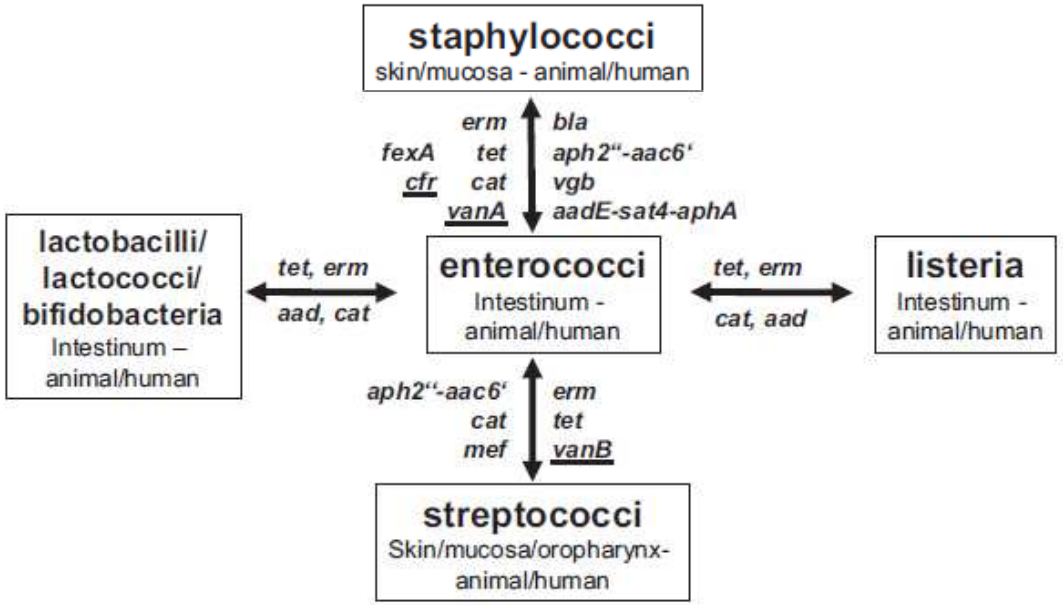


Fig. 2. Resistance gene pool shared in Gram-positive bacteria. The second line describes the habitat of the corresponding bacterium. Resistances against: *aad*, streptomycin; *aac6-aph2*, gentamicin/tobramycin; *bla*, penicillins; *cat*, chloramphenicol; *cfr*, florfenicol/linezolid; *erm*, macrolide-lincosamide-streptogramin B (MLS_B); *fexA*, florfenicol/chloramphenicol, *mef*, macrolides; *sat4*, nourseothricin; *tet*, tetracycline; *vanA*, vancomycin/teicoplanin; *vanB*, Vancomycin; *vgb*, streptogramin B. Some determinants represent several classes and types of resistance genes such as *erm* representing *erm*(A)/(B)/(C) or *tet* which stands for *tet*(M)/(O)/(W) (ribosomal protection) and *tet*(K)/(L) (efflux pumps) being summarized here for the sake of space. Underlined resistance genes are of special concern encoding resistance to important therapeutic substances or antibiotics of last resort.

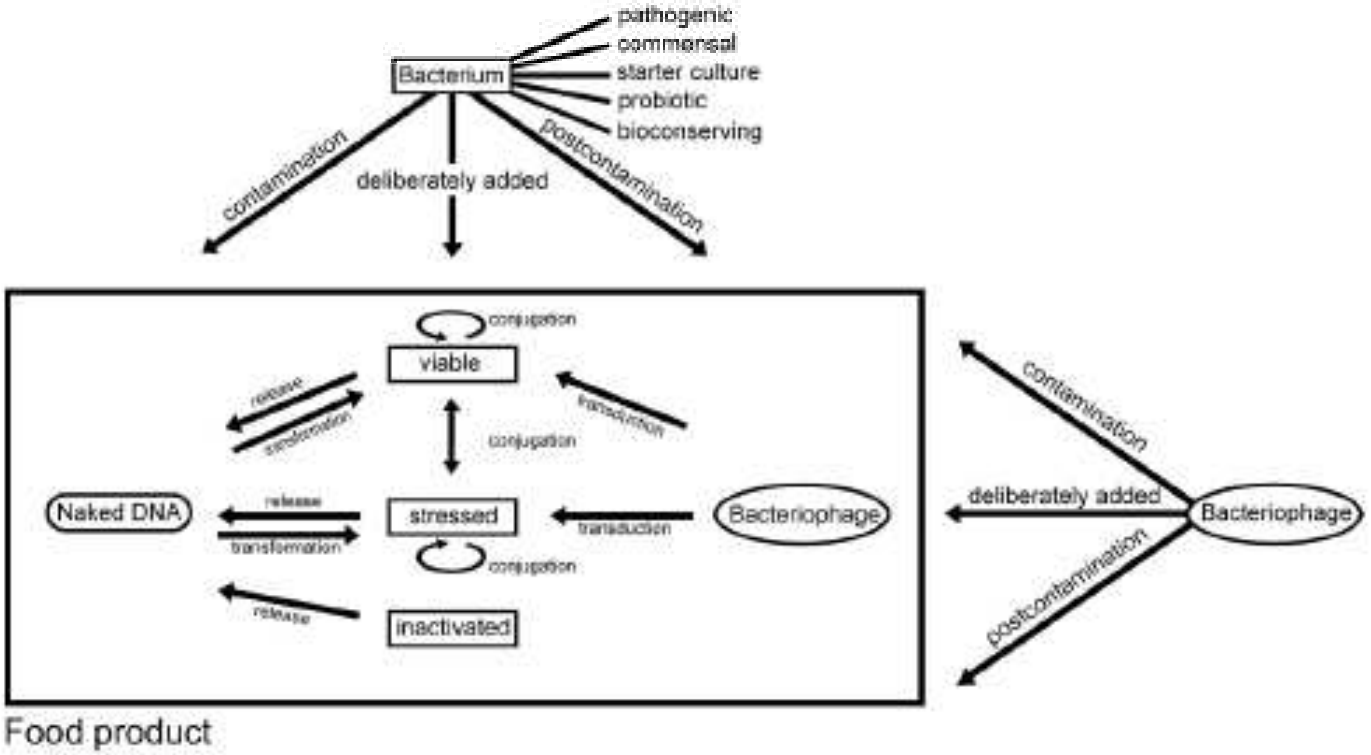
International Journal of
Environmental Research and
Public Health
ISSN 1660-4601
www.mdpi.com/journal/ijerph

Review

Antimicrobial Resistance in the Food Chain: A Review

Claire Verraes [1,*], Sigrid Van Boxstael [2], Eva Van Meervenne [2,3], Els Van Coillie [3], Patrick Butaye [4,5], Boudewijn Catry [6], Marie-Athénaïs de Schaetzen [7], Xavier Van Huffel [1], Hein Imberechts [4,8], Katelijne Dierick [6], Georges Daube [7,8], Claude Saegerman [7,8], Jan De Block [3], Jeroen Dewulf [5,8] and Lieve Herman [3,8]

Figure 1. Overview of horizontal gene transfer in food products.



Conclusion

- Alimentation
  - Voie d'exposition / évolution
    - Bactéries zoonotiques
    - Bactéries / Eléments mobiles / Gènes de résistance
- Evaluation du risque
  - Exposition x Danger
  - Surveillance / Caractérisation
- Prévention du risque
  - HACCP
  - Hygiène de la cuisine (Stockage, Instruments)
  - Préparation

- Enterococcus – Werner
- Verraes
- Mughini Salmonella
- Mughini Campylobacter