

ESBL carriage in pig slaughterhouse workers is associated with occupational exposure

Type de document	Article de revue
Auteur	W. Dohmen
Auteur	L. VAN Gompel
Auteur	H. Schmitt
Auteur	A. Liakopoulos
Auteur	L. Heres
Auteur	B. A. Urlings
Auteur	D. Mevius
Auteur	M. J. M. Bonten
Auteur	D. J. J. Heederik
Résumé	We investigated the prevalence of extended-spectrum β -lactamase (ESBL) carriage in slaughterhouse workers and the association with occupational exposure to slaughter animals and products. Stool samples from 334 employees in a Dutch pig slaughterhouse were obtained. Presence of ESBL was determined by selective plating, microarray analysis, and gene sequencing. Questionnaires were used to collect personal and occupational information. The overall prevalence of ESBL carriage was 4.8% (16/334). All ESBL-producing isolates were <i>Escherichia coli</i> . The ESBL genes detected were bla CTX-M-1 (n = 8), bla CTX-M-15 (n = 3), bla CTX-M-27 (n = 2), bla CTX-M-24 (n = 1), bla CTX-M-55 (n = 1), and bla SHV-12 (n = 1). A higher prevalence of ESBL was seen in workers in jobs with as tasks 'removal of lungs, heart, liver, tongue' (33%), and 'removal of head and spinal cord' (25%). For further analysis, participants were divided in two groups based on potential exposure to ESBL as related to their job title. One group with an assumed higher exposure to ESBL (e.g. stable work, stabbing, dehairing, removal of organs) and another group with an assumed lower exposure to ESBL (e.g. refrigeration, packaging and expedition). In the 'higher exposure' group, ten out of 95 (10.5%) were carrying ESBL vs. six out of 233 (2.6%) in the 'lower exposure' group. Human ESBL carriage was significantly associated with job exposure in the slaughterhouse (OR 4.5, CI 1.6-12.6). Results suggest that ESBL carriage in slaughterhouse workers overall is comparable with the Dutch population. Within the slaughterhouse population a difference in carriage exists depending on their position along the slaughter line and tasks involved.
Date	2017-07
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 28462735 PMCID: PMC9203444
Volume	145
Pages	2003-2010
Publication	Epidemiology and Infection
DOI	10.1017/S0950268817000784
Numéro	10
Abrév. de revue	Epidemiol Infect
ISSN	1469-4409
Date d'ajout	01/08/2024 à 16:35:41
Modifié le	01/08/2024 à 16:35:41

Marqueurs :

Abattoirs, Adult, Animals, Antimicrobial resistance, beta-Lactamases, bla CTX-M-1, *Escherichia coli*, *Escherichia coli* Infections, Feces, Female, Humans, Male, Netherlands, occupational epidemiology, Occupational Exposure, pig abattoir workers, *Sus scrofa*, zoonosis

Pièces jointes

- PubMed entry

Air exposure as a possible route for ESBL in pig farmers

Type de document	Article de revue
Auteur	Wietse Dohmen
Auteur	Heike Schmitt
Auteur	Marc Bonten
Auteur	Dick Heederik
Résumé	Livestock can carry extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae, with blaCTX-M-1 being most prevalent. ESBL carriage in farmers is associated with ESBL carriage in animals, with direct animal-human contact considered as the dominant route of transmission. However, inhalation of stable air might represent another route of transmission. We, therefore, quantified presence of blaCTX-M group 1 genes (CTX-M-gr1) in dust and the association with CTX-M-gr1 carriage in pig farmers, family members and employees. We included 131 people living and/or working on 32 conventional Dutch pig production farms (farmers, family members and employees) during two sampling moments over a 12-month interval. Human stool samples, rectal swabs from 60 pigs per farm, and 2-5 dust samples collected using an electrostatic dust collector (EDC) (as a proxy for presence of viable CTX-M-gr1 carrying bacteria in air) were obtained per farm. Presence of ESBL-producing <i>Escherichia coli</i> (<i>E. coli</i>) in stool samples and rectal swabs was determined by selective plating and CTX-M-gr1 was identified by PCR. Dust samples were analyzed directly by PCR for presence of CTX-M-gr1. Questionnaires were used to collect information on nature, intensity and duration of animal contact. Overall human prevalence of CTX-M-gr1 carriage was 3.6%. CTX-M-gr1 was detected in dust on 26% of the farms and in pigs on 35% of the farms, on at least one sampling moment. Human CTX-M-gr1 carriage and presence of CTX-M-gr1 in dust were associated univariately (OR=12.4, 95% CI=2.7-57.1). In multivariate analysis human CTX-M-gr1 carriage was associated with the number of working hours per week (OR=1.03, 95% CI=1.00-1.06), presence of CTX-M-gr1 carrying pigs on the farm (OR=7.4, 95% CI=1.1-49.7) and presence of CTX-M-gr1 in dust (OR=3.5, 95% CI=0.6-20.9). These results leave open the possibility of airborne CTX-M-gr1 transmission from animals to humans next to direct contact.
Date	2017-05
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 28273621
Volume	155
Pages	359-364
Publication	Environmental Research
DOI	10.1016/j.envres.2017.03.002
Abrév. de revue	Environ Res
ISSN	1096-0953
Date d'ajout	01/08/2024 à 16:35:57
Modifié le	01/08/2024 à 16:35:57

Possibility of Air transmissino but no quantitative exposure measurement

Marqueurs :

Adolescent, Adult, Aged, Air Pollutants, Airborne transmission, Animals, Antimicrobial resistance, beta-Lactamases, DNA, Bacterial, Dust, Environmental Monitoring, *Escherichia coli*, *Escherichia coli* Proteins, Extended-spectrum beta-lactamase, Farmers, Feces, Female, Humans, Male, Middle Aged, Netherlands, Occupational Exposure, Pig farmers, Swine, Young Adult, Zoonosis

Pièces jointes

- PubMed entry

Carriage of extended-spectrum β -lactamases in pig farmers is associated with occurrence in pigs

Type de document	Article de revue
Auteur	W. Dohmen
Auteur	M. J. M. Bonten
Auteur	M. E. H. Bos

Auteur	S. van Marm
Auteur	J. Scharringa
Auteur	J. A. Wagenaar
Auteur	D. J. J. Heederik
Résumé	Livestock may serve as a reservoir for extended-spectrum β-lactamase-producing Enterobacteriaceae (ESBL-PE). The objectives of this study were to determine the prevalence of carriage with ESBL-PE in pig farmers, family members and employees, and its association with carriage in pigs. Rectal swabs were taken from 2388 pigs (398 pooled samples) on 40 pig farms and faecal samples were obtained from 142 humans living or working on 34 of these farms. Presence of ESBL-PE was determined by selective plating (agar). ESBL genes were analysed by PCR or microarray analysis, and gene sequencing. Genotypes and plasmids were determined by multilocus sequence typing and PCR-based replicon typing for selected isolates. ESBL genes were detected in Escherichia coli from eight humans (6%) (blaCTX-M-1, n = 6; blaTEM-52, n = 1 and blaCTX-M-14, n = 1) on six farms. In 157 pig isolates (107 pooled samples) on 18 farms (45%) ESBL genes were detected (blaCTX-M-1, n = 12; blaTEM-52, n = 6; and blaCTX-M-14, n = 3). Human and pig isolates within the same farm harboured similar ESBL gene types and had identical sequence and plasmid types on two farms (e.g. E. coli ST-453, blaCTX-M-1, IncI1), suggesting clonal transmission. For the remaining farms, sequence types, but not plasmid types, differed. Human ESBL carriage was associated with average number of hours working on the farm per week (OR = 1.04, 95% CI 1.02-1.06) and presence of ESBLs in pigs (OR = 12.5, 95% CI 1.4-111.7). Daily exposure to pigs carrying ESBL-PE is associated with ESBL carriage in humans.
Date	2015-10
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 26033669
Volume	21
Pages	917-923
Publication	Clinical Microbiology and Infection: The Official Publication of the European Society of Clinical Microbiology and Infectious Diseases
DOI	10.1016/j.cmi.2015.05.032
Numéro	10
Abrév. de revue	Clin Microbiol Infect
ISSN	1469-0691
Date d'ajout	01/08/2024 à 16:36:09
Modifié le	01/08/2024 à 16:36:09

Marqueurs :

Adolescent, Adult, Aged, Animal reservoirs, animals, Animals, antimicrobial resistance, beta-Lactamases, Carrier State, Child, Cross-Sectional Studies, CTX-M, Enterobacteriaceae, Enterobacteriaceae Infections, epidemiology, Escherichia coli, Farmers, Feces, Female, Genotype, Humans, Male, Microarray Analysis, Middle Aged, Occupational Exposure, Plasmids, Polymerase Chain Reaction, Prevalence, Rectum, Sequence Analysis, DNA, Swine, Young Adult, zoonosis

Pièces jointes

- PubMed entry

Assessment of the Exposure of Turkey Farmers to Antimicrobial Resistance Associated with Working Practices

Type de document	Article de revue
Auteur	Giorgio Franceschini
Auteur	Marta Bottino
Auteur	Ilary Millet
Auteur	Elisa Martello
Auteur	Francesca Zaltron
Auteur	Anna Rosa Favretto
Auteur	Nicoletta Vonesch
Auteur	Paola Tomao
Auteur	Alessandro Mannelli
Résumé	The objective of the present study was the identification of farming practices in the production of turkeys for human consumption, and their ranking in terms of the occupational probability of exposure to antimicrobial resistant (AMR) bacteria, for farm workers. We gathered evidence and data from scientific literature, on risk factors for AMR in farmers, and on the prevalence of those hazards across farming phases. We administered semi-structured interviews to public and private veterinarians in Northern Italy, to obtain detailed information on turkey farming phases, and on working practices. Data were then integrated into a semi-quantitative Failure Modes and Effect Analysis (FMEA). Those working practices, which are characterized by direct contact with numerous animals, and which are carried out frequently, with rare use of personal protection devices resulted as associated with the greatest probability of exposure to AMR. For methicillin resistant Staphylococcus aureus (MRSA), these included vaccination and administration of any individual therapy, and removal and milling of litter, given the exposure of farmers to high dust level. Indeed, levels of occupational exposure to MRSA are enhanced by its transmission routes, which include direct contact with animal, as well as airborne transmission. Level of exposure to extended spectrum beta lactamase (ESBL) is more strictly associated with direct contact and the oral-fecal route. Consequently, exposure to ESBL resulted and associated with the routinely tipping over of poults turned on their back, and with the individual administration of therapies.
Date	2019-02-01
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 30717204 PMID: PMC6466403
Volume	6
Pages	13
Publication	Veterinary Sciences
DOI	10.3390/vetsci6010013
Numéro	1
Abrév. de revue	Vet Sci
ISSN	2306-7381
Date d'ajout	01/08/2024 à 16:35:19
Modifié le	01/08/2024 à 16:35:19

Semi quantitative anlysis for ranking farming practices

Marqueurs :

animal farms, antimicrobial resistance, farmers, FMEA, risk assessment, workers

Pièces jointes

- PubMed entry

One Health-based management for sustainably mitigating tetracycline-resistant Aeromonas hydrophila-induced health risk

Type de document	Article de revue
Auteur	Tien-Hsuan Lu
Auteur	Chi-Yun Chen
Auteur	Wei-Min Wang
Auteur	Chung-Min Liao
Résumé	Aeromonas hydrophila has ability to spread tetracycline resistance (tetR) under stresses of oxytetracycline (OTC), one of the most important antibiotics in aquaculture industry. Even though environmental reservoir of Aeromonas allows it to be at interfaces across One Health components, a robust modelling framework for rigorously assessing health risks is currently lacking. We proposed a One Health-based approach and leveraged recent advances in quantitative microbial risk assessment appraised by available dataset to interpret interactions at the human-animal-environment interfaces in various exposure scenarios. The dose-response models were constructed considering the effects on mortality for aquaculture species and tetR genes transfer for humans. A scenario-specific risk assessment on pond species-associated A. hydrophila infection and human gut-associated tetR

genes transfer was examined. Risk-based control strategies were involved to test their effectiveness. We showed that farmed shrimp exposed to tetracycline-resistant *A. hydrophila* in OTC-contaminated water experienced higher infection risk (relative risk: 1.25-1.34). The tetR genes transfer risk for farmers in shrimp ponds (~2 × 10-4) and swimmers in coastal areas (~4 × 10-6) during autumn exceeded acceptable risk (10-6). This cautionary finding underscores the importance of accounting for monitoring, assessing, and mitigating occupational health hazards among workers in shrimp farming sectors within future One Health-based strategies for managing water infection risks. We recommend that OTC emission rate together with *A. hydrophila* concentration should be reduced by up to 70-99% to protect human, farmed shrimp, and environmental health. Our predictive framework can be adopted for other systems and be used as a "risk detector" for assessing tetR-related health risks that invoke potential risk management on addressing sustainable mitigation on offsetting residual OTC emission and tetR genes spread in a species-human-environmental health system.

Date	2024-05-15
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 38599271
Volume	349
Pages	123943
Publication	Environmental Pollution (Barking, Essex: 1987)
DOI	10.1016/j.envpol.2024.123943
Abrév. de revue	Environ Pollut
ISSN	1873-6424
Date d'ajout	01/08/2024 à 16:27:48
Modifié le	01/08/2024 à 16:27:48

exposure assessment based on water ingested/activity * conc.
inactivation in gastronomical tract + plasmid transfer

Marqueurs :

Aeromonas hydrophila, Animals, Anti-Bacterial Agents, Aquaculture, Gram-Negative Bacterial Infections, Health risk assessment, Humans, Modelling, One Health, Oxytetracycline, Risk Assessment, Tetracycline resistance, Tetracycline Resistance

Pièces jointes

◦ PubMed entry

Farm dust resistomes and bacterial microbiomes in European poultry and pig farms

Type de document	Article de revue
Auteur	Roosmarijn E. C. Luiken
Auteur	Liese Van Gompel
Auteur	Alex Bossers
Auteur	Patrick Munk
Auteur	Philip Joosten
Auteur	Rasmus Borup Hansen
Auteur	Berith E. Knudsen
Auteur	Silvia García-Cobos
Auteur	Jeroen Dewulf
Auteur	Frank M. Aarestrup
Auteur	Jaap A. Wagenaar
Auteur	Lidwien A. M. Smit
Auteur	Dik J. Mevius
Auteur	Dick J. J. Heederik
Auteur	Heike Schmitt
Auteur	EFFORT-group
Résumé	BACKGROUND: Livestock farms are a reservoir of antimicrobial resistant bacteria from feces. Airborne dust-bound bacteria can spread across the barn and to the outdoor environment. Therefore, exposure to farm dust may be of concern for animals, farmers and neighboring residents. Although dust is a potential route of transmission, little is known about the resistome and bacterial microbiome of farm dust. OBJECTIVES: We describe the resistome and bacterial microbiome of pig and poultry farm dust and their relation with animal feces resistomes and bacterial microbiomes, and on-farm antimicrobial usage (AMU). In addition, the relation between dust and farmers' stool resistomes was explored. METHODS: In the EFFORT-study, resistomes and bacterial microbiomes of indoor farm dust collected on Electrostatic Dust fall Collectors (EDCs), and animal feces of 35 conventional broiler and 44 farrow-to-finish pig farms from nine European countries were determined by shotgun metagenomic analysis. The analysis also included 79 stool samples from farmers working or living at 12 broiler and 19 pig farms and 46 human controls. Relative abundance of and variation in resistome and bacterial composition of farm dust was described and compared to animal feces and farmers' stool. RESULTS: The farm dust resistome contained a large variety of antimicrobial resistance genes (ARGs); more than the animal fecal resistome. For both poultry and pigs, composition of dust resistomes finds (partly) its origin in animal feces as dust resistomes correlated significantly with fecal resistomes. The dust bacterial microbiome also correlated significantly with the dust resistome composition. A positive association between AMU in animals on the farm and the total abundance of the dust resistome was found. Occupational exposure to pig farm dust or animal feces may contribute to farmers' resistomes, however no major shifts in farmers resistome towards feces or dust resistomes were found in this study. CONCLUSION: Poultry and pig farm dust resistomes are rich and abundant and associated with the fecal resistome of the animals and the dust bacterial microbiome.
Date	2020-10
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 32738764
Volume	143
Pages	105971
Publication	Environment International
DOI	10.1016/j.envint.2020.105971
Abrév. de revue	Environ Int
ISSN	1873-6750
Date d'ajout	01/08/2024 à 16:31:14
Modifié le	01/08/2024 à 16:31:14

Marqueurs :

Air, Animals, Anti-Bacterial Agents, Bacteria, Chickens, Drug Resistance, Bacterial, Dust, Europe, Farm, Farms, Metagenomics, Microbiome, Microbiota, One health, Poultry, Resistome, Swine

Pièces jointes

◦ PubMed entry

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

Type de document	Article de revue
Auteur	Lapo Mughini-Gras
Auteur	Alejandro Dorado-García
Auteur	Engeline van Duijkeren
Auteur	Gerrita van den Bunt
Auteur	Cindy M Dierikx
Auteur	Marc J M Bonten
Auteur	Martin C J Bootsma

Auteur

Heike Schmitt

Auteur

Tine Hald

Auteur

Eric G Evers

Auteur

Aline de Koeijer

Auteur

Wilfrid van Pelt

Auteur

Eelco Franz

Auteur

Dik J Mevius

Auteur

Dick J J Heederik

Résumé

Background Extended-spectrum β -lactamase-producing *Escherichia coli* (ESBL-EC), plasmid-mediated AmpC-producing *E coli* (pAmpC-EC), and other bacteria are resistant to important β -lactam antibiotics. ESBL-EC and pAmpC-EC are increasingly reported in animals, food, the environment, and community-acquired and health-care-associated human infections. These infections are usually preceded by asymptomatic carriage, for which attributions to animal, food, environmental, and human sources remain unquantified. Methods In this population-based modelling study, we collected ESBL and pAmpC gene data on the Netherlands population for 2005–17 from published datasets of gene occurrences in *E coli* isolates from different sources, and from partners of the ESBL Attribution Consortium and the Dutch National Antimicrobial Surveillance System. Using these data, we applied an established source attribution model based on ESBL-EC and pAmpC-EC prevalence and gene data for humans, including high-risk populations (ie, returning travellers, clinical patients, farmers), farm and companion animals, food, surface freshwater, and wild birds, and human exposure data, to quantify the overall and gene-specific attributable sources of community-acquired ESBL-EC and pAmpC-EC intestinal carriage. We also used a simple transmission model to determine the basic reproduction number (R0) in the open community. Findings We identified 1220 occurrences of ESBL-EC and pAmpC-EC genes in humans, of which 478 were in clinical patients, 454 were from asymptomatic carriers in the open community, 103 were in poultry and pig farmers, and 185 were in people who had travelled out of the region. We also identified 6275 occurrences in non-human sources, including 479 in companion animals, 4026 in farm animals, 66 in wild birds, 1430 from food products, and 274 from surface freshwater. Most community-acquired ESBL-EC and pAmpC-EC carriage was attributed to human-to-human transmission within or between households in the open community (60·1%, 95% credible interval 40·0–73·5), and to secondary transmission from high-risk groups (6·9%, 4·1–9·2). Food accounted for 18·9% (7·0–38·3) of carriage, companion animals for 7·9% (1·4–19·9), farm animals (non-occupational contact) for 3·6% (0·6–9·9), and swimming in freshwater and wild birds (ie, environmental contact) for 2·6% (0·2–8·7). We derived an R0 of 0·63 (95% CI 0·42–0·77) for intracommunity transmission. Interpretation Although humans are the main source of community-acquired ESBL-EC and pAmpC-EC carriage, the attributable non-human sources underpin the need for longitudinal studies and continuous monitoring, because intracommunity ESBL-EC and pAmpC-EC spread alone is unlikely to be self-maintaining without transmission to and from non-human sources. Funding IHealth4Food, Dutch Ministry of Economic Affairs, and the EU's Horizon-2020 through One-Health European Joint Programme.

Date

2019-08-01

Titre abrégé

Attributable sources of community-acquired carriage of <i>Escherichia coli</i> containing β -lactam antibiotic resistance genes

Catalogue de bibl.

ScienceDirect

URL

<https://www.sciencedirect.com/science/article/pii/S2542519619301305>

Consulté le

01/08/2024 à 16:29:49

Volume

3

Pages

e357-e369

Publication

The Lancet Planetary Health

DOI

10.1016/S2542-5196(19)30130-5

Numéro

8

Abrév. de revue

The Lancet Planetary Health

ISSN

2542-5196

Date d'ajout

01/08/2024 à 16:29:49

Modifié le

01/08/2024 à 16:29:49

Pièces jointes

- ScienceDirect Snapshot

Antimicrobial drug resistance of *Escherichia coli* isolated from poultry abattoir workers at risk and broilers on antimicrobials

Type de document

Article de revue

Auteur

J. W. Oguttu

Auteur

C. M. Veary

Auteur

J. A. Picard

Résumé

Antimicrobial usage in food animals increases the prevalence of antimicrobial drug resistance among their enteric bacteria. It has been suggested that this resistance can in turn be transferred to people working with such animals, e.g., abattoir workers. Antimicrobial drug resistance was investigated for *Escherichia coli* from broilers raised on feed supplemented with antimicrobials, and the people who carry out evisceration, washing and packing of intestines in a high-throughput poultry abattoir in Gauteng, South Africa. Broiler carcasses were sampled from 6 farms, on each of which broilers are produced in a separate 'grow-out cycle'. Per farm, 100 caeca were randomly collected 5 minutes after slaughter and the contents of each were selectively cultured for *E. coli*. The minimum inhibitory concentration (MIC) of each isolate was determined for the following antimicrobials: doxycycline, trimethoprim, sulphamethoxazole, ampicillin, enrofloxacin, fosfomycin, ceftriaxone and nalidixic acid. The same was determined for the faeces of 29 abattoir workers and 28 persons used as controls. The majority of isolates from broilers were resistant, especially to antimicrobials that were used on the farms in the study. Overall median MICs and the number of resistant isolates from abattoir workers (packers plus eviscerators) tended to be higher than for the control group. However, no statistically significant differences were observed when the median MICs of antimicrobials used regularly in poultry and percentage resistance were compared, nor could an association between resistance among the enteric *E. coli* from packers and those from broilers be demonstrated.

Date

2008-12

Langue

eng

Catalogue de bibl.

PubMed

Extra

PMID: 19496314

Volume

79

Pages

161-166

Publication

Journal of the South African Veterinary Association

DOI

10.4102/jsava.v79i4.266

Numéro

4

Abrév. de revue

J S Afr Vet Assoc

ISSN

1019-9128

Date d'ajout

01/08/2024 à 16:36:42

Modifié le

01/08/2024 à 16:36:42

Marqueurs :

Abattoirs, Animals, Anti-Bacterial Agents, Case-Control Studies, Cecum, Chickens, Colony Count, Microbial, Disease Reservoirs, Dose-Response Relationship, Drug, Drug Resistance, Bacterial, Drug Resistance, Multiple, Bacterial, *Escherichia coli*, *Escherichia coli* Infections, Food Microbiology, Humans, Microbial Sensitivity Tests, Occupational Exposure, Poultry Diseases, Risk Assessment

Pièces jointes

- PubMed entry

Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms

Type de document

Article de revue

Auteur

Jian Sun

Auteur

Xiao-Ping Liao

Auteur

Alarie W. D'Souza

Auteur

Manish Boolchandani

Auteur

Sheng-Hui Li

Auteur

Ke Cheng

Auteur

José Luis Martínez

4 sur 6

02/08/2024, 12:07

Auteur

Li

Liang

Auteur

Feng

You-Jun

Auteur

Fang

Liang-Xing

Auteur

Huang

Ting

Auteur

Xia

Jing

Auteur

Yu

Yang

Auteur

Zhou

Yu-Feng

Auteur

Sun

Yong-Xue

Auteur

Deng

Xian-Bo

Auteur

Zeng

Zhen-Ling

Auteur

Jiang

Hong-Xia

Auteur

Fang

Bing-Hu

Auteur

Tang

You-Zhi

Auteur

Lian

Xin-Lei

Auteur

Zhang

Rong-Min

Auteur

Fang

Zhi-Wei

Auteur

Yan

Qiu-Long

Auteur

Dantas

Gautam

Auteur

Liu

Ya-Hong

Résumé

Anthropogenic environments have been implicated in enrichment and exchange of antibiotic resistance genes and bacteria. Here we study the impact of confined and controlled swine farm environments on temporal changes in the gut microbiome and resistome of veterinary students with occupational exposure for 3 months. By analyzing 16S rRNA and whole metagenome shotgun sequencing data in tandem with culture-based methods, we show that farm exposure shapes the gut microbiome of students, resulting in enrichment of potentially pathogenic taxa and antimicrobial resistance genes. Comparison of students' gut microbiomes and resistomes to farm workers' and environmental samples revealed extensive sharing of resistance genes and bacteria following exposure and after three months of their visit. Notably, antibiotic resistance genes were found in similar genetic contexts in student samples and farm environmental samples. Dynamic Bayesian network modeling predicted that the observed changes partially reverse over a 4-6 month period. Our results indicate that acute changes in a human's living environment can persistently shape their gut microbiota and antibiotic resistome.

Date

2020-03-18

Langue

eng

Catalogue de bibl.

PubMed

Extra

PMID: 32188862 PMCID: PMC7080799

Volume

11

Pages

1427

Publication

Nature Communications

DOI

10.1038/s41467-020-15222-y

Numéro

1

Abrév. de revue

Nat Commun

ISSN

2041-1723

Date d'ajout

01/08/2024 à 16:33:01

Modifié le

01/08/2024 à 16:33:01

Marqueurs :

Adult, Animals, Anti-Bacterial Agents, Bacteria, Drug Resistance, Bacterial, Farms, Gastrointestinal Microbiome, Gastrointestinal Tract, Humans, Male, Occupational Exposure, Schools, Veterinary, Students, Swine, Young Adult

Pièces jointes

- PubMed entry

Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers: A metagenome-wide cross-sectional study

Type de document

Article de revue

Auteur

Gompel

Liese Van

Auteur

Luiken

Roosmarijn E. C.

Auteur

Hansen

Rasmus B.

Auteur

Munk

Patrick

Auteur

Bouwknegt

Martijn

Auteur

Heres

Lourens

Auteur

Greve

Gerdit D.

Auteur

Scherpenisse

Peter

Auteur

Gortemaker

Betty G. M. Jongerius-

Auteur

Zijdeveld

Monique H. G. Tersteeg-

Auteur

Cobos

Silvia García-

Auteur

Dohmen

Wietske

Auteur

García

Alejandro Dorado-

Auteur

Wagenaar

Jaap A.

Auteur

Urlings

Bert A. P.

Auteur

Aarestrup

Frank M.

Auteur

Mevius

Dik J.

Auteur

Heederik

Dick J. J.

Auteur

Schmitt

Heike

Auteur

Bossers

Alex

Auteur

Smit

Lidwien A. M.

Résumé

BACKGROUND: By studying the entire human faecal resistome and associated microbiome, the diversity and abundance of faecal antimicrobial resistance genes (ARGs) can be comprehensively characterized. Prior culture-based studies have shown associations between occupational exposure to livestock and carriage of specific antimicrobial resistant bacteria. Using shotgun metagenomics, the present study investigated 194 faecal resistomes and bacteriomes from humans occupationally exposed to ARGs in livestock (i.e. pig and poultry farmers, employees and family members and pig slaughterhouse workers) and a control population (Lifelines cohort) in the Netherlands. In addition, we sought to identify determinants for the human resistome and bacteriome composition by applying a combination of multivariate (NMDS, PERMANOVA, SIMPER and DESeq2 analysis) and multivariable regression analysis techniques. RESULTS: Pig slaughterhouse workers and pig farmers carried higher total ARG abundances in their stools compared to broiler farmers and control subjects. Tetracycline, β -lactam and macrolide resistance gene clusters dominated the resistome of all studied groups. No significant resistome alpha diversity differences were found among the four populations. However, the resistome beta diversity showed a separation of the mean resistome composition of pig and pork exposed workers from broiler farmers and controls, independent of their antimicrobial use. We demonstrated differences in resistome composition between slaughter line positions, pig versus poultry exposed workers, as well as differences between farmers and employees versus family members. In addition, we found a significant correlation between the bacteriome and resistome, and significant differences in the bacteriome composition between and within the studied subpopulations. Finally, an in-depth analysis of pig and poultry farms - of which also farm livestock resistomes were analysed - showed positive associations between the number of on-farm working hours and human faecal AMR loads. CONCLUSION: We found that the total normalized faecal ARG carriage was larger in persons working in the Dutch pork production chain compared to poultry farmers and controls. Additionally, we showed significant differences in resistome and bacteriome composition of pig and pork exposed workers compared to a control group, as well as within-population (farms, slaughterhouse) compositional differences. The number of on-farm working hours and the farm type (pig or broiler) that persons live or work on are determinants for the human faecal resistome. Overall, our results may suggest direct or indirect livestock contact as a determinant for human ARG carriage. Future studies should further focus on the connection between the human and livestock resistome (i.e. transmission routes) to substantiate the evidence for livestock-associated resistome acquisition.

Date

2020-10

Langue

eng

Titre abrégé

Description and determinants of the faecal resistome and microbiome of farmers and slaughterhouse workers

Catalogue de bibl.

PubMed

Extra PMID: 32679392
Volume 143
Pages 105939
Publication Environment International
DOI 10.1016/j.envint.2020.105939
Abrév. de revue Environ Int
ISSN 1873-6750
Date d'ajout 01/08/2024 à 16:31:44
Modifié le 01/08/2024 à 16:31:44

Marqueurs :

Abattoirs, Animals, Anti-Bacterial Agents, Antimicrobial resistance, Chickens, Cross-Sectional Studies, Drug Resistance, Bacterial, Farmers, Humans, Macrolides, Metagenome, Microbiome, Microbiota, Netherlands, Occupational exposure, Resistome, Slaughterhouse workers, Swine

Pièces jointes

- PubMed entry

Occupational Exposure and Carriage of Antimicrobial Resistance Genes (tetW, ermB) in Pig Slaughterhouse Workers

Type de document	Article de revue
Auteur	Liese Van Gompel
Auteur	Wietske Dohmen
Auteur	Roosmarijn E. C. Luiken
Auteur	Martijn Bouwknegt
Auteur	Lourens Heres
Auteur	Eri van Heijnsbergen
Auteur	Betty G. M. Jongerius-Gortemaker
Auteur	Peter Scherpenisse
Auteur	Gerdit D. Greve
Auteur	Monique H. G. Tersteeg-Zijderveld
Auteur	Katharina Wadepohl
Auteur	Ana Sofia Ribeiro Duarte
Auteur	Violeta Muñoz-Gómez
Auteur	Jennie Fischer
Auteur	Magdalena Skarżyńska
Auteur	Dariusz Wasyl
Auteur	Jaap A. Wagenaar
Auteur	Bert A. P. Urlings
Auteur	Alejandro Dorado-García
Auteur	Inge M. Wouters
Auteur	Dick J. J. Heederik
Auteur	Heike Schmitt
Auteur	Lidwien A. M. Smit
Résumé	OBJECTIVES: Slaughterhouse staff is occupationally exposed to antimicrobial resistant bacteria. Studies reported high antimicrobial resistance gene (ARG) abundances in slaughter pigs. This cross-sectional study investigated occupational exposure to tetracycline (tetW) and macrolide (ermB) resistance genes and assessed determinants for faecal tetW and ermB carriage among pig slaughterhouse workers. METHODS: During 2015-2016, 483 faecal samples and personal questionnaires were collected from workers in a Dutch pig abattoir, together with 60 pig faecal samples. Human dermal and respiratory exposure was assessed by examining 198 carcass, 326 gloves, and 33 air samples along the line, next to 198 packed pork chops to indicate potential consumer exposure. Samples were analyzed by qPCR (tetW, ermB). A job exposure matrix was created by calculating the percentage of tetW and ermB positive carcasses or gloves for each job position. Multiple linear regression models were used to link exposure to tetW and ermB carriage. RESULTS: Workers are exposed to tetracycline and macrolide resistance genes along the slaughter line. Tetw and ermB gradients were found for carcasses, gloves, and air filters. One packed pork chop contained tetW, ermB was non-detectable. Human faecal tetW and ermB concentrations were lower than in pig faeces. Associations were found between occupational tetW exposure and human faecal tetW carriage, yet, not after model adjustments. Sampling round, nationality, and smoking were determinants for ARG carriage. CONCLUSION: We demonstrated clear environmental tetracycline and macrolide resistance gene exposure gradients along the slaughter line. No robust link was found between ARG exposure and human faecal ARG carriage.
Date	2020-02-20
Langue	eng
Catalogue de bibl.	PubMed
Extra	PMID: 31883001 PMCID: PMC9194797
Volume	64
Pages	125-137
Publication	Annals of Work Exposures and Health
DOI	10.1093/annweh/wxz098
Numéro	2
Abrév. de revue	Ann Work Expo Health
ISSN	2398-7316
Date d'ajout	01/08/2024 à 16:34:30
Modifié le	01/08/2024 à 16:34:30

Marqueurs :

Abattoirs, air, Animals, Anti-Bacterial Agents, Cross-Sectional Studies, dermal exposure, Drug Resistance, Bacterial, faecal carriage, gloves, macrolide resistance, Macrolides, Occupational Exposure, respiratory exposure, retail meat, Swine, tetracycline resistance

Pièces jointes

- PubMed entry