The relevance of transmission routes of antibiotic resistant bacteria calculated using different methodologies and the relevance of routes per pathogen: a systematic review and meta-analysis

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Introduction

Antibiotic resistant bacteria (ARB) are a major global problem, stressing the need to understand acquisition routes between hosts and reservoirs. While many studied risk factors for ARB acquisition, infection or colonisation, the urgency to reduce ARB calls for a quantification of acquisition routes' relevance, which is less known but pivotal for cost-effective interventions.

This review collects estimates on acquisition routes' contributions of ARB in humans, animals, water and the environment. For each estimate, we determined the methodology used, e.g., statistical measures such as odds ratios (ORs) and modelling methods such as R_0. Secondly, we assess if different methodologies used to measure exposure result in different transmission route estimates. Thirdly, we rank transmission routes per pathogen to compare the importance of routes per pathogen.

Methods

PubMed and EMBASE were searched, resulting in 6017 articles published up until December 20th, 2018. Full text screening was performed on 518 articles and 275 are included.

Results

We extracted 741 estimates, 716 were for one bacteria species/group, mostly produced with statistical methods (556), of which risk (242) and ORs (239) were most common, followed by genetic overlap (87), modelling (62) and bacterial intake (17). *S. aureus* (273), *E. coli* (156) and Enterobacteriaceae (99) were mostly studied. Occupational exposure (157) was the most studied route followed by travelling (110) and contacting a colonised person (93). The United States (141), the Netherlands (87) and Germany (60) were the most studied countries. Comparing methods was difficult as not all studied the same routes and due to study heterogeneity not all estimates could be pooled.

Conclusion

A missing link exists between routes and their occurrence, which disables estimation of transmission routes' importance. To create effective policies reducing ARB, estimates of transmission should be weighed by the frequency of exposure occurrence.

Introduction

The emergence and transmission of antibiotic-resistant (ABR) pathogens is a major global problem, stressing the need to understand the transmission routes between hosts and reservoirs. Antibiotic resistance is not only found in humans, but also in animals, water and the environment and can be transmitted between and within these reservoirs, with different relevance attributed to each route of transmission (1).

While many studies have researched risk factors for acquisition, infection or colonisation with ABR pathogens, the global urgency to reduce the prevalence of antibiotic resistance calls for research on the quantification of the occurrence of transmission routes and their relative importance, which is less well known (2). This knowledge on the One Health interplay of ABR pathogens as well as human-human transmission, however, is pivotal to develop targeted interventions for the most relevant routes to effectively reduce ABR infections and create cost-effective intervention policies.

Although a previous review mapped transmission routes of ABR bacteria (3), the contribution of transmission routes to the total number of acquisitions of ABR bacteria remains unknown. There has been no systematic review of the evidence regarding the relevance of transmission routes or their contribution to the ABR burden of disease. To form a comprehensive foundation of the contribution of different transmission routes to the total ABR burden, a bridge has to be created between the occurrence of exposure and the probability to become colonised when exposed.

Moreover, the impact of different methodologies for estimating transmission routes on the estimates of the relative importance of various routes has not been explored previously. While some studies assess the risk of colonization with ABR bacteria using colonization status as an outcome, other studies assess the risk of colonization using the identical genetic structure of the bacteria between source and receiver as an outcome. Such methodological differences lead to a potential discrepancy between results and can impair comparability.

The aim of this research is threefold. Firstly, we aim to determine the contribution of transmission routes to the acquisition of ABR bacteria by humans, animals, water and the environment via a systematic review of the literature. Secondly, we aim to assess whether the different methodologies used to measure exposure, acquisition or colonization result in different estimates of transmission routes' importance. Methods are conceptualized as methods to measure exposure resulting in an acquisition, for example statistical effect measures such as the odds ratio (OR) and modelling methods such as R_0, the expected number of secondary cases caused by a typical infected individual during its period of infectiousness in a completely susceptible population (4).

Methods

Search strategy

We performed a systematic review in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) protocol (5). The protocol for this systematic review was registered on PROSPERO (CRD42019136298) and can be accessed at http://www.crd.york.ac.uk/PROSPERO/display_record.php?ID=CRD42019136298 (6).

We identified quantified estimates of transmission routes from humans, animals and environmental reservoirs that resulted in an acquisition of ABR bacteria. An acquisition is conceptualized as one or more of: exposure, intake, infection, acquisition, carriage and colonisation. Antibiotic resistance is defined as the resistance of bacteria to one or more antibiotics for which the bacterium is not intrinsic resistant.

On the 20th of December 2018, we firstly searched PubMed using the search terms shown in Appendix 1 resulting in 4554 articles. We did not exclude articles based on publication date, publication type, sample size, significance level or quality. Secondly, Embase was searched using the search terms shown in Appendix 2, which resulted in 5180 articles. Removal of duplicates in Endnote and Rayyan resulted in a final set of 6017 articles for title/abstract screening. Two researchers separately in- or excluded a random subset of 50 of the 6017 articles, there was an agreement of 100%. Thereafter, one researcher performed the title/abstract screening in Rayyan. Rayyan is a free web application designed to keep track of the articles in- and excluded and is usable for the initial screening of abstracts in a review (7). In cases of doubt on whether to in- or exclude an abstract/article, the second researcher was asked for advice. Five-hundred-and-twelve articles were included for full-text screening. After the full-text screening, a total of 275 articles were included. Figure 1 shows a flow diagram of the articles in the review process.

Study selection

Inclusion criteria for the final set of articles were 1) the presence of quantified estimates of 2) a clear acquisition route 3) of an ABR bacteria. Antimicrobial resistance of the bacteria is defined as resistance to one or more antibiotics, if the study included resistant and non-resistant pathogens the notation "^{rs}" is placed after the transmission estimate to indicate so.

Papers were excluded if they only reported prevalence estimates of the percentage of the source colonised/infected with ARB, for example 10% of the cows on the farm were colonised with MRSA, because this is not a quantification of the occurrence of a transmission route. We excluded studies on horizontal plasmid transfer, within-person transfer of the infection, for example from nasal to anal colonization within the same person, and antibiotics as a source of acquisition as these routes do not comprise transmission. Colonization pressure was excluded because we considered this transmission route too indirect. After applying these inclusion and exclusion criteria, 275 studies and 716 estimates remained.

Data extraction

We extracted the method of estimation, the transmission estimate, the 95% CI, the transmission route, the pathogen, whether the articles studies only resistant pathogens or gave a pooled estimated for resistant and susceptible pathogens, the country under study, the size of the study population, the author, the year of publication, the title of the paper, the animal involved in the transmission route and in case of travelling as a transmission route, whether a pe-travel screening took place. Study characteristics and outcomes were saved in a data extraction table using Microsoft Excel.

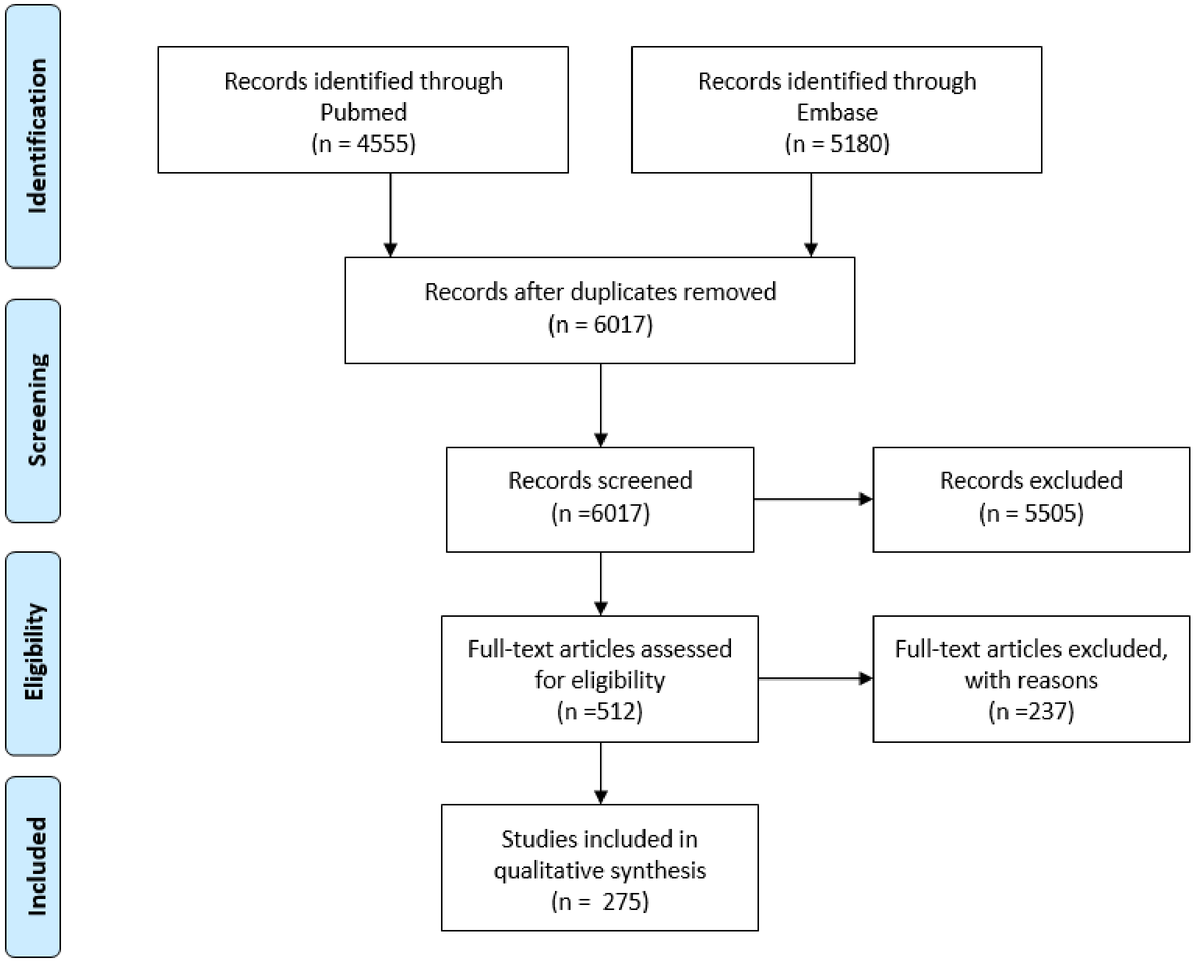

Figure 1. Prisma flow diagram of articles during the review.

Quality assessment

Only the quality of travel studies was assessed by using a $^{+}$ or $^{-}$ to indicate whether pre-travel screening was performed or not.

Data synthesis and analyses

Reservoirs

The following 12 reservoirs and cross-reservoirs in which transmission occurs were identified, 1) animal, 2) animal and food, 3) animal and human, 4) animal, human and water, 5) animal and environment, 6) animal and water, 7) human, 8) human and environment, 9) human and food, 10) human and water, 11) environment, and 12) environment and water. Travelling and interventions studies were not categorized in a reservoirs.

Transmission routes

In order to describe all identified transmission routes identified, grouping was needed to describe the overall evidence on transmission routes of ABR bacteria holistically. The transmission routes were grouped and assigned to a reservoirs as following; 1) air to animal (animal and environment), 2) animal to air (animal and environment), 3) animal to water (animal and water), 4) animal to animal (animal), 5) animal to environment (animal and environment), 6) sharing water source with animals (animal, human and water), 7) non-commercial animal keeping (animal and human), 8) breast feeding (human), 9) contact with an infected person (human), 10) contaminated hospital room to human (human and environment) 11) eating meat to humans (human and food), 12) environment to animal (animal and environment), 13) environment to plant (environment), 14) environment to environment (environment), 15) environment to human (human and environment), 16) family member colonised (human), 17) family member with occupational exposure (animal and human), 18) fomites (human and environment), 19) food to animal (animal and food), 20) human to air (human and environment), 21) human to nearby environment (human and environment), 22) human to animal (animal and human), 23) intervention, 24) livestock to drinking water (animal and water) 25) milk to human (human and food), 26) mother animal to baby animal (animal), 27) nearby environment to animal (animal and environment), 28) nearby environment to human (human and environment), 29) nearby farm to human (animal and human), 30) nearby farm to animal (animal), 31) occupational exposure (animal and human), 32) organ transfer (human), 33) other: animal meat to animal (animal and food), 34) other: bathing and showering (human), 35) other: crowding (human), 36) other: antibacterial soap (human), 37) pet to human (animal and human), 38) prior patient in room was colonised (human and environment), 39) space sharing (human) and, 40) travelling. A description of each route can be found in table 1. Appendix 3 shows which studies were grouped under which route.

Methods of estimation

We identified four main methods; genes (identical genetic overlap between ABR genes in source and AMR genes in receiver), intake (the dose of AMR bacteria in the source estimated to be taken in by humans), modelling (mathematical modelling estimates regarding the intake or proportion of cases accountable for be a source) and statistical inference. Statistical methods included the following five sub methods odds ratio's (ORs), risks, prevalence ratio's (PRs), risk ratio's (RR) and transmission rate's (TRs). Modelling methods included R0, attributable percentage of the total number of cases to this route, transmission rates (TRs), cases per day, incidence, incidence rate ratios (IRRs) and acquisition rates (ARs).

Pathogens

To estimate transmission routes per pathogen, each estimate was categorized per bacteria species if two or more estimates on this species were present, otherwise the estimate was categorized as "other". The following 19 groups were identified *Staphylococcus aureus (S. Aureus), Escherichia coli (E. coli),* Enterobacteriaceae which included estimates pooled for multiple species of Enterobacteriaceae, vancomycin resistant enterococci (VRE), staphylococci, *Pseudomonas aeruginosa* (*P. aeruginosa), Acinetobacter baumannii (A. baumannii), Acinetobacter calcoaceticus (A. calcoaceticus) , Campylobacter, Enterococcus faecalis (E. faecalis), Enterococcus faecium (E. faecium), Streptococcus pneumoniae (S. pneumoniae),* group B streptococci, salmonella, *Staphylococcus epidermidis (S. epidermidis), Staphylococcus pseudintermedius (S. pseudintermedius), Staphylococcus haemolyticus (S haemolyticus)*, genes (e.g. blaTEM) and other (*Enterococci*, *Mycoplasma hominis*, *Ureaplasma urealyticum*, *Klebsiella pneumoniae*, *Staphylococcus hominis*, *Staphylococcus cohnii*, *Klebsiella oxytoca, Haemophilus influenzae*).

Travelling

To assess travelling as transmission route, we grouped the countries of destination in one of the following 11 group; South Asia (Afghanistan, Bangladesh, Bhutan, Maldives, Nepal, India, Pakistan and Sri Lanka), South East Asia (Indonesia, Cambodia, Laos, Myanmar, Malaysia, Thailand, Vietnam, Australia, Brunei, the Philippines and Singapore), West Asia (Bahrain, Iran, Israel, Jordan, Kuwait, Lebanon, Oman, Qatar, Palestinian territories, Syria, Turkey, Iraq, Saudi Arabia, United Arab Emirates, and Yemen), Central & East Asia (China, Hong Kong, Mongolia, Uzbekistan, Turkmenistan, Tajikistan, Kyrgyzstan, Kazakhstan, East Turkestan, North Korea, South Korea, Japan, and Taiwan), Asia unspecified, Latin America (central Amerika, Mexico and south Amerika), north America, America unspecified, Africa (entire African continent), Europe and multiple regions (multiple of the above regions).

Meta-analysis

Random effects meta-analyses using the maximum-likelihood estimator were performed per methodology per transmission route per pathogen and only if the studies had the same outcome measure or outcome measures that could be transformed into each other, for example exposure in the last year vs. exposure in the last week cannot be transformed to be similar but infections per day and infections per week in the hospital can. Meta-analyses were performed per method per route per pathogen even when only two estimated were present. Transmission estimates on more than one bacteria species were excluded from the meta-analysis (*n=25)*. All analysis where performed using R version 3.6.1.

Results

Study population

We included 275 studies which contained 716 transmission estimates on 40 identified transmission routes. Most studies occurred in the United States (*n*=141), the Netherlands (*n*=87) and Germany (*n*=60) as shown in figure 2.

Most estimates, 78%, were produced using statistics, amongst which risks (44%) and OR (43%) were the preferred methods as described table 1. The least estimates, 2%, were produced using bacteria intake as method of estimation. The three most commonly studied transmission route are occupational exposure (21%), travelling (15%) and contact with an infected person (13%) as described in table A, appendix 2. Of the estimates on travelling, 64% (*n=70)* were based on pre- and post-travel bacteria screening.

Table 1. *Frequencies of methods of estimation*

Method of estimation (*n*)		Specification (*n*)	
Statistics	556	Odds ratio	239
		Risk	242
		Prevalence ratio	63
		Transmission rate	5
		Risk ratio	3
		Risk difference	4
Genes	87	Identical overlap	86
		Attributable % (Importance of route)	1
Modelling	56	R0	21
		Attributable % (Importance of route)	10
		Transmission rate	8
		Cases per day	6
		Incidence	4
		Incidence rate ratio	6
		Acquisition rate	1
Bacteria intake	17		
Total	716		

The three most commonly studied bacteria were *S. aureus* (38%), *E. coli* (22%) and Enterobacteriaceae (17%) as described in figure 3 and table B, appendix 2 A list of all articles included is reported in appendix 3.

Cross-reservoir

Cross-reservoir transmission between animal and humans was studied the most (29%). Transmission between the, such as rooms or utensils, and humans was also studied often (9%), after which the following reservoirs with at least 1% of studies followed; transmission between water and humans (2%), water and animals (2%), animals and the environment (6%). Figure 4 shows which studies researched transmission in one reservoir or between two reservoirs.

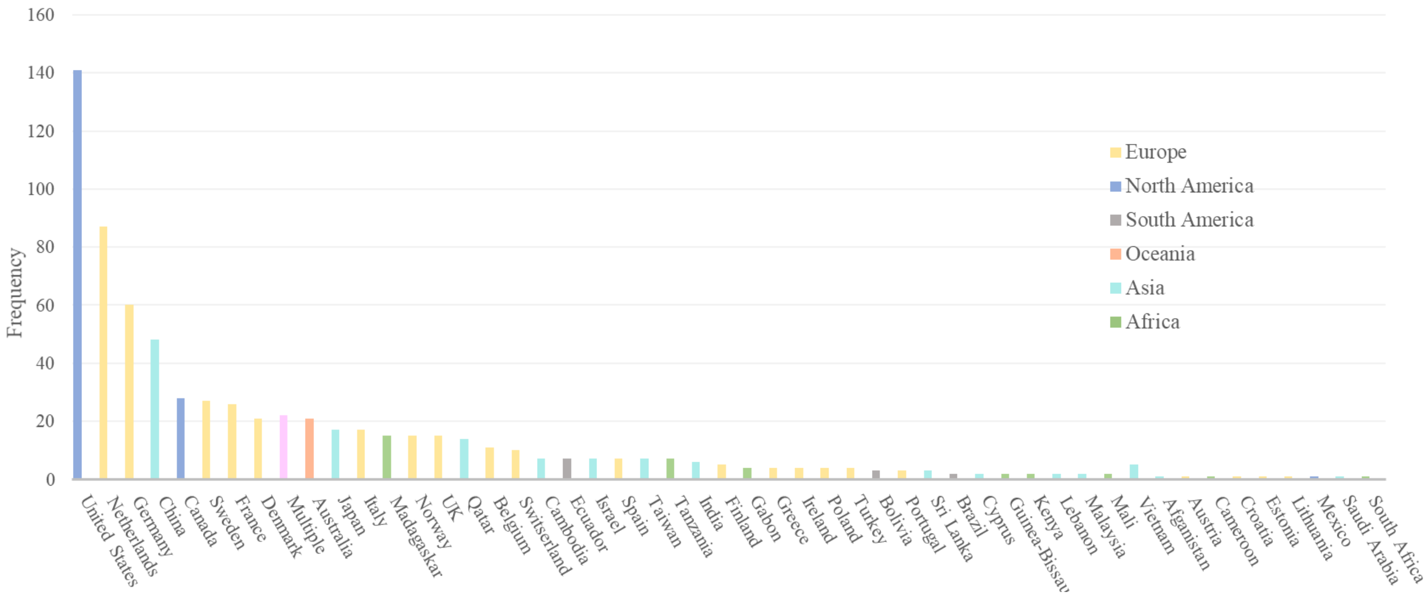

Figure 2. Countries per transmission route estimate *(n=716)*

Note: 5 studies were executed in laboratories and 8 were simulation studies and therefore not displayed in this figure.

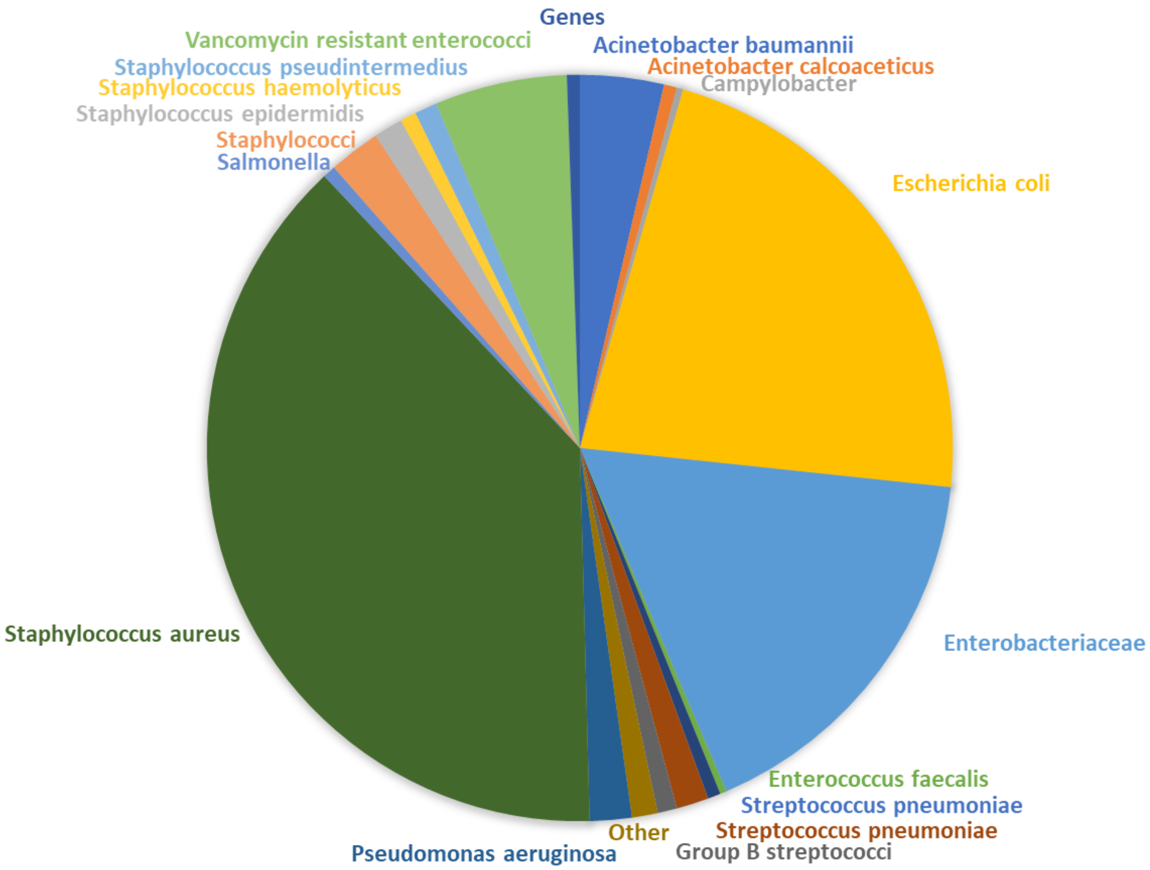

Figure 3. Chard of all bacteria studied

Transmission routes

Besides the acquisition of *E. coli* and Enterobacteriaceae when travelling to regions in Asia, *E. coli* transmission through breastfeeding (11.12, 95% CI [1.207-102.458], *A. baumannii* transmission through contact with an infected person (4.514, 95% CI [1.033-19.731], and *E. coli* transmission through a colonized household member (4.107, 95% CI [2.279-7.402]) yielded the highest ORs. Pig to air transmission of *S. aureus* (0.867, 95% CI [0.865-0.869]), chicken to environment transmission of *E. coli* (0.581, 95% CI [0.166-0.906]) and human to nearby environment transmission of *S. aureus* (0.525, 95% CI [0.312-0.73]) yielded the highest risk. Furthermore, the transmission of *S. aureus* through occupational exposure to pigs (2.761, 95% CI [1.897-4.017]), transmission of Enterobacteriaceae through a household member (1.921 95% CI [1.469-2.619]) and transmission of staphylococci through occupational exposure to pigs (1.522, 95% CI [1.272-1.821]) had the highest PR. Transmission of *S. Aureus* through breastfeeding (0.72, 95% CI [0.518-0.86]), transmission of *S. aureus* through occupational exposure to pigs (0.424, 95% CI [0.117-0.805]) and transmission of *S. aureus* through contact with a household member (0.394, 95% CI [0.284-0.517]) had the highest genetic overlap. Pig to pig transmission had the highest R0 (4.037, 95% CI[2.784-5.885].

In total, 91 random effects meta-analyses were performed. No meta-analysis was performed on bacteria intake as no more than two estimates on transmission routes using similar outcome measures were identified. Table 2 shows a full list of all transmission routes and pooled estimates.

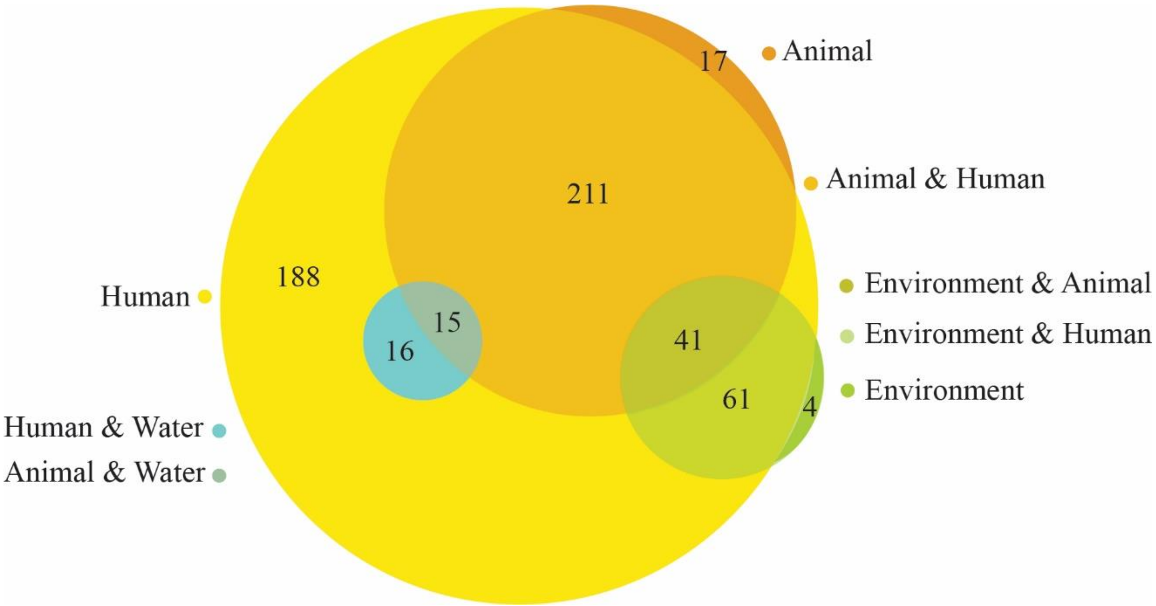

Figure 4. Reservoirs and cross-reservoir transmission in the study

Table 2. Meta-analysis on transmission routes per pathogen with ≥2 estimates

Transmission route	Definition	Total (*n*)	Pathogen	Method of estimation (n)	Pooled estimate	Lower limit	Upper limit
Animal to air	Transmission of animal to air						
	Poultry	2	*E. coli*	Risk (2)	0.126	0.075	0.205
	Pig	2	*E. coli*	Risk (2)	0.229	0.132	0.368
		1	Enterobacteriaceae	Risk (1)			
		3	*S. aureus*	Risk (3)	0.867	0.865	0.869
	Cattle	21	*S. aureus*	Risk (21)	0.459	0.219	0.720
Animal to animal	Transmission from animal to animal by other routes than birth						
	Poultry	4	*E. coli*	Genes (1) Risk (1) Transmission rate (2) [1]			
	Pet[2]	2	*S. aureus*	Risk (1) Genes (1)			
		3	*S. pseudintermedius*	Risk (2) Genes (1)	0.333	0.183	0.527
	Cattle	2	*S. aureus*	Transmission rate (2) [1]			
	Pig	2	*S. aureus*	R0(2) [2]	4.037	2.784	5.885
Animal to environment	Transmission from any animal to the environment (soil) through faeces or other routes						
	Pig	2	*E. coli*	Risk (2)	0.077	0.044	0.131
	Poultry	4	*E. coli*	Risk (4)[3]	0.581	0.166	0.906
	Animal compost	1	*E. coli*	Genes (1)			
	Pet	1	Enterobacteriaceae	Genes (1)			
Sharing water source with animals	Transmission through sharing water source with animals	5	*E. coli*	OR (5)[4]			

Non-commercial animal keeping	Contact of humans with animals, but not in a commercial farm setting and neither with pets, e.g. keeping horses or poultry at home	1	*E. coli*	OR (1)			
		3	Enterobacteriaceae	OR (3)[1]			
Breastfeeding	Transmission through breastfeeding from human mother to child	4	*E. coli*	OR (3)			
				Genes (1)	11.12	1.207	102.458
		2	Enterobacteriaceae	OR (2)	0.466	0.238	0.915
		4	*S. aureus*	OR (1)			
				PR (1)			
				Genes (2)	0.72	0.518	0.86
		3	*S. pneumoniae*	OR (3)	1.675	0.982	2.856
Contact with infected person	Contact with an infected person that is not a household member	7	*E. coli*	Genes (4)	0.222	0.014	0.85
				Risk (3)	0.241	0.172	0.326
		6	Enterobacteriaceae	OR (1)			
				Genes (4)	0.169	0.075	0.339
		42	*S. aureus*	Acquisition rate (1)			
				Cases per day (4)[1]			
				Genes (7)	0.356	0.135	0.662
				IOR (3)[5]			
				OR (2)	1.444	0.785	2.658
				TR (4)[1]			
				R_0 (11)[12]	0.642	0.487	0.846
				Risk (8)	0.098	0.056	0.166
				RR (2)[13]	1.061	1.012	1.113
		16	VRE	Risk (9)	0.087	0.049	0.148
				Genes (1)			
				R_0 (4)[5]			
				IOR (1)			

					TR (1)			
			10	*A. baumannii*	OR (2)	4.514	1.033	19.731
					Risk (5)	0.067	0.017	0.231
					R0 (2)[5]			
					IOR (1)			
			1	*A. calcoaceticus*	Genes (1)			
			7	*P. aeruginosa*	Risk (2)	0.029	0.005	0.151
					Genes (2)	0.28	0.22	0.35
					IOR (2)[5]			
					Transmission rate (1)			
			2	*S. epidermidis*	Risk (2)	0.095	0.052	0.168
Eating meat to human	Transmission from consuming meat as human[6]							
		White	5	*E. coli*	OR(2)	2.378	0.666	8.491
					Genes(1)			
					PR(1)			
		Red	13	*E. coli*	OR(6)	1.238	0.546	2.805
					PR(5)	1.185	0.977	1.314
		Fish	1	*E. coli*	OR(1)			
		Insects	1	*E. coli*				
		General	4	*E. coli*	OR(3)	0.68	0.416	1.111
Family member colonised	Transmission from a colonised family member to another family member		5	*E. coli*	OR (4)	4.107	2.279	7.402
					Risk (1)			
			4	Enterobacteriaceae	PR (2)	1.921	1.409	2.619
					Risk (1)			
					Genes(1)			
			18	*S. aureus*	OR (7)[7]	2.08	1.002	4.32
					Risk (2)	0.02	0.01	0.042
					Genes(8)[14]	0.394	0.284	0.517
			2	*P. aeruginosa*	Genes (2)	1	0.002	1

Family member occupational exposure	Transmission from a family member with occupational exposure, e.g. farming, to another family member						
	Farming[8]	4	*S. aureus*	OR (4)	2.351	1.269	4.496
	Hospital staff	3	*S. aureus*	OR (3)[15]	3.984	1.799	8.821
		2	VRE	Risk (1)			
				RR (1)			
Human to nearby environment	Transmission from humans to a nearby environment, e.g. a keyboard or bed	2	Enterobacteriaceae	Risk (1)			
				Genes (1)			
		3	*S. aureus*	Risk (3)	0.525	0.312	0.73
		11	VRE	Genes (1)			
				R_0 (2)[5]			
				Risk (8)	0.295	0.159	0.481
		13	*A. baumannii*	Risk (13)	0.164	0.025	0.599
		2	*A. calcoaceticus*	Risk (2)	0.122	0.070	0.203
Livestock to drinking water	Transmission from livestock on property on nearby property to drinking water for humans						
	Cattle	4	*E. coli*	OR (4)	1.411	1.025	1.942
	Pig	4	*E. coli*	OR (4)	3.324	1.590	6.949
	Poultry	4	*E. coli*	OR (4)	2.102	1.306	3.385
Mother to child	Transmission of the mother through birth to her child	1	*E. coli*	OR (1)			
		5	Enterobacteriaceae	OR (1)			
				Risk (3)[1]			
				Genes (1)			
		6	*S. aureus*	OR (2)	2.857	1.623	5.031
				Risk (3)	0.059	0.038	0.09
				Genes (1)			
		6	Group B streptococci	Risk (6)	0.263	0.133	0.451

Occupational exposure	Exposure to ABR bacteria on the work floor, analysed separately for veterinarians, farmers of poultry, pigs and cows[10]							
		Cattle	4	*S. aureus*	OR (4)	2.78	0.904	8.554
					PR (1)			
			1	Staphylococci	Risk (1)			
		Pig	1	*E. coli*	Risk (1)			
			2	Enterobacteriaceae	OR (2)	1.04	1.021	1.061
					Risk (3)	0.047	0.003	0.474
					Genes (1)			
			38	*S. aureus*	OR (17)	3.614	2.061	6.335
					PR (16)	2.761	1.897	4.017
					Risk (10)	0.306	0.123	0.581
					Genes (4)	0.424	0.117	0.805
			9	Staphylococci	Risk (3)	0.444	0.066	0.901
					Genes (1)			
					PR (5)	1.522	1.272	1.821
			5	*S. haemolyticus*	PR (5)[1]			
			5	*S. epidermidis*	PR (5)[1]			
		Poultry	15	*E. coli*	OR (14)	1.761	1.367	2.27
					Genes (1)			
			10	*S. aureus*	OR (7)	3.719	1.577	8.77
					PR (3)	0.753	0.318	1.782
			1	VRE	PR (1)			
		Other[9]	5	*S. aureus*	OR (3)			
					Risk (4)			
		Livestock[1]	4	*E. coli*	OR (1)			
					PR (2)			
					Genes (1)			
			18	*S. aureus*	OR (10)			
					PR (2)			

					Risk (6)			
					Genes (2)			
			1	Enterobacteriaceae	OR (1)			
		Cook/ food handler[1]	2	*E. coli*	PR (1)			
					Risk (1)			
			1	Enterobacteriaceae	Risk (1)			
			2	*S. aureus*	OR (2)			
		Veterinarian staff	4	*S. aureus*	OR (4)	6	0.874	41.2
					Risk (5)	0.085	0.04	0.17
			1	Staphylococci	Risk (1)			
Pet to human	Transmission from pets to human		3	*E. coli*	OR (2)	1.118	0.802	1.559
					Genes (1)			
			2	Enterobacteriaceae	OR (2)[1]			
			16	*S. aureus*	Risk (5)[11]	0.043	0.011	0.151
					PR (1)			
					Genes (6)	0.145	0.068	0.282
			4	Staphylococci	OR (2)	0.54	0.415	0.703
					Risk (1)			
					Genes (1)			
		Horse	3	*S. aureus*	Genes (3)	0.059	0.027	0.125
		Pet pig	1	*S. aureus*	Genes (1)			
Prior colonised patient in room	Transmission through your room potentially being colonised as the former patient staying in the room is known the be colonised		1	*A. baumannii*	OR (1)			
			1	*P. aeruginosa*	OR (1)			
Space sharing	Sharing a space, e.g. room or ward, with a colonised person but direct contact is not necessarily the case							
		Sharing a room	1	*E. coli*	OR (1)	2.764	1.781	4.287
			3	Enterobacteriaceae	OR (3)			

			1	VRE	OR (1)			
		Other[1]	1	Enterobacteriaceae	OR (1)			
			2	*S. aureus*	OR (2)			
			1	*A. baumannii*	OR (1)			
			1	VRE	OR (1)			
Contaminated room	Being present in a contaminated room		2	VRE	OR (2)[1]			
			2	*P. aeruginosa*	OR (1)			
					Genes(1)			
Travelling	Travelling to a foreign country							
		South Asia	2	*S. aureus*	OR (2)	1.952	0.395	9.643
			6	*E. coli*	OR (3)	25.445	10.057	64.377
					Risk (3)	0.755	0.409	0.932
			8	Enterobacteriaceae	OR (3)	4.387	1.674	11.494
					Risk (5)	0.766	0.709	0.815
		South East Asia	1	*E. coli*	Risk (1)			
			1	*S. aureus*	OR (1)			
			7	Enterobacteriaceae	OR (4)	22.793	5.224	99.45
					Risk (3)	0.362	0.327	0.398
		Western Asia	1	*E. coli*	Risk (1)			
			6	Enterobacteriaceae	OR (3)	4.729	0.541	41.331
					Risk (3)	0.3	0.168	0.477
		Central & East Asia	3	Enterobacteriaceae	Risk (3)	0.539	0.424	0.65
		Asia (unspecified)	2	*E. coli*	Risk (2)	0.143	0.088	0.224
					PR (1)			
			6	Enterobacteriaceae	OR (3)	4.094	2.37	7.07
					Risk (3)	0.172	0.101	0.277
		Latin America	4	*E. coli*	Risk (3)	0.028	0.001	0.393
					PR (1)			
			1	*S. aureus*	OR (1)			
			11	Enterobacteriaceae	OR (2)	0.595	0.327	1.08
					Risk (9)	0.126	0.077	0.2
		North America	1	*E. coli*	Risk (1)			
			1	Enterobacteriaceae	Risk (1)			
		America	1	*E. coli*	PR (1)			

	2	Enterobacteriaceae	OR (2)	6.176	0.603	63.241
Africa	5	*E. coli*	OR(1)			
			Risk (4)	0.134	0.043	0.345
	1	*S. aureus*	OR (1)			
	16	Enterobacteriaceae	OR (4)	3.658	2.359	5.673
			Risk (12)	0.179	0.113	0.273
Europe	5	*E. coli*	Risk (4)	0	0	0.938
			PR (1)			
	5	Enterobacteriaceae	OR (3)	1.033	0.654	1.629
			Risk (2)	0.167	0.064	0.369
Multiple regions[1]	4	*E. coli*	OR (1)			
			PR (3)			
	7	Enterobacteriaceae	OR (4)			
			Risk (2)			
			PR (1)			

Notes: [1] Could not be pooled due to dissimilarities or because estimates arose from the same study under different conditions, [2] Dogs or cats, [3] Only (2)part of the studies were pooled due to dissimilarities with other studies, [4] Not pooled as this was one study with no reference group without exposure, but compared water sharing with wildlife and livestock to water sharing with livestock only for different kinds of resistant E. coli [5] could not be pooled due to missing sample sizes [6]meta-analyses pooled for meat (pork, poultry, veal, beef) eaten on at least a weekly basis (OR *n* = 11, PR *n* = 5) [7]meta-analtsis based on 6 studies as one was based on OR of parents vs. siblings to get infected when a child is infected [8] 5 swine, 1 poultry, 1 cattle [9] Agriculture, irrigation worker, manure handling, multiple groups [10] Being a vet was considered a separate group, not matter which animals were names as exposure [11] 3 of these were pooled, other was on a goat which were kept as pets/close to home but are not comparable to cats and dogs and the other estimate was particular on not having pets [12] Due to missing sample sizes and confidence intervals, only 3 estimates could be pooled.[13] The RR of Calfee et al. 2003 was based on close, similar to household, contact vs. less close contacts, so this estimate could also have been grouped as family member colonized [14] Based on seven of the eight estimates as one was not similar to the others, it estimated the importance of the route rather than transmission probability [15] Based on 2 as 1 was explicitly on household members *not* being health care workers

VRE; vancomycin resistant enterococci

Discussion

This systematic review shows which transmission routes have been studied the most and which methods of estimation have commonly been used. Breastfeeding, occupational exposure to animals and transmission between household members were identified by multiple methods as the highest risk routes. Statistical methods, especially ORs and risks, are most often used the estimate the importance of transmission routes. Cross-reservoir transmission between humans and animals has been studied most commonly, whereas studies on transmission from the environment are scarce, as also indicated by a previous meta-analysis which only included significant transmission estimates (3).

Studies such as McCallum et al. 2002, in which no identical overlap in *P. aeruginosa* was found even though two household members were colonised, and Ozaki et al. 2009, in which four families members carried MRSA but only three of them where genetically identical and one was acquired outside the family, indicate that risk estimates are common overestimates of transmission routes, and that genetic overlap is a more accurate method of estimating routes of acquisition of ABR bacteria. Other studies (30,52), also indicate this overestimation of risk estimates compared to identical genetic overlap.

Our review emphasizes a gap in the current knowledge on transmission routes. A bridge between the frequency of exposure and the risk to get colonised when exposed is missing. Moreover, the starting point of the transmission circle remains mostly unidentified, except when genetic overlap as a method of estimation is used. Looking at routes previously identified as high risk, breastfeeding only occurs in the first years of life whereas transmission between households occurs throughout life. Both these routes have a high genetic overlap and a high OR and PR, indicating that not only are they often the source of transmission but they also have a high chance of transmission upon occurrence. To make policies aimed at reducing ABR bacteria, a coherent picture of the occurrence of exposure and risk of colonization when exposed should be created.

Furthermore, comparison of methods of estimation to estimate whether some methods result in over- or underestimation was not possible as the transmission routes estimates were often not identified for all methods of estimation.

Strengths of this review include the assessment and comparison of various methods of estimation, reservoirs and transmission routes so that a coherent overview of the current literature on ABR bacteria is provided. The first limitation of our study is that we do not stratify for the length of exposure or time between exposure and measurements for travelling and occupational exposure. The pooled estimates are therefore more difficult to interpret. Secondly, we do not consider the use of antibiotics as a transmission route. We focus on transmission instead of mutation or creation. Further, although all measures were taken to limit discrepancies, data collection was done by one reviewer which might have caused discrepancies in data collection and analysis. Fourthly, the extensive literature on the transmission of ABR bacteria precludes our search terms from identifying all studies in this area. By including synonyms, we tried to identify as many of the studies as possible. Moreover, we did not include a formal quality assessment due to the diverse nature of our studies.

To conclude, on the one hand, there is a plethora of estimates and studies on risk factors and transmission routes of ABR bacteria. On the other, this review indicates that the relevance of routes on a population scale is missing.

References

1. Holmes AH, Moore LSP, Sundsfjord A, Steinbakk M, Regmi S, Karkey A, et al. Understanding the mechanisms and drivers of antimicrobial resistance. Lancet (London, England). 2016 Jan;387(10014):176–87.

2. Pelupessy I, Bonten MJM, Diekmann O. How to assess the relative importance of different colonization routes of pathogens within hospital settings. Proc Natl Acad Sci U S A. 2002 Apr;99(8):5601–5.

3. Chatterjee A, Modarai M, Naylor NR, Boyd SE, Atun R, Barlow J, et al. Quantifying drivers of antibiotic resistance in humans: a systematic review. Lancet Infect Dis. 2018 Dec;18(12):e368–78.

4. Diekmann O, Heesterbeek JA, Metz JA. On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations. J Math Biol. 1990;28(4):365–82.

5. Moher D, Liberati A, Tetzlaff J, Altman DG, Group TP. Preferred Reporting Items for Systematic Reviews and Meta-Analyses: The PRISMA Statement. PLOS Med [Internet]. 2009 Jul 21;6(7):e1000097. Available from: https://doi.org/10.1371/journal.pmed.1000097

6. Godijk NG, Bootsma MCJ. What is the estimated importance of transmission routes for antimicrobial-resistant bacteria according to different methodologies? PROSPERO 2019 CRD42019136298 [Internet]. Available from: https://www.crd.york.ac.uk/prospero/display_record.php?ID=CRD42019136298

7. Ouzzani M, Hammady H, Fedorowicz Z, Elmagarmid A. Rayyan---a web and mobile app for systematic reviews. Syst Rev [Internet]. 2016;5(1):210. Available from: http://dx.doi.org/10.1186/s13643-016-0384-4

8. Lo W-U, Ho P-L, Chow K-H, Lai EL, Yeung F, Chiu SS. Fecal carriage of CTXM type extended-spectrum beta-lactamase-producing organisms by children and their household contacts. J Infect. 2010 Apr;60(4):286–92.

9. Alves M, Lemire A, Decré D, Margetis D, Bigé N, Pichereau C, et al. Extended-spectrum beta-lactamase - producing enterobacteriaceae in the intensive care unit: Acquisition does not mean cross-transmission. BMC Infect Dis. 2016 Apr;16(1):147.

10. Cochard H, Aubier B, Quentin R, van der Mee-Marquet N. Extended-Spectrum β -Lactamase–

Producing Enterobacteriaceae in French Nursing Homes: An Association between High Carriage Rate among Residents, Environmental Contamination, Poor Conformity with Good Hygiene Practice, and Putative Resident-to-Resident Tra. Infect Control Hosp Epidemiol. 2014 Apr;35(4):384–9.

11. Cuny C, Nathaus R, Layer F, Strommenger B, Altmann D, Witte W. Nasal colonization of humans with methicillin-resistant Staphylococcus aureus (MRSA) CC398 with and without exposure to pigs. PLoS One [Internet]. 2009 Aug 27;4(8):e6800–e6800. Available from: https://pubmed.ncbi.nlm.nih.gov/19710922

12. Gustafsson EB, Ringberg H, Johansson PJH. MRSA in children from foreign countries adopted to Swedish families. Acta Paediatr Int J Paediatr. 2007 Jan;96(1):105–8.

13. Johansson PJH, Gustafsson EB, Ringberg H. High prevalence of MRSA in household contacts. Scand J Infect Dis. 2007;39(9):764–8.

14. Mitsuda T, Arai K, Ibe M, Imagawa T, Tomono N, Yokota S. The influence of methicillin-resistant Staphylococcus aureus (MRSA) carriers in a nursery and transmission of MRSA to their households. J Hosp Infect. 1999 May;42(1):45–51.

15. Nerby JM, Gorwitz R, Lesher L, Juni B, Jawahir S, Lynfield R, et al. Risk factors for household transmission of community-associated methicillin-resistant Staphylococcus aureus. Pediatr Infect Dis J. 2011 Nov;30(11):927–32.

16. Stone ND, Lewis DR, Johnson TM 2nd, Hartney T, Chandler D, Byrd-Sellers J, et al. Methicillin-resistant Staphylococcus aureus (MRSA) nasal carriage in residents of Veterans Affairs long-term care facilities: role of antimicrobial exposure and MRSA acquisition. Infect Control Hosp Epidemiol. 2012 Jun;33(6):551–7.

17. Snyder GM, Thorn KA, Furuno JP, Perencevich EN, Roghmann M-C, Strauss SM, et al. Detection of Methicillin-Resistant Staphylococcus aureus and Vancomycin-Resistant Enterococci on the Gowns and Gloves of Healthcare Workers . Infect Control Hosp Epidemiol. 2008 Jul;29(7):583–9.

18. Senn L, Clerc O, Zanetti G, Basset P, Prod’hom G, Gordon NC, et al. The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant Staphylococcus aureus. MBio. 2016 Jan;7(1):e02039-15.

19. Frénay HME, Vandenbroucke-Grauls CMJE, Molkenboer MJCH, Verhoef J. Long-term carriage, and transmission of methicillin-resistant Staphylococcus aureus after discharge from hospital. J Hosp Infect. 1992 Nov;22(3):207–15.

20. McBryde ES, Bradley LC, Whitby M, McElwain DLS. An investigation of contact transmission of methicillin-resistant Staphylococcus aureus. J Hosp Infect. 2004 Nov 1;58(2):104–8.

21. Gastelum DT, Dassey D, Mascola L, Yasuda LM. Transmission of community-associated methicillin-resistant Staphylococcus aureus from breast milk in the neonatal intensive care unit. Pediatr Infect Dis J. 2005 Dec;24(12):1122–4.

22. Pierce R, Lessler J, Popoola VO, Milstone AM. Meticillin-resistant Staphylococcus aureus (MRSA) acquisition risk in an endemic neonatal intensive care unit with an active surveillance culture and decolonization programme. J Hosp Infect. 2017 Jan;95(1):91–7.

23. Calfee DP, Durbin LJ, Germanson TP, Toney DM, Smith EB, Farr BM. Spread of methicillin-resistant Staphylococcus aureus (MRSA) among household contacts of individuals with nosocomially acquired MRSA. Infect Control Hosp Epidemiol. 2003 Jun;24(6):422–6.

24. Crombach WHJ, Dijkshoorn L, van Noort-Klaassen M, Niessen J, van Knippenberg-Gordebeke G. Control of an epidemic spread of a multi-resistant strain of Acinetobacter calcoaceticus in a hospital. Intensive Care Med. 1989;15(3):166–70.

25. Morgan DJ, Liang SY, Smith CL, Johnson JK, Harris AD, Furuno JP, et al. Frequent Multidrug-Resistant Acinetobacter baumannii Contamination of Gloves, Gowns, and Hands of Healthcare Workers . Infect Control Hosp Epidemiol. 2010 Jul;31(7):716–21.

26. Griffith SJ, Nathan C, Selander RK, Chamberlin W, Gordon S, Kabins S, et al. The Epidemiology of Pseudomonas Aeruginosa in Oncology Patients in a General Hospital. J Infect Dis. 1989 Dec;160(6):1030–6.

27. Coleman BL, Salvadori MI, McGeer AJ, Sibley KA, Neumann NF, Bondy SJ, et al. The role of drinking water in the transmission of antimicrobial-resistant E. coli. Epidemiol Infect [Internet]. 2012;140(4):633–42. Available from: https://www.ncbi.nlm.nih.gov/pubmed/21733246

28. Fornasini M, Reves RR, Murray BE, Morrow AL, Pickering LK. Trimethoprim-Resistant Escherichia coli in Households of Children Attending Day Care Centers. J Infect Dis. 1992 Aug;166(2):326–30.

29. Lietzau S, Raum E, von Baum H, Marre R, Brenner H. Clustering of antibiotic resistance of E. coli in couples: Suggestion for a major role of conjugal transmission. BMC Infect Dis. 2006 Jul;6:119.

30. Tandé D, Boisramé-Gastrin S, Münck MR, Héry-Arnaud G, Gouriou S, Jallot N, et al. Intrafamilial transmission of extended-spectrum-β-lactamase-producing Escherichia coli and Salmonella enterica Babelsberg among the families of internationally adopted children. J Antimicrob Chemother [Internet]. 2010;65(5):859–65. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L359507100

31. Ferreira JP, Anderson KL, Correa MT, Lyman R, Ruffin F, Reller LB, et al. Transmission of mrsa between companion animals and infected human patients presenting to outpatient medical care facilities. PLoS One. 2011;6(11):e26978.

32. Cluzet VC, Gerber JS, Nachamkin I, Metlay JP, Zaoutis TE, Davis MF, et al. Risk factors for recurrent colonization with methicillin-resistant Staphylococcus aureus in community-dwelling adults and children. Infect Control Hosp Epidemiol. 2015 Jul;36(7):786–93.

33. Walter J, Espelage W, Adlhoch C, Cuny C, Schink S, Jansen A, et al. Persistence of nasal colonisation with methicillin resistant Staphylococcus aureus CC398 among participants of veterinary conferences and occurrence among their household members: A prospective cohort study, Germany 2008–2014. Vet Microbiol. 2017;200:13–8.

34. Schaumburg F, Alabi AS, Mombo-Ngoma G, Kaba H, Zoleko RM, Diop DA, et al. Transmission of Staphylococcus aureus between mothers and infants in an African setting. Clin Microbiol Infect. 2014 Jun;20(6):O390-6.

35. Zetsma JW, Spanjaard L, Dankert J. [Carrier state and spread of methicillin resistant Staphylococcus aureus following hospital discharge]. Ned Tijdschr Geneeskd. 1993 Nov;137(47):2428–31.

36. Chidekel AS, Steele-Moore L, Padman R, Pellegrino V, Berg D, Klein J. Nasopharyngeal colonization in children with cystic fibrosis: Antibiotic resistance and intrafamilial spread. Infect Dis Clin Pract [Internet]. 2000;9(8):333–6. Available from: https://journals.lww.com/infectdis/Fulltext/2000/09080/Nasopharyngeal_Colonization_in_Children_with.9.aspx

37. Alam MT, Read TD, Petit RA, Boyle-Vavra S, Miller LG, Eells SJ, et al. Transmission and microevolution of USA300 MRSA in U.S. households: Evidence from whole-genome sequencing.

MBio. 2015 Mar;6(2):e00054.

38. Davis MF, Misic AM, Morris DO, Moss JT, Tolomeo P, Beiting DP, et al. Genome sequencing reveals strain dynamics of methicillin-resistant Staphylococcus aureus in the same household in the context of clinical disease in a person and a dog. Vet Microbiol. 2015 Nov;180(3–4):304–7.

39. Eveillard M, Martin Y, Hidri N, Boussougant Y, Joly-Guillou M-L. Carriage of methicillin-resistant Staphylococcus aureus among hospital employees: prevalence, duration, and transmission to households. Infect Control Hosp Epidemiol. 2004 Feb;25(2):114–20.

40. Ozaki K, Takano M, Higuchi W, Takano T, Yabe S, Nitahara Y, et al. Genotypes, intrafamilial transmission, and virulence potential of nasal methicillin-resistant Staphylococcus aureus from children in the community. J Infect Chemother. 2009 Apr;15(2):84–91.

41. Toleman MS, Reuter S, Coll F, Harrison EM, Blane B, Brown NM, et al. Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant Staphylococcus aureus USA300 in the East of England. J Infect Dis. 2016 Aug;214(3):447–53.

42. McCallum SJ, Gallagher MJ, Corkill JE, Hart CA, Ledson MJ, Walshaw MJ. Spread of an epidemic Pseudomonas aeruginosa strain from a patient with cystic fibrosis (CF) to non-CF relatives. Thorax. 2002 Jun;57(6):559–60.

43. Kunze M, Ziegler A, Fluegge K, Hentschel R, Proempeler H, Berner R. Colonization, serotypes and transmission rates of group B streptococci in pregnant women and their infants born at a single University Center in Germany. J Perinat Med [Internet]. 2011;39(4):417–22. Available from: http://ovidsp.ovid.com/ovidweb.cgi?T=JS&PAGE=reference&D=emed13&NEWS=N&AN=362125172

44. Kunze M, Zumstein K, Markfeld-Erol F, Elling R, Lander F, Prömpeler H, et al. Comparison of pre- and intrapartum screening of group B streptococci and adherence to screening guidelines: a cohort study. Eur J Pediatr [Internet]. 2015;174(6):827–35. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L604109627 http://dx.doi.org/10.1007/s00431-015-2548-y

45. Facchinetti F, Piccinini F, Mordini B, Volpe A. Chlorhexidine vaginal flushings versus systemic ampicillin in the prevention of vertical transmission of neonatal group B streptococcus, at term. J Matern Neonatal Med [Internet]. 2002;11(2):84–8. Available from:

http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L34836873

46. Kadanali A, Altoparlak U, Kadanali S. Maternal carriage and neonatal colonisation of group B streptococcus in eastern Turkey: prevalence, risk factors and antimicrobial resistance. Int J Clin Pr. 2005;59(4):437–40.

47. Eren A, Küçükercan M, Oğuzoğlu N, Ünal N, Karateke A. The carriage of group B streptococci in Turkish pregnant women and its transmission rate in newborns and serotype distribution. Turk J Pediatr. 2005;47(1):28–33.

48. Strus M, Pawlik D, Brzychczy-Włoch M, Gosiewski T, Rytlewski K, Lauterbach R, et al. Group B streptococcus colonization of pregnant women and their children observed on obstetric and neonatal wards of the University hospital in krakow, Poland. J Med Microbiol. 2009;58(2):228–33.

49. Rasamiravaka T, Andriatsitohanana TT, Rasamindrakotroka A. Evaluation of methicillin-resistant staphylococcus aureus nasal carriage in malagasy pig and poultry non-industrial farmers. J Infect Dev Ctries. 2017;11(2):129–35.

50. Ho J, O'Donoghue MM, Boost M V. Occupational exposure to raw meat: A newly-recognized risk factor for Staphylococcus aureus nasal colonization amongst food handlers. Int J Hyg Environ Health. 2014;217(2–3):347–53.

51. Boost M V., O'Donoghue MM, James A. Prevalence of Staphylococcus aureus carriage among dogs and their owners. Epidemiol Infect. 2008;136(7):953–64.

52. Mutters NT, Brooke RJ, Frank U, Heeg K. Low risk of apparent transmission of vancomycin-resistant Enterococci from bacteraemic patients to hospitalized contacts. Am J Infect Control. 2013 Sep;41(9):778–81.

53. Rosen K, Roesler U, Merle R, Friese A. Persistent and transient airborne MRSA colonization of piglets in a newly established animal model. Front Microbiol. 2018;9(JUL):1542.

54. Dierikx CM, van der Goot J, van Essen-Zandbergen A, Mevius DJ. Dynamics of cefotaxime resistant Escherichia coli in broilers in the first week of life. Vet Microbiol. 2018 Aug;222:64–8.

55. van Duijkeren E, Kamphuis M, van der Mije IC, Laarhoven LM, Duim B, Wagenaar JA, et al. Transmission of methicillin-resistant Staphylococcus pseudintermedius between infected dogs and cats and contact pets, humans and the environment in households and veterinary clinics. Vet

Microbiol. 2011 Jun;150(3–4):338–43.

56. Loeffler A, Pfeiffer DU, Lindsay JA, Soares-Magalhaes R, Lloyd DH. Lack of transmission of methicillin-resistant Staphylococcus aureus (MRSA) between apparently healthy dogs in a rescue kennel. Vet Microbiol. 2010 Feb;141(1–2):178–81.

57. Broens EM, Graat EAM, van de Giessen AW, Broekhuizen-Stins MJ, de Jong MCM. Quantification of transmission of livestock-associated methicillin resistant Staphylococcus aureus in pigs. Vet Microbiol. 2012 Mar;155(2–4):381–8.

58. Huijbers PMC, Graat EAM, van Hoek AHAM, Veenman C, de Jong MCM, van Duijkeren E. Transmission dynamics of extended-spectrum β-lactamase and AmpC β-lactamase-producing Escherichia coli in a broiler flock without antibiotic use. Prev Vet Med. 2016 Sep;131:12–9.

59. Riccobono E, Pallecchi L, Mantella A, Bartalesi F, Zeballos IC, Trigoso C, et al. Carriage of antibiotic-resistant Escherichia coli among healthy children and home-raised chickens: A household study in a resource-limited setting. Microb Drug Resist. 2012 Feb;18(1):83–7.

60. Weese JS, Dick H, Willey BM, McGeer A, Kreiswirth BN, Innis B, et al. Suspected transmission of methicillin-resistant Staphylococcus aureus between domestic pets and humans in veterinary clinics and in the household. Vet Microbiol. 2006 Jun;115(1–3):148–55.

61. Windahl U, Ågren J, Holst BS, Börjesson S. Colonization with methicillin-resistant Staphylococcus pseudintermedius in multi-dog households: A longitudinal study using whole genome sequencing. Vet Microbiol. 2016 Jun;189:8–14.

62. Graveland H, Wagenaar JA, Verstappen KMHW, Oosting-van Schothorst I, Heederik DJJ, Bos MEH. Dynamics of MRSA carriage in veal calves: a longitudinal field study. Prev Vet Med. 2012 Dec;107(3–4):180–6.

63. Gao LL, Tan Y, Zhang XD, Hu JQ, Miao ZM, Wei LM, et al. Emissions of Escherichia coli carrying extended-spectrum β-lactamase resistance from pig farms to the surrounding environment. Int J Environ Res Public Health. 2015 Apr;12(4):4203–13.

64. Laube H, Friese A, von Salviati C, Guerra B, Rösler U. Transmission of ESBL/AmpC-producing Escherichia coli from broiler chicken farms to surrounding areas. Vet Microbiol. 2014 Aug;172(3–4):519–27.

65. Moodley A, Guardabassi L. Transmission of IncN plasmids carrying blaCTX-M-1 between

commensal escherichia coli in pigs and farm workers. Antimicrob Agents Chemother. 2009 Apr;53(4):1709–11.

66. Gao L, Hu J, Zhang X, Wei L, Li S, Miao Z, et al. Application of swine manure on agricultural fields contributes to extended- spectrum ß-lactamase producing Escherichia coli spread in Tai'an, China. Front Microbiol. 2015;6(MAR):313.

67. Leite-Martins L, Meireles D, Bessa LJ, Mendes Â, De Matos AJ, Martins Da Costa P. Spread of multidrug-resistant Enterococcus faecalis within the household setting. Microb Drug Resist. 2014 Oct;20(5):501–7.

68. Schmithausen RM, Schulze-Geisthoevel SV, Stemmer F, El-Jade M, Reif M, Hack S, et al. Analysis of Transmission of MRSA and ESBL-E among Pigs and Farm Personnel. PLoS One. 2015;10(9):e0138173.

69. Davis MF, Pisanic N, Rhodes SM, Brown A, Keller H, Nadimpalli M, et al. Occurrence of Staphylococcus aureus in swine and swine workplace environments on industrial and antibiotic-free hog operations in North Carolina, USA: A One Health pilot study. Environ Res. 2018 May;163:88–96.

70. Fu J, Yang D, Jin M, Liu W, Zhao X, Li C, et al. Aquatic animals promote antibiotic resistance gene dissemination in water via conjugation: Role of different regions within the zebra fish intestinal tract, and impact on fish intestinal microbiota. Mol Ecol. 2017 Oct;26(19):5318–33.

71. Parm U, Metsvaht T, Sepp E, Ilmoja ML, Pisarev H, Pauskar M, et al. Risk factors associated with gut and nasopharyngeal colonization by common Gram-negative species and yeasts in neonatal intensive care units patients. Early Hum Dev. 2011 Jun;87(6):391–9.

72. Chen CJ, Hsu KH, Lin TY, Hwang KP, Chen PY, Huang YC. Factors associated with nasal colonization of methicillin-resistant Staphylococcus aureus among healthy children in Taiwan. J Clin Microbiol. 2011 Jan;49(1):131–7.

73. Isendahl J, Turlej-Rogacka A, Manjuba C, Rodrigues A, Giske CG, Nauclér P. Fecal Carriage of ESBL-Producing E. coli and K. pneumoniae in Children in Guinea-Bissau: A Hospital-Based Cross-Sectional Study. PLoS One. 2012;7(12):e51981.

74. Hijazi SM, Fawzi MA, Ali FM, Abd El Galil KH. Multidrug-resistant ESBL-producing Enterobacteriaceae and associated risk factors in community infants in Lebanon. J Infect Dev

Ctries. 2016 Sep;10(9):947–55.

75. Koliou MG, Andreou K, Lamnisos D, Lavranos G, Iakovides P, Economou C, et al. Risk factors for carriage of Streptococcus pneumoniae in children. BMC Pediatr. 2018 Apr;18(1):144.

76. Nakamura K, Kaneko M, Abe Y, Yamamoto N, Mori H, Yoshida A, et al. Outbreak of extended-spectrum beta-lactamase-producing Escherichia coli transmitted through breast milk sharing in a neonatal intensive care unit. J Hosp Infect. 2016 Jan;92(1):42–6.

77. Nordberg V, Quizhpe Peralta A, Galindo T, Turlej-Rogacka A, Iversen A, Giske CG, et al. High Proportion of Intestinal Colonization with Successful Epidemic Clones of ESBL-Producing Enterobacteriaceae in a Neonatal Intensive Care Unit in Ecuador. PLoS One. 2013;8(10):e76597.

78. Çftç E, Aysev ÜDD, İnce E, Gürz H. Investigation of risk factors for penicillin-resistant Streptococcus pneumoniae carriage in Turkish children. Pediatr Int. 2001 Aug;43(4):385–90.

79. Benito D, Lozano C, Jiménez E, Albújar M, Gómez A, Rodríguez JM, et al. Characterization of Staphylococcus aureus strains isolated from faeces of healthy neonates and potential mother-to-infant microbial transmission through breastfeeding. FEMS Microbiol Ecol. 2015 Mar;91(3).

80. Gueimonde M, Salminen S, Isolauri E. Presence of specific antibiotic (tet) resistance genes in infant faecal microbiota. FEMS Immunol Med Microbiol. 2006 Oct;48(1):21–5.

81. Schwartz-Neiderman A, Braun T, Fallach N, Schwartz D, Carmeli Y, Schechner V. Risk factors for Carbapenemase-Producing Carbapenem-Resistant Enterobacteriaceae (CP-CRE) acquisition among contacts of newly diagnosed CP-CRE patients. Infect Control Hosp Epidemiol. 2016 Oct;37(10):1219–25.

82. Grabsch EA, Burrell LJ, Padiglione A, O’Keeffe JM, Ballard S, Grayson ML. Risk of Environmental and Healthcare Worker Contamination With Vancomycin-Resistant Enterococci During Outpatient Procedures and Hemodialysis. Infect Control Hosp Epidemiol. 2006 Mar;27(3):287–93.

83. El Shafie SS, Alishaq M, Leni Garcia M. Investigation of an outbreak of multidrug-resistant Acinetobacter baumannii in trauma intensive care unit. J Hosp Infect. 2004 Feb;56(2):101–5.

84. Rydberg J, Cederberg Å. Intrafamilial spreading of escherichia coli resistant to trimethoprim. Scand J Infect Dis. 1986;18(5):457–60.

85. Jackson SS, Harris AD, Magder LS, Stafford KA, Johnson JK, Miller LG, et al. Bacterial burden is associated with increased transmission to health care workers from patients colonized with vancomycin-resistant Enterococcus. Am J Infect Control. 2019 Jan;47(1):13–7.

86. Torres E, López-Cerero L, Morales I, Navarro MD, Rodríguez-Baño J, Pascual A. Prevalence and transmission dynamics of Escherichia coli ST131 among contacts of infected community and hospitalized patients. Clin Microbiol Infect. 2018 Jun;24(6):618–23.

87. Zhou Q, Moore C, Eden S, Tong A, McGeer A. Factors Associated With Acquisition of Vancomycin-Resistant Enterococci (VRE) in Roommate Contacts of Patients Colonized or Infected with VRE in a Tertiary Care Hospital. Infect Control Hosp Epidemiol. 2008 May;29(5):398–403.

88. Hedin G, Hambraeus A. Multiply antibiotic-resistant Staphylococcus epidermidis in patients, staff and environment--a one-week survey in a bone marrow transplant unit. J Hosp Infect. 1991 Feb;17(2):95–106.

89. Domenech de Celles M, Salomon J, Marinier A, Lawrence C, Gaillard J-L, Herrmann J-L, et al. Identifying more epidemic clones during a hospital outbreak of multidrug-resistant Acinetobacter baumannii. PLoS One. 2012;7(9):e45758.

90. Christopher S, Verghis RM, Antonisamy B, Sowmyanarayanan TV, Brahmadathan KN, Kang G, et al. Transmission dynamics of methicillin-resistant Staphylococcus aureus in a medical intensive care unit in India. PLoS One. 2011;6(7):e20604.

91. Austin DJ, Bonten MJ, Weinstein RA, Slaughter S, Anderson RM. Vancomycin-resistant enterococci in intensive-care hospital settings: transmission dynamics, persistence, and the impact of infection control programs. Proc Natl Acad Sci U S A. 1999 Jun;96(12):6908–13.

92. Plipat N, Spicknall IH, Koopman JS, Eisenberg JNS. The dynamics of methicillin-resistant Staphylococcus aureus exposure in a hospital model and the potential for environmental intervention. BMC Infect Dis. 2013 Dec;13(1):595.

93. Mikolajczyk RT, Kauermann G, Sagel U, Kretzschmar M. Mixture Model to Assess the Extent of Cross-Transmission of Multidrug-Resistant Pathogens in Hospitals. Infect Control Hosp Epidemiol. 2009 Aug;30(8):730–6.

94. Cheah ALY, Cheng AC, Spelman D, Nation RL, Kong DCM, McBryde ES. Mathematical

modelling of vancomycin-resistant enterococci transmission during passive surveillance and active surveillance with contact isolation highlights the need to identify and address the source of acquisition. BMC Infect Dis. 2018 Oct;18(1):511.

95. Cooper BS, Kypraios T, Batra R, Wyncoll D, Tosas O, Edgeworth JD. Quantifying type-specific reproduction numbers for nosocomial pathogens: Evidence for heightened transmission of an Asian sequence type 239 MRSA clone. PLoS Comput Biol. 2012;8(4):e1002454.

96. Domenech de Celles M, Opatowski L, Salomon J, Varon E, Carbon C, Boelle P-Y, et al. Intrinsic epidemicity of Streptococcus pneumoniae depends on strain serotype and antibiotic susceptibility pattern. Antimicrob Agents Chemother. 2011 Nov;55(11):5255–61.

97. Forrester M, Pettitt AN. Use of Stochastic Epidemic Modeling to Quantify Transmission Rates of Colonization With Methicillin-Resistant Staphylococcus Aureus in an Intensive Care Unit . Infect Control Hosp Epidemiol. 2005 Jul;26(7):598–606.

98. Pettitt AN, Forrester ML, Gibson GJ. Bayesian inference of hospital-acquired infectious diseases and control measures given imperfect surveillance data. Biostatistics. 2007 Apr;8(2):383–401.

99. Hetem DJ, Westh H, Boye K, Jarløv JO, Bonten MJM, Bootsma MCJ. Nosocomial transmission of community-associated methicillin-resistant Staphylococcus aureus in Danish hospitals. J Antimicrob Chemother. 2012 Jul;67(7):1775–80.

100. Mikolajczyk RT, Sagel U, Bornemann R, Krämer A, Kretzschmar M. A statistical method for estimating the proportion of cases resulting from cross-transmission of multi-resistant pathogens in an intensive care unit. J Hosp Infect. 2007 Feb;65(2):149–55.

101. Simon CP, Percha B, Riolo R, Foxman B. Modeling bacterial colonization and infection routes in health care settings: Analytic and numerical approaches. J Theor Biol. 2013 Oct;334:187–99.

102. López-García M, Kypraios T. A unified stochastic modelling framework for the spread of nosocomial infections. J R Soc Interface. 2018 Jun;15(143).

103. McBryde ES, Pettitt AN, McElwain DLS. A stochastic mathematical model of methicillin resistant Staphylococcus aureus transmission in an intensive care unit: Predicting the impact of interventions. J Theor Biol. 2007 Apr;245(3):470–81.

104. Wang L, Ruan S. Modeling Nosocomial Infections of Methicillin-Resistant Staphylococcus aureus with Environment Contamination. Sci Rep. 2017 Apr;7(1):580.

105. Givon-Lavi N, Fraser D, Porat N, Dagan R. Spread of Streptococcus pneumoniae and antibiotic-resistant S. pneumoniae from day-care center attendees to their younger siblings. J Infect Dis. 2002 Dec;186(11):1608–14.

106. Normark BH, Christensson B, Sandgren A, Noreen B, Sylvan S, Burman LG, et al. Clonal Analysis of Streptococcus pneumoniae Nonsusceptible to Penicillin at Day-Care Centers with Index Cases, in a Region with Low Incidence of Resistance: Emergence of an Invasive Type 35B Clone among Carriers. Microb Drug Resist. 2003;9(4):337–44.

107. Johnson JK, Smith G, Lee MS, Venezia RA, Stine OC, Nataro JP, et al. The Role of Patient-to-Patient Transmission in the Acquisition of Imipenem-Resistant Pseudomonas aeruginosa Colonization in the Intensive Care Unit . J Infect Dis. 2009 Sep;200(6):900–5.

108. Kojima Y, Harada S, Aoki K, Ishii Y, Sawa T, Hasegawa K, et al. Spread of CTX-M-15 extended-spectrum β-lactamase-producing Escherichia coli isolates through household contact and plasmid transfer. J Clin Microbiol [Internet]. 2014/02/19. 2014 May;52(5):1783–5. Available from: https://pubmed.ncbi.nlm.nih.gov/24554749

109. Maataoui N, Mayet A, Duron S, Delacour H, Mentré F, Laouenan C, et al. High acquisition rate of extended-spectrum β-lactamase-producing Enterobacteriaceae among French military personnel on mission abroad, without evidence of inter-individual transmission. Clin Microbiol Infect. 2019 May;25(5):631.e1-631.e9.

110. Cooper BS, Medley GF, Stone SP, Kibbler CC, Cookson BD, Roberts JA, et al. Methicillin-resistant Staphylococcus aureus in hospitals and the community: stealth dynamics and control catastrophes. Proc Natl Acad Sci U S A. 2004 Jul;101(27):10223–8.

111. Kariuki S, Revathi G, Kariuki N, Kiiru J, Mwituria J, Muyodi J, et al. Invasive multidrug-resistant non-typhoidal Salmonella infections in Africa: Zoonotic or anthroponotic transmission? J Med Microbiol. 2006 May;55(5):585–91.

112. Geffers C, Farr BM. Risk of transmission of nosocomial methicillin-resistant Staphylococcus aureus (MRSA) from patients colonized with MRSA. Vol. 26, Infection control and hospital epidemiology. United States; 2005. p. 114–5.

113. Martinez JA, Ruthazer R, Hansjosten K, Barefoot L, Snydman DR. Role of environmental contamination as a risk factor for acquisition of vancomycin-resistant enterococci in patients treated in a medical intensive care unit. Arch Intern Med. 2003 Sep;163(16):1905–12.

114. Salm F, Deja M, Gastmeier P, Kola A, Hansen S, Behnke M, et al. Prolonged outbreak of clonal MDR Pseudomonas aeruginosa on an intensive care unit: Contaminated sinks and contamination of ultra-filtrate bags as possible route of transmission? Antimicrob Resist Infect Control. 2016;5(1):53.

115. Leistner R, Meyer E, Gastmeier P, Pfeifer Y, Eller C, Dem P, et al. Risk factors associated with the community-acquired colonization of extended-spectrum beta-lactamase (ESBL) positive Escherichia Coli. an exploratory case-control study. PLoS One. 2013;8(9):e74323.

116. Nadimpalli M, Vuthy Y, de Lauzanne A, Fabre L, Criscuolo A, Gouali M, et al. Meat and Fish as Sources of Extended-Spectrum beta-Lactamase-Producing Escherichia coli, Cambodia. Emerg Infect Dis. 2019 Jan;25(1).

117. Samore MH, Tonnerre C, Hannah EL, Stoddard GJ, Borotkanics RJ, Haddadin B, et al. Impact of outpatient antibiotic use on carriage of ampicillin-resistant Escherichia coli. Antimicrob Agents Chemother. 2011 Mar;55(3):1135–41.

118. Börjesson S, Ny S, Egervärn M, Bergström J, Rosengren Å, Englund S, et al. Limited dissemination of extended-spectrum β-lactamase–and plasmid-encoded AmpC–producing escherichia coli from food and farm animals, sweden. Emerg Infect Dis. 2016 Apr;22(4):634–40.

119. Sorensen TL, Blom M, Monnet DL, Frimodt-Moller N, Poulsen RL, Espersen F. Transient intestinal carriage after ingestion of antibiotic-resistant Enterococcus faecium from chicken and pork. N Engl J Med. 2001 Oct;345(16):1161–6.

120. Duckro AN, Blom DW, Lyle EA, Weinstein RA, Hayden MK. Transfer of vancomycin-resistant enterococci via health care worker hands. Arch Intern Med. 2005 Feb;165(3):302–7.

121. Kotay S, Chai W, Guilford W, Barry K, Mathers AJ. Spread from the sink to the patient: In situ study using green fluorescent protein (GFP)-expressing Escherichia coli to model bacterial dispersion from hand-washing sink-trap reservoirs. Appl Environ Microbiol. 2017 Apr;83(8).

122. Habteselassie MY, Bischoff M, Applegate B, Reuhs B, Turco RF. Understanding the role of agricultural practices in the potential colonization and contamination by Escherichia coli in the rhizospheres of fresh produce. J Food Prot. 2010 Nov;73(11):2001–9.

123. Samore MH, Magill MK, Alder SC, Severina E, Morrison-De Boer L, Lyon JL, et al. High rates of multiple antibiotic resistance in Streptococcus pneumoniae from healthy children living in isolated

rural communities: association with cephalosporin use and intrafamilial transmission. Pediatrics. 2001 Oct;108(4):856–65.

124. Stewardson AJ, Vervoort J, Adriaenssens N, Coenen S, Godycki-Cwirko M, Kowalczyk A, et al. Effect of outpatient antibiotics for urinary tract infections on antimicrobial resistance among commensal Enterobacteriaceae: a multinational prospective cohort study. Clin Microbiol Infect. 2018 Sep;24(9):972–9.

125. Paltansing S, Vlot JA, Kraakman MEM, Mesman R, Bruijning ML, Bernards AT, et al. Extended-spectrum beta-lactamase-producing enterobacteriaceae among travelers from the Netherlands. Emerg Infect Dis. 2013 Aug;19(8):1206–13.

126. Garcia-Graells C, Antoine J, Larsen J, Catry B, Skov R, Denis O. Livestock veterinarians at high risk of acquiring methicillin-resistant Staphylococcus aureus ST398. Epidemiol Infect. 2012 Mar;140(3):383–9.

127. Lo W-T, Lin W-J, Tseng M-H, Wang S-R, Wang C-C. Dissemination of Methicillin-resistant Staphylococcus aureus among Healthy Children in Northern Taiwan. J Med Sci. 2010 Jan 1;30.

128. Lu PL, Tsai JC, Chiu YW, Chang FY, Chen YW, Hsiao CF, et al. Methicillin-resistant Staphylococcus aureus carriage, infection and transmission in dialysis patients, healthcare workers and their family members. Nephrol Dial Transplant. 2008 May;23(5):1659–65.

129. Neyra RC, Frisancho JA, Rinsky JL, Resnick C, Carroll KC, Rule AM, et al. Multidrug-resistant and methicillin-resistant Staphylococcus aureus (MRSA) in hog slaughter and processing plant workers and their community in North Carolina (USA). Environ Health Perspect. 2014 May;122(5):471–7.

130. Würtz ET, Bønløkke JH, Urth TR, Larsen J, Islam MZ, Sigsgaard T, et al. No apparent transmission of livestock-associated methicillin-resistant Staphylococcus aureus CC398 in a survey of staff at a regional Danish hospital. Antimicrob Resist Infect Control. 2017;6(1):126.

131. Baran JJ, Ramanathan J, Riederer KM, Khatib R. Stool colonization with vancomycin-resistant enterococci in healthcare workers and their households. Infect Control Hosp Epidemiol. 2002 Jan;23(1):23–6.

132. Maree CL, Eells SJ, Tan J, Bancroft EA, Malek M, Harawa NT, et al. Risk factors for infection and colonization with community-associated methicillin-resistant Staphylococcus aureus in the

Los Angeles County jail: a case-control study. Clin Infect Dis. 2010 Dec;51(11):1248–57.

133. Nilsson P, Laurell MH. Carriage of penicillin-resistant Streptococcus pneumoniae by children in day-care centers during an intervention program in Malmo, Sweden. Pediatr Infect Dis J. 2001 Dec;20(12):1144–9.

134. Rackham D, Ray S, Franks A, Bielak K, Pinn T. Community-Associated methicillin-resistant staphylococcus aureus nasal carriage in a college student athlete population. Clin J Sport Med. 2010 May;20(3):185–8.

135. Groat EF, Williams NJ, Pinchbeck G, Simpson A, Schmidt VM. Canine raw meat diets and antimicrobial resistant E. coli: is there a link? BSAVA Congr Proc 2016 [Internet]. 2018;57:540–540. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L617436536

136. Olkkola S, Kovanen S, Roine J, Hanninen M-L, Hielm-Bjorkman A, Kivisto R. Population Genetics and Antimicrobial Susceptibility of Canine Campylobacter Isolates Collected before and after a Raw Feeding Experiment. PLoS One. 2015;10(7):e0132660.

137. Fukuda A, Usui M, Okamura M, Dong-Liang H, Tamura Y. Role of Flies in the Maintenance of Antimicrobial Resistance in Farm Environments. Microb Drug Resist. 2019;25(1):127–32.

138. Barbarin AM, Hu B, Nachamkin I, Levy MZ. Colonization of Cimex lectularius with methicillin-resistant Staphylococcus aureus. Vol. 16, Environmental microbiology. England; 2014. p. 1222–4.

139. Lis DO, Pacha JZ, Idzik D. Methicillin resistance of airborne coagulase-negative staphylococci in homes of persons having contact with a hospital environment. Am J Infect Control. 2009 Apr;37(3):177–82.

140. Kennedy M, Ramsheh MY, Williams CML, Auty J, Haldar K, Abdulwhhab M, et al. Face mask sampling reveals antimicrobial resistance genes in exhaled aerosols from patients with chronic obstructive pulmonary disease and healthy volunteers. BMJ Open Respir Res. 2018;5(1):e000321.

141. Thom KA, Johnson JK, Lee MS, Harris AD. Environmental contamination because of multidrug-resistant Acinetobacter baumannii surrounding colonized or infected patients. Am J Infect Control. 2011 Nov;39(9):711–5.

142. Bures S, Fishbain JT, Uyehara CFT, Parker JM, Berg BW. Computer keyboards and faucet handles as reservoirs of nosocomial pathogens in the intensive care unit. Am J Infect Control.

2000 Dec;28(6):465–71.

143. Shahbazian JH, Hahn PD, Ludwig S, Ferguson J, Baron P, Christ A, et al. Multidrug and mupirocin resistance in environmental methicillin-resistant Staphylococcus aureus (MRSA) isolates from homes of people diagnosed with community-onset MRSA infection. Appl Environ Microbiol. 2017 Nov;83(22).

144. Levin AS, Gobara S, Mendes CMF, Cursino MR, Sinto S. Environmental Contamination by Multidrug-Resistant Acinetobacter baumannii in an Intensive Care Unit . Infect Control Hosp Epidemiol. 2001 Nov;22(11):717–20.

145. Zimbudzi E, Stuart RL, Korman TM, Kotsanas D. Contamination of renal patients' hospital chart covers with vancomycin-- resistant enterococci: Handle with care. Australas Med J. 2011;4(10):538–41.

146. Chalfine A, Kitzis M-D, Bezie Y, Benali A, Perniceni L, Nguyen J-C, et al. Ten-year decrease of acquired methicillin-resistant Staphylococcus aureus (MRSA) bacteremia at a single institution: the result of a multifaceted program combining cross-transmission prevention and antimicrobial stewardship. Antimicrob Resist Infect Control. 2012;1(1):18.

147. Duggal S, Kaur N, Hans C. An investigation of MRSA from the burns ward: The importance of hand hygiene. J Clin Diagnostic Res [Internet]. 2011;5(3):476–9. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L361974465

148. Batra R, Cooper BS, Whiteley C, Patel AK, Wyncoll D, Edgeworth JD. Efficacy and Limitation of a Chlorhexidine-Based Decolonization Strategy in Preventing Transmission of Methicillin-Resistant Staphylococcus aureus in an Intensive Care Unit . Clin Infect Dis [Internet]. 2010;50(2):210–7. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L358066902 http://dx.doi.org/10.1086/648717

149. D'Agata EM, Horn MA, Webb GF. The impact of persistent gastrointestinal colonization on the transmission dynamics of vancomycin-resistant enterococci. J Infect Dis. 2002;185(6):766–73.

150. Perencevich EN, Fisman DN, Lipsitch M, Harris AD, Morris, Jr. JG, Smith DL. Projected Benefits of Active Surveillance for Vancomycin-Resistant Enterococci in Intensive Care Units. Clin Infect Dis. 2004;38(8):1108–15.

151. Montecalvo MA, Jarvis WR, Uman J, Shay DK, Petrullo C, Rodney K, et al. Infection-control measures reduce transmission of vancomycin-resistant enterococci in an endemic setting. Ann Intern Med. 1999;131(4):269–72.

152. Coleman BL, Louie M, Salvadori MI, McEwen SA, Neumann N, Sibley K, et al. Contamination of Canadian private drinking water sources with antimicrobial resistant Escherichia coli. Water Res. 2013;47(9):3026–36.

153. Caudell MA, Mair C, Subbiah M, Matthews L, Quinlan RJ, Quinlan MB, et al. Identification of risk factors associated with carriage of resistant Escherichia coli in three culturally diverse ethnic groups in Tanzania: a biological and socioeconomic analysis. Lancet Planet Heal. 2018;2(11):e489–97.

154. Moodley A, Latronico F, Guardabassi L. Experimental colonization of pigs with methicillin-resistant Staphylococcus aureus (MRSA): insights into the colonization and transmission of livestock-associated MRSA. Epidemiol Infect. 2011;139(10):1594–600.

155. Corrò M, Skarin J, Börjesson S, Rota A. Occurrence and characterization of methicillin-resistant Staphylococcus pseudintermedius in successive parturitions of bitches and their puppies in two kennels in Italy. BMC Vet Res. 2018;14(1):308.

156. Tameliene R, Barčaite E, Stoniene D, Buinauskiene J, Markuniene E, Kudrevičiene A, et al. Escherichia coli colonization in neonates: Prevalence, perinatal transmission, antimicrobial susceptibility, and risk factors. Med. 2012;48(2):71–6.

157. Denkel LA, Schwab F, Kola A, Leistner R, Garten L, von Weizsäcker K, et al. The mother as most important risk factor for colonization of very low birth weight (VLBW) infants with extended-spectrum b-lactamase-producing Enterobacteriaceae (ESBL-E). J Antimicrob Chemother [Internet]. 2014;69(8):2230–7. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L373579825 http://dx.doi.org/10.1093/jac/dku097

158. Bourgeois-Nicolaos N, Lucet JC, Daubié C, Benchaba F, Rajguru M, Ruimy R, et al. Maternal vaginal colonisation by Staphylococcus aureus and newborn acquisition at delivery. Paediatr Perinat Epidemiol [Internet]. 2010;24(5):488–91. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L359285405 http://dx.doi.org/10.1111/j.1365-3016.2010.01139.x

159. Chua KB, Ngeow YF, Ng KB, Chye JK, Lim CT. Ureaplasma urealyticum and Mycoplasma hominis isolation from cervical secretions of pregnant women and nasopharyngeal secretions of their babies at delivery. Singapore Med J [Internet]. 1998;39(7):300–2. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L28454895

160. Jiménez-Rámila C, López-Cerero L, Aguilar Martín M V., Vera Martín C, Serrano L, Pascual, et al. Vagino-rectal colonization and maternal–neonatal transmission of Enterobacteriaceae producing extended-spectrum β-lactamases or carbapenemases: a cross-sectional study. J Hosp Infect. 2019;101(2):167–74.

161. Kothari C, Gaind R, Singh LC, Sinha A, Kumari V, Arya S, et al. Community acquisition of beta-lactamase producing Enterobacteriaceae in neonatal gut. BMC Microbiol. 2013;17(13):136.

162. Morel AS, Wu F, Della-Latta P, Cronquist A, Rubenstein D, Saiman L. Nosocomial transmission of methicillin-resistant Staphylococcus aureus from a mother to her preterm quadruplet infants. Am J Infect Control. 2002;30(3):170–3.

163. Peretz A, Skuratovsky A, Khabra E, Adler A, Pastukh N, Barak S, et al. Peripartum maternal transmission of extended-spectrum β-lactamase organism to newborn infants. Diagn Microbiol Infect Dis [Internet]. 2017;87(2):168–71. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L613873082 http://dx.doi.org/10.1016/j.diagmicrobio.2016.11.004

164. Kurita H, Kurashina K, Honda T. Nosocomial transmission of methicillin-resistant Staphylococcus aureus via the surfaces of the dental operatory. Br Dent J. 2006;201(5):297–300.

165. Zhou ZY, Hu BJ, Gao XD, Bao R, Chen M, Li HY. Sources of sporadic Pseudomonas aeruginosa colonizations/infections in surgical ICUs: Association with contaminated sink trap. J Infect Chemother [Internet]. 2016;22(7):450–5. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L610371805 http://dx.doi.org/10.1016/j.jiac.2016.03.016

166. Rubini S, Ravaioli C, Previato S, D'Incau M, Tassinari M, Guidi E, et al. Prevalence of Salmonella strains in wild animals from a highly populated area of north-eastern Italy. Ann Ist Super Sanita. 2016;52(2):277–80.

167. Wielders CCH, van Hoek AHAM, Hengeveld PD, Veenman C, Dierikx CM, Zomer TP, et al. Extended-spectrum β-lactamase- and pAmpC-producing Enterobacteriaceae among the

general population in a livestock-dense area. Clin Microbiol Infect [Internet]. 2017 Feb 1;23(2):120.e1-120.e8. Available from: https://doi.org/10.1016/j.cmi.2016.10.013

168. Reynaga E, Torres C, Garcia-Nuñez M, Navarro M, Vilamala A, Puigoriol E, et al. Clinical impact and prevalence of MRSA CC398 and differences between MRSA-TetR and MRSA-TetS in an area of Spain with a high density of pig farming: a prospective cohort study. Clin Microbiol Infect. 2017;23(9):678.e1-678.e4.

169. Diercke M, Rocker D, Köck R, Pulz M. Livestock-associated methicillin-resistant Staphylococcus aureus in patients admitted to hospitals in the Ems-Dollart-Region, 2011. Int J Med Microbiol [Internet]. 2012;302:138–9. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L70938327 http://dx.doi.org/10.1016/j.ijmm.2012.08.002

170. Founou LL, Founou RC, Essack SY, Djoko CF. Mannitol-fermenting methicillin-resistant staphylococci (MRS) in pig abattoirs in Cameroon and South Africa: A serious food safety threat. Int J Food Microbiol. 2018;285:50–60.

171. Jayaweera JAAS, Kumbukgolla WW. Antibiotic resistance patterns of methicillin-resistant Staphylococcus aureus (MRSA) isolated from livestock and associated farmers in Anuradhapura, Sri Lanka. Germs. 2017;7(3):132–9.

172. Dohmen W, Bonten MJM, Bos MEH, van Marm S, Scharringa J, Wagenaar JA, et al. Carriage of extended-spectrum beta-lactamases in pig farmers is associated with occurrence in pigs. Clin Microbiol Infect. 2015 Oct;21(10):917–23.

173. Mascaro V, Leonetti M, Nobile CGA, Barbadoro P, Ponzio E, Recanatini C, et al. Prevalence of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) among farm and slaughterhouse workers in Italy. J Occup Environ Med. 2018;60(8):E416–25.

174. Moodley A, Nightingale EC, Stegger M, Nielsen SS, Skov RL, Guardabassi L. High risk for nasal carriage of methicillin-resistant Staphylococcus aureus among Danish veterinary practitioners. Scand J Work Environ Heal. 2008;34(2):151–7.

175. Rasamiravaka T, Nirinarimanana AJ, Rasamindrakotroka A. Evaluation of methicillin-resistant Staphylococcus Aureus nasal carriage in malagasy veterinary students: MRSA nasal carriage inmalagasy veterinary students. African J Clin Exp Microbiol [Internet]. 2016;17(4):250–5. Available from:

http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L611514485 http://dx.doi.org/10.4314/ajcem.v17i4.5

176. Rosenberg Goldstein RE, Micallef SA, Gibbs SG, He X, George A, Sapkota A, et al. Occupational exposure to Staphylococcus aureus and Enterococcus spp. among spray irrigation workers using reclaimed water. Int J Environ Res Public Health. 2014;11(4):4340–55.

177. van Rijen MM, Van Keulen PH, Kluytmans JA. Increase in a Dutch hospital of methicillin-resistant Staphylococcus aureus related to animal farming. Clin Infect Dis. 2008;46(2):261–3.

178. Ye X, Fan Y, Wang X, Liu W, Yu H, Zhou J, et al. Livestock-associated methicillin and multidrug resistant S. aureus in humans is associated with occupational pig contact, not pet contact. Sci Rep. 2016;6(6):19184.

179. Ye X, Wang X, Fan Y, Peng Y, Li L, Li S, et al. Genotypic and Phenotypic Markers of Livestock-Associated Methicillin-Resistant Staphylococcus aureus CC9 in Humans. Appl Env Microbiol. 2016;82(13):3892–9.

180. Price LB, Graham JP, Lackey LG, Roess A, Vailes R, Silbergeld E. Elevated risk of carrying gentamicin-resistant escherichia coli among U.S. poultry workers. Environ Health Perspect. 2007;115(12):1738–42.

181. Trung NV, Matamoros S, Carrique-Mas JJ, Nghia NH, Nhung NT, Chieu TTB, et al. Zoonotic transmission of mcr-1 colistin resistance gene from small-scale poultry farms, Vietnam. Emerg Infect Dis. 2017;23(3):529–32.

182. Moser KA, Zhang L, Spicknall I, Braykov NP, Levy K, Marrs CF, et al. The Role of Mobile Genetic Elements in the Spread of Antimicrobial-Resistant Escherichia coli from Chickens to Humans in Small-Scale Production Poultry Operations in Rural Ecuador. Am J Epidemiol. 2018;187(3):558–67.

183. Wardyn SE, Forshey BM, Farina SA, Kates AE, Nair R, Quick MK, et al. Swine farming is a risk factor for infection with and high prevalence of carriage of multidrug-resistant staphylococcus aureus. Clin Infect Dis. 2015;61(1):59–66.

184. Rinsky JL, Nadimpalli M, Wing S, Hall D, Baron D, Price LB, et al. Livestock-Associated Methicillin and Multidrug Resistant Staphylococcus aureus Is Present among Industrial, Not Antibiotic-Free Livestock Operation Workers in North Carolina. PLoS One. 2013;8(7):e67641.

185. Hatcher SM, Rhodes SM, Stewart JR, Silbergeld E, Pisanic N, Larsen J, et al. The Prevalence of Antibiotic-Resistant Staphylococcus aureus Nasal Carriage among Industrial Hog Operation Workers, Community Residents, and Children Living in Their Households: North Carolina, USA. Env Heal Perspect. 2017;125(4):560–9.

186. Li L, Chen Z, Guo D, Li S, Huang J, Wang X, et al. Nasal carriage of methicillin-resistant coagulase-negative staphylococci in healthy humans is associated with occupational pig contact in a dose-response manner. Vet Microbiol. 2017;208:231–8.

187. Borgen K, Simonsen GS, Sundsfjord A, Wasteson Y, Olsvik O, Kruse H. Continuing high prevalence of VanA-type vancomycin-resistant enterococci on Norwegian poultry farms three years after avoparcin was banned. J Appl Microbiol. 200AD;89(3):478–85.

188. Fischer J, Hille K, Mellmann A, Schaumburg F, Kreienbrock L, Koeck R. Nasal colonization of pig-exposed persons with Enterobacteriaceae and associated antimicrobial resistance. Int J Med Microbiol [Internet]. 2015;305:93. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L72056533%5Cnhttp://bb2sz3ek3z.search.serialssolutions.com?sid=EMBASE&issn=14384221&id=doi:&atitle=Nasal+colonization+of+pig-exposed+persons+with+Enterobacteriaceae+and+associated+an

189. Frana TS, Beahm AR, Hanson BM, Kinyon JM, Layman LL, Karriker LA, et al. Isolation and Characterization of Methicillin-Resistant Staphylococcus aureus from Pork Farms and Visiting Veterinary Students. PLoS One. 2013;8(1):e53738.

190. Wulf MWH, Sørum M, Van Nes A, Skov R, Melchers WJG, Klaassen CHW, et al. Prevalence of methicillin-resistant Staphylococcus aureus among veterinarians: An international study. Clin Microbiol Infect [Internet]. 2008;14(1):29–34. Available from: https://www.ncbi.nlm.nih.gov/pubmed/17986212

191. Fang HW, Chiang PH, Huang YC. Livestock-associated methicillin-resistant Staphylococcus aureus ST9 in pigs and related personnel in Taiwan. PLoS One [Internet]. 2014;9(2). Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L372555436 http://dx.doi.org/10.1371/journal.pone.0088826

192. Khanna T, Friendship R, Dewey C, Weese JS. Methicillin resistant Staphylococcus aureus colonization in pigs and pig farmers. Vet Microbiol. 2008;128(3–4):298–303.

193. W. W, F. L. Emergence of caMRSA infections in humans caused by MRSA CC398 which has its main reservoir in animals. Int J Med Microbiol [Internet]. 2009;299:105. Available from: http://ovidsp.ovid.com/ovidweb.cgi?T=JS&PAGE=reference&D=emed9&NEWS=N&AN=70139900

194. Cuny C, Abdelbary M, Koeck R, Layer F, Werner G, Witte W. Methicillin resistant Staphylococcus aureus from infections in horses in Germany : Significance for infections in humans. Int J Med Microbiol [Internet]. 2015;305:172. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L72056738%255Cnhttp://bb2sz3ek3z.search.serialssolutions.com?sid=EMBASE&issn=14384221&id=doi:&atitle=Methicillin+resistant+Staphylococcus+aureus+from+infections+in+horses+in+Germany+%253

195. Drougka E, Foka A, Koutinas CK, Jelastopulu E, Giormezis N, Farmaki O, et al. Interspecies spread of Staphylococcus aureus clones among companion animals and human close contacts in a veterinary teaching hospital. A cross-sectional study in Greece. Prev Vet Med. 2016;126:190–8.

196. Oppliger A, Moreillon P, Charrière N, Giddey M, Morisset D, Sakwinska O. Antimicrobial resistance of Staphylococcus aureus strains acquired by pig farmers from pigs. Appl Environ Microbiol. 2012;78(22):8010–4.

197. Nakane K, Kawamura K, Goto K, Arakawa Y. Long-term colonization by blaCTX-M-harboring Escherichia coli in healthy Japanese people engaged in food handling. Appl Environ Microbiol. 2016;82(6):1818–27.

198. Castro A, Santos C, Meireles H, Silva J, Teixeira P. Food handlers as potential sources of dissemination of virulent strains of Staphylococcus aureus in the community. J Infect Public Health. 2016;9(2):153–60.

199. Zurfluh K, Stephan R, Widmer A, Poirel L, Nordmann P, Nüesch HJ, et al. Screening for fecal carriage of MCR-producing Enterobacteriaceae in healthy humans and primary care patients. Antimicrob Resist Infect Control [Internet]. 2017;6(1). Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L614855993 http://dx.doi.org/10.1186/s13756-017-0186-z

200. Cuny C, Arnold P, Hermes J, Eckmanns T, Mehraj J, Schoenfelder S, et al. Occurrence of cfr-mediated multiresistance in staphylococci from veal calves and pigs, from humans at the corresponding farms, and from veterinarians and their family members. Vet Microbiol.

2017;200:88–94.

201. Brennan GI, Abbott Y, Burns A, Leonard F, McManus BA, O'Connell B, et al. The emergence and spread of multiple livestock-associated clonal complex 398 methicillin-resistant and methicillin-susceptible staphylococcus aureus strains among animals and humans in the Republic of Ireland, 2010-2014. PLoS One. 2016;11(2):e0149396.

202. Knetsch CW, Connor TR, Mutreja A, van Dorp SM, ers IM, Browne HP, et al. Whole genome sequencing reveals potential spread of Clostridium difficile between humans and farm animals in the Netherlands, 2002 to 2011. Euro Surveill. 2014;19(45):20954.

203. Lozano C, Aspiroz C, Lasarte JJ, Gomez-Sanz E, Zarazaga M, Torres C. Dynamic of nasal colonization by methicillin-resistant Staphylococcus aureus ST398 and ST1 after mupirocin treatment in a family in close contact with pigs. Comp Immunol Microbiol Infect Dis. 2011;34(1):e1-7.

204. Tzavaras I, Siarkou VI, Zdragas A, Kotzamanidis C, Vafeas G, Bourtzi-Hatzopoulou E, et al. Diversity of vanA-type vancomycin-resistant Enterococcus faecium isolated from broilers, poultry slaughterers and hospitalized humans in Greece. J Antimicrob Chemother. 2012;67(8):1811–8.

205. Kock R, Schaumburg F, Mellmann A, Koksal M, Jurke A, Becker K, et al. Livestock-associated methicillin-resistant Staphylococcus aureus (MRSA) as causes of human infection and colonization in Germany. PLoS One. 2013;8(2):e55040.

206. Wang J, Lin D-C, Guo X-M, Wei H-K, Liu X-Q, Chen X-J, et al. Distribution of the Multidrug Resistance Gene cfr in Staphylococcus Isolates from Pigs, Workers, and the Environment of a Hog Market and a Slaughterhouse in Guangzhou, China. Foodborne Pathog Dis. 2015 Jul;12(7):598–605.

207. Mularoni A, Bertani A, Vizzini G, Gona F, Campanella M, Spada M, et al. Outcome of Transplantation Using Organs from Donors Infected or Colonized with Carbapenem-Resistant Gram-Negative Bacteria. Am J Transplant. 2015;15(10):2674–82.

208. Goldberg E, Bishara J, Lev S, Singer P, Cohen J. Organ transplantation from a donor colonized with a multidrug-resistant organism: A case report. Transpl Infect Dis. 2012;14(3):296–9.

209. Cui M, Wu C, Zhang J, Zhang C, Li R, Wai-Chi Chan E, et al. Distinct mechanisms of acquisition of mcr-1 -bearing plasmid by Salmonella strains recovered from animals and food samples. Sci

Rep. 2017;7(1):13199.

210. Mork RL, Hogan PG, Muenks CE, Boyle MG, Thompson RM, Morelli JJ, et al. Comprehensive modeling reveals proximity, seasonality, and hygiene practices as key determinants of MRSA colonization in exposed households. Pediatr Res. 2018;84(5):668–76.

211. Gandolfi-Decristophoris P, De Benedetti A, Petignat C, Attinger M, Guillaume J, Fiebig L, et al. Evaluation of pet contact as a risk factor for carriage of multidrug-resistant staphylococci in nursing home residents. Am J Infect Control [Internet]. 2012;40(2):128–33. Available from: https://www.ncbi.nlm.nih.gov/pubmed/21824684

212. Morita JE, Fujioka RS, Tice AD, Berestecky J, Sato D, Seifried SE, et al. Survey of methicillin-resistant Staphylococcus aureus (MRSA) carriage in healthy college students, Hawai'i. Hawaii Med J. 2007;66(8):213–5.

213. De Martino L, Lucido M, Mallardo K, Facello B, Mallardo M, Iovane G, et al. Methicillin-resistant staphylococci isolated from healthy horses and horse personnel in Italy. J Vet Diagn Invest. 2010;22(1):77–82.

214. Loncaric I, Brunthaler R, Spergser J. Suspected goat-to-human transmission of methicillin-resistant staphylococcus aureus sequence type 398. J Clin Microbiol [Internet]. 2013;51(5):1625–6. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L368805609 http://dx.doi.org/10.1128/JCM.03052-12

215. Morris DO, Lautenbach E, Zaoutis T, Leckerman K, Edelstein PH, Rankin SC. Potential for pet animals to harbour methicillin-resistant Staphylococcus aureus when residing with human MRSA patients. Zoonoses Public Heal. 2012;59(4):286–93.

216. Boehmer T, Vogler AJ, Thomas A, Sauer S, Hergenroether M, Straubinger RK, et al. Phenotypic characterization and whole genome analysis of extended-spectrum betalactamase-producing bacteria isolated from dogs in Germany. PLoS One [Internet]. 2018;13(10). Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L624555301 http://dx.doi.org/10.1371/journal.pone.0206252

217. Damborg P, Top J, Hendrickx APA, Dawson S, Willems RJL, Guardabassi L. Dogs are a reservoir of ampicillin-resistant Enterococcus faecium lineages associated with human infections. Appl Environ Microbiol. 2009;75(8):2360–5.

218. Gordoncillo MJ, Abdujamilova N, Perri M, Donabedian S, Zervos M, Bartlett PC. Detection of Methicillin-Resistant Staphylococcus aureus (MRSA) in Backyard Pigs and Their Owners, Michigan, USA. Zoonoses Public Health. 2012;59(3):212–6.

219. Van den Eede A, Martens A, Floré K, Denis O, Gasthuys F, Haesebrouck F, et al. MRSA carriage in the equine community: An investigation of horse-caretaker couples. Vet Microbiol. 2013;163(3–4):313–8.

220. Walther B, Hermes J, Cuny C, Wieler LH, Vincze S, Elnaga YA, et al. Sharing more than friendship - nasal colonization with coagulase-positive staphylococci (CPS) and co-habitation aspects of dogs and their owners. PLoS One [Internet]. 2012;7(4). Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L364660931 http://dx.doi.org/10.1371/journal.pone.0035197

221. Shorman M, Al-Tawfiq JA. Risk factors associated with vancomycin-resistant enterococcus in intensive care unit settings in Saudi Arabia. Interdiscip Perspect Infect Dis. 2013;2013:369674.

222. Nseir S, Blazejewski C, Lubret R, Wallet F, Courcol R, Durocher A. Risk of acquiring multidrug-resistant Gram-negative bacilli from prior room occupants in the intensive care unit. Clin Microbiol Infect [Internet]. 2011;17(8):1201–8. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L70195056 http://dx.doi.org/10.1111/j.1469-0691.2010.03238.x http://apac-tc.hosted.exlibrisgroup.com/openurl/61BON/BOND_SERVICES_PAGE?&sid=EMBASE&issn=1198743X&id=doi:10.1111

223. Morales Barroso I, López-Cerero L, Navarro MD, Gutiérrez-Gutiérrez B, Pascual A, Rodríguez-Baño J. Intestinal colonization due to Escherichia coli ST131: Risk factors and prevalence. Antimicrob Resist Infect Control [Internet]. 2018;7(1). Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L624939884 http://dx.doi.org/10.1186/s13756-018-0427-9

224. Torres-Gonzalez P, Cervera-Hernandez ME, Niembro-Ortega MD, Leal-Vega F, Cruz-Hervert LP, Garcia-Garcia L, et al. Factors Associated to Prevalence and Incidence of Carbapenem-Resistant Enterobacteriaceae Fecal Carriage: A Cohort Study in a Mexican Tertiary Care Hospital. PLoS One. 2015;10(10):e0139883.

225. Ben-David D, Masarwa S, Navon-Venezia S, Mishali H, Fridental I, Rubinovitch B, et al.

Carbapenem-Resistant Klebsiella pneumoniae in Post-Acute-Care Facilities in Israel . Infect Control Hosp Epidemiol. 2011;32(9):845–53.

226. Papadimitriou-Olivgeris M, Drougka E, Fligou F, Kolonitsiou F, Liakopoulos A, Dodou V, et al. Risk factors for enterococcal infection and colonization by vancomycin-resistant enterococci in critically ill patients. Infection. 2014;42(6):1013–22.

227. Jiménez-Truque N, Saye EJ, Soper N, Saville BR, Thomsen I, Edwards KM, et al. Association Between Contact Sports and Colonization with Staphylococcus aureus in a Prospective Cohort of Collegiate Athletes. Sport Med [Internet]. 2017;47(5):1011–9. Available from: https://www.ncbi.nlm.nih.gov/pubmed/27577687

228. Fossi Djembi L, Hodille E, Chomat-Jaboulay S, Coudrais S, De Santis N, Gardes S, et al. Factors associated with Vancomycin-resistant Enterococcus acquisition during a large outbreak. J Infect Public Health. 2017;10(2):185–90.

229. Ulstad CR, Solheim M, Berg S, Lindbæk M, Dahle UR, Wester AL. Carriage of ESBL/AmpC-producing or ciprofloxacin non-susceptible Escherichia coli and Klebsiella spp. in healthy people in Norway. Antimicrob Resist Infect Control. 2016;5(1):57.

230. Vading M, Kabir MH, Kalin M, Iversen A, Wiklund S, Nauclér P, et al. Frequent acquisition of low-virulence strains of ESBL-producing Escherichia coli in travellers. J Antimicrob Chemother. 2016;71(12):3548–55.

231. Peirano G, Gregson DB, Kuhn S, Erkooi OG, Nobrega DB, Pitout JDD. Rates of colonization with extended-spectrum beta-lactamase-producing Escherichia coli in Canadian travellers returning from South Asia: a cross-sectional assessment. C Open. 2017;5(4):E850-e855.

232. Macfadden DR, Bogoch II, Brownstein JS, Daneman N, Fisman D, German M, et al. A passage from India: Association between air traffic and reported cases of New Delhi Metallo-beta-lactamase 1 from 2007 to 2012. Travel Med Infect Dis. 2015;13(4):295–9.

233. Epelboin L, Robert J, Tsyrina-Kouyoumdjian E, Laouira S, Meyssonnier V, Caumes E. High Rate of Multidrug-Resistant Gram-Negative Bacilli Carriage and Infection in Hospitalized Returning Travelers: A Cross-Sectional Cohort Study. J Travel Med. 2015;22(5):292–9.

234. Lorme F, Maataoui N, Rondinaud E, Esposito-Farèse M, Clermont O, Ruppe E, et al. Acquisition of plasmid-mediated cephalosporinase producing Enterobacteriaceae after a travel to the tropics.

PLoS One. 2018;13(12):e0206909.

235. Nurjadi D, Friedrich-Jänicke B, Schäfer J, Van Genderen PJJ, Goorhuis A, Perignon A, et al. Skin and soft tissue infections in intercontinental travellers and the import of multi-resistant Staphylococcus aureus to Europe. Clin Microbiol Infect. 2015;21(6):567.e1-567.e10.

236. Ostholm-Balkhed A, Tarnberg M, Nilsson M, Nilsson LE, Hanberger H, Hallgren A, et al. Travel-associated faecal colonization with ESBL-producing Enterobacteriaceae: incidence and risk factors. J Antimicrob Chemother. 2013;68(9):2144–53.

237. Yaita K, Aoki K, Suzuki T, Nakaharai K, Yoshimura Y, Harada S, et al. Epidemiology of extended-spectrum β-lactamase producing Escherichia coli in the stools of returning Japanese travelers, and the risk factors for colonization. PLoS One [Internet]. 2014;9(5). Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L373153348 http://dx.doi.org/10.1371/journal.pone.0098000

238. Sannes MR, Belongia EA, Kieke B, Smith K, Kieke A, Vandermause M, et al. Predictors of Antimicrobial-Resistant Escherichia coli in the Feces of Vegetarians and Newly Hospitalized Adults in Minnesota and Wisconsin . J Infect Dis. 2008;197(3):430–4.

239. Islam S, Selvarangan R, Kanwar N, McHenry R, Chappell JD, Halasa N, et al. Intestinal Carriage of Third-Generation Cephalosporin-Resistant and Extended-Spectrum β-Lactamase-Producing Enterobacteriaceae in Healthy US Children. J Pediatric Infect Dis Soc. 2018;7(3):234–40.

240. Tängdén T, Cars O, Melhus Å, Löwdin E. Foreign travel is a major risk factor for colonization with Escherichia coli producing CTX-M-type extended-spectrum β-lactamases: A prospective study with Swedish volunteers. Antimicrob Agents Chemother [Internet]. 2010;54(9):3564–8. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L359442396 http://dx.doi.org/10.1128/AAC.00220-10

241. Pires J, Kuenzli E, Kasraian S, Tinguely R, Furrer H, Hilty M, et al. Polyclonal intestinal colonization with extended-spectrum cephalosporin-resistant enterobacteriaceae upon traveling to India. Front Microbiol. 2016;7(JUL):1069.

242. Lausch KR, Fuursted K, Larsen CS, Storgaard M. Colonisation with multi-resistant Enterobacteriaceae in hospitalised Danish patients with a history of recent travel: A cross-sectional study. Travel Med Infect Dis. 2013;11(5):320–3.

243. Arcilla MS, van Hattem JM, Haverkate MR, Bootsma MCJ, van Genderen PJJ, Goorhuis A, et al. Import and spread of extended-spectrum β-lactamase-producing Enterobacteriaceae by international travellers (COMBAT study): a prospective, multicentre cohort study. Lancet Infect Dis. 2017;17(1):78–85.

244. Blyth DM, Mende K, Maranich AM, Beckius ML, Harnisch KA, Rosemann CA, et al. Antimicrobial resistance acquisition after international travel in U.S. travelers. Trop Dis Travel Med Vaccines. 2016;2:4.

245. Bevan ER, McNally A, Thomas CM, Piddock LJV, Hawkey PM. Acquisition and loss of CTX-M-producing and non-producing escherichia coli in the fecal microbiome of travelers to South Asia. MBio. 2018;9(6).

246. Lubbert C, Straube L, Stein C, Makarewicz O, Schubert S, Mossner J, et al. Colonization with extended-spectrum beta-lactamase-producing and carbapenemase-producing Enterobacteriaceae in international travelers returning to Germany. Int J Med Microbiol. 2015;305(1):148–56.

247. Nakayama T, Kumeda Y, Kawahara R, Yamaguchi T, Yamamoto Y. Carriage of colistin-resistant, extended-spectrum β-lactamase-producing escherichia coli harboring the mcr-1 resistance gene after short-term international travel to Vietnam. Infect Drug Resist [Internet]. 2018;11:391–5. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L621430027 http://dx.doi.org/10.2147/IDR.S153178

248. Valverde A, Turrientes MC, Norman F, Pérez Molina JA, Coque T, Baquero F, et al. Intestinal Colonisation with multidrug-resistant Enterobacteriaceae in travellers, immigrants and “visiting friends and relatives”: Dominance of E. coli producing CTX-M enzymes. Clin Microbiol Infect [Internet]. 2012;18:763–4. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L70824278 http://dx.doi.org/10.1111/j.1469-0691.2012.03802.x

249. Johnning A, Kristiansson E, Angelin M, Marathe N, Shouche YS, Johansson A, et al. Quinolone resistance mutations in the faecal microbiota of Swedish travellers to India. BMC Microbiol. 2015;15(1):15–85.

250. Sun Q, Tarnberg M, Zhao L, Stalsby Lundborg C, Song Y, Grape M, et al. Varying high levels of faecal carriage of extended-spectrum beta-lactamase producing Enterobacteriaceae in rural

villages in Shandong, China: implications for global health. PLoS One. 2014;9(11):e113121.

251. O’Flaherty E, Solimini AG, Pantanella F, De Giusti M, Cummins E. Human exposure to antibiotic resistant-Escherichia coli through irrigated lettuce. Environ Int. 2019;122:270–80.

252. Dekić S, Klobučar G, Ivanković T, Zanella D, Vucić M, Bourdineaud JP, et al. Emerging human pathogen Acinetobacter baumannii in the natural aquatic environment: a public health risk? Int J Environ Health Res. 2018;28(3):315–22.

253. Goldstein RR, Kleinfelter L, He X, Micallef SA, George A, Gibbs SG, et al. Higher prevalence of coagulase-negative staphylococci carriage among reclaimed water spray irrigators. Sci Total Environ. 2017;595:35–40.

254. Leonard AFC, Zhang L, Balfour AJ, Garside R, Hawkey PM, Murray AK, et al. Exposure to and colonisation by antibiotic-resistant E. coli in UK coastal water users: Environmental surveillance, exposure assessment, and epidemiological study (Beach Bum Survey). Environ Int. 2018;114:326–33.

255. Yang F, Huang L, Li L, Yang Y, Mao D, Luo Y. Discharge of KPC-2 genes from the WWTPs contributed to their enriched abundance in the receiving river. Sci Total Environ [Internet]. 2017;581:136–43. Available from: http://www.embase.com/search/results?subaction=viewrecord&from=export&id=L614013670 http://dx.doi.org/10.1016/j.scitotenv.2016.12.063

Appendix 1.

Search in Pubmed, 20-12-2018

(((((((((((((resistant[Title/Abstract]) OR resistance[Title/Abstract])) AND ((((((bacterial[Title/Abstract]) OR antibiotic[Title/Abstract]) OR drug[Title/Abstract]) OR antibacterial[Title/Abstract]) OR antimicrobial[Title/Abstract]) OR microbial[Title/Abstract]))) OR antibiotic resistance, bacterial[MeSH Terms]))) AND ((((((((acquiring[Title/Abstract]) OR acquisition[Title/Abstract]) OR transmission[Title/Abstract]) OR spread[Title/Abstract]) OR dissemination[Title/Abstract]) OR exposure[Title/Abstract]) OR exposed[Title/Abstract]) OR intake[Title/Abstract]))) AND (((((((colonization[Title/Abstract]) OR colonized[Title/Abstract]) OR colonisation[Title/Abstract]) OR colonised[Title/Abstract]) OR carriage[Title/Abstract]) OR carrying[Title/Abstract])))) NOT ((((((((((((fung*[Title/Abstract]) OR viral[Title/Abstract]) OR virus[Title/Abstract]) OR implant*[Title/Abstract]) OR HIV[Title/Abstract]) OR molecular[Title]) OR cancer[Title/Abstract]) OR tumor[Title/Abstract]) OR tumour[Title/Abstract]) OR neoplasm[Title/Abstract]) OR neoplasms[Title/Abstract])))) AND (((english[Language]) OR dutch[Language]))

Results:4555

After removing dublicates: 4550

Search in Embase, 20-12-2018

(('bacterial':ab,ti OR 'antibiotic':ab,ti OR 'drug':ab,ti OR 'antibacterial':ab,ti OR 'antimicrobial':ab,ti OR 'microbial':ab,ti) AND ('resistant':ab,ti OR 'resistance':ab,ti) OR 'antibiotic resistance'/exp) AND ('acquiring':ab,ti OR 'acquisition':ab,ti OR 'transmission':ab,ti OR 'spread':ab,ti OR 'dissemination':ab,ti OR 'exposure':ab,ti OR 'exposed':ab,ti OR 'intake':ab,ti) AND ('colonization':ab,ti OR 'colonized':ab,ti OR 'colonisation':ab,ti OR 'colonised':ab,ti OR 'carriage':ab,ti OR 'carrying':ab,ti) NOT ('fung*':ab,ti OR 'viral':ab,ti OR 'virus':ab,ti OR 'implant*':ab,ti OR 'hiv':ab,ti OR 'molecular':ti OR 'cancer':ab,ti OR 'tumor':ab,ti OR 'tumour':ab,ti OR 'neoplasm':ab,ti OR 'neoplasms':ab,ti) AND ([dutch]/lim OR [english]/lim)

Results: 5180

After removing duplicates: 5121

After merging results from Pubmed and Embase: 9683 results
After removing duplicates: 6017 results

Appendix 2.

Table A. *Frequencies of each transmission route identified*

Transmission route	Frequency
Air to animal	3
Animal to air	29
Animal to water	2
Animal to animal	13
Animal to environment	8
Breast feeding	17
Contaminated room	4
Contact with infected person	93
Eating meat to human	24
Environment to animal	1
Environment to plant	2
Environment to environment	2
Environment to human	2
Family member colonised	33
Family member with occupational exposure	11
Fomites	12
Food to animal	5
Human to air	6
Human to nearby environment	30
Human to animal	1
Intervention	17
Livestock to drinking water	12
Milk to human	1
Animal mother to child	3
Mother to child during birth	20
Nearby environment to animal	1
Nearby environment to human	4
Nearby farm to human	10
Nearby farm to animal	1
Non-commercial animal keeping	4

Occupation exposure	157
Organ transfer	3
Other: animal to meat of animal	1
Other: bathing/showering	3
Other: crowding	1
Other: antibacterial soap	3
Pet to human	28
Prior colonised patient in room	3
Sharing water source with animals	5
Space sharing	11
Travelling	110
Pre-travel screening : 70	
No pre-travel screening: 40	
Travelling: eating food with local population	1
Contacting foreign healthcare service while travelling	1
Vegetables to human	4
Water to plant	2
Water to animal	1
Water (drinking) to human	6
Water (exposure) to human	5
Total	716

Table B. *Frequencies of bacteria studied for transmission routes included in quantitative synthesis*

Bacteria	Frequencies
Acinetobacter baumannii	26
Acinetobacter calcoaceticus	4
Campylobacter	2
E. coli	159
Enterobacteriaceae (unspecified)[1]	121
Enterococcus faecalis	2
Enterococcus faecium	4
Genes	4
Group B streptococci	6
S. aureus	275
Pseudomonas aeruginosa	13
Salmonella	4
Staphylococcus epidermidis	9
Staphylococcus haemolyticus	5
Staphylococcus pseudintermedius	7
Staphylococci	16
Streptococcus pneumoniae	10
VRE	41
Other[1]	8
Total	716

Notes: [1]*Multiple Enterobacteriaceae or unspecified*, [2]*Enterococci, Mycoplasma hominis, Ureaplasma urealyticum, Klebsiella pneumoniae, Staphylococcus hominis, Staphylococcus cohnii, Klebsiella oxytoca, Haemophilus influenzae*

Appendix 3

Table C. *List of studies of which estimates were included in the qualitative synthesis*

Author	Citation	Title	Transmission route	Bacteria group	Method of estimation
Rosen	(53)	Persistent and Transient Airborne MRSA Colonization of Piglets in a Newly Established Animal Model.	Air to animal	*S. aureus*	Bacteria load
Dierikx	(54)	Dynamics of cefotaxime resistant Escherichia coli in broilers in the first week of life.	Animal to animal	E. coli	Risk
van Duijkeren	(55)	Transmission of methicillin-resistant Staphylococcus pseudintermedius between infected dogs and cats and contact pets, humans and the environment in households and veterinary clinics	Animal to animal, pet to human	Staphylococcus pseudintermedius	Risk
Loeffler	(56)	Lack of transmission of methicillin-resistant Staphylococcus aureus (MRSA) between apparently healthy dogs in a rescue kennel	Animal to animal	*S. aureus*	Risk
Broens	(57)	Quantification of transmission of livestock-associated methicillin resistant Staphylococcus aureus in pigs.	Animal to animal	*S. aureus*	R0
Huijbers	(58)	Transmission dynamics of extended-spectrum β-lactamase and AmpC β-lactamase-producing Escherichia coli in a broiler flock without antibiotic use	Animal to animal, environment to animal	*E. coli*	transmission rate, R0
Riccobono	(59)	Carriage of Antibiotic-Resistant Escherichia coli Among Healthy Children and Home-Raised Chickens: A Household Study in a Resource-Limited Setting	Animal to animal, occupational exposure, contact with infected person	*E. coli*	Genes
Weese	(60)	Suspected transmission of methicillin-resistant Staphylococcus aureus between domestic pets and humans in veterinary clinics and in the household	Animal to animal, pet to human	*S. aureus*	Genes
Windahl	(61)	Colonization with methicillin-resistant Staphylococcus pseudintermedius in multi-dog households: A longitudinal study using whole genome sequencing	Animal to animal	*Staphylococcus pseudintermedius*	Genes
Graveland	(62)	Dynamics of MRSA carriage in veal calves: a longitudinal field study.	Animal to animal, Animal to air	*S. aureus*	transmission rate (week)

Gao	(63)	Emissions of Escherichia coli Carrying Extended-Spectrum β-Lactamase Resistance from Pig Farms to the Surrounding Environment	Animal to environment, animal to air, animal to water	*E. coli*	Risk
Laube	(64)	Transmission of ESBL/AmpC-producing Escherichia coli from broiler chicken farms to surrounding areas.	Animal to environment, animal to air	*E. coli*	Risk
Moodley	(65)	Transmission of IncN plasmids carrying blaCTX-M-1 between commensal Escherichia coli in pigs and farm workers.	Animal to environment, animal to air, occupational exposure	*E. coli*	Risk
Gao	(66)	Application of swine manure on agricultural fields contributes to extended-spectrum β-lactamase-producing Escherichia coli spread in Tai'an, China	Animal to environment	*E. coli*	Genes
Leite-Martins	(67)	Spread of multidrug-resistant Enterococcus faecalis within the household setting.	Animal to environment, occupational exposure	*Enterococcus faecalis*	Genes
Schmithausen	(68)	Analysis of Transmission of MRSA and ESBL-E among Pigs and Farm Personnel	Animal to air, occupational exposure	*S. aureus*, Enterobacteriaceae	Risk
Davis	(69)	Occurrence of Staphylococcus aureus in swine and swine workplace environments on industrial and antibiotic-free hog operations in North Carolina, USA: A One Health pilot study	Animal to air, occupational exposure	*S. aureus*	Risk
Fu	(70)	Aquatic animals promote antibiotic resistance gene dissemination in water via conjugation: Role of different regions within the zebra fish intestinal tract, and impact on fish intestinal microbiota	Animal to water	*E. coli*	Bacteria intake
Parm	(71)	Risk factors associated with gut and nasopharyngeal colonization by common Gram-negative species and yeasts in neonatal intensive care units patients	Breast feeding	Other	OR
Chen	(72)	Factors associated with nasal colonization of methicillin-resistant Staphylococcus aureus among healthy children in Taiwan.	Breast feeding	*S. aureus*	OR
Isendahl	(73)	Fecal carriage of ESBL-producing E. coli and K. pneumoniae in children in Guinea-Bissau: a hospital-based cross-sectional study.	Breast feeding, fomites	Enterobacteriaceae	OR
Hijazi	(74)	Multidrug-resistant ESBL-producing Enterobacteriaceae and associated risk factors in community infants in Lebanon	Breast feeding, pet to human	Enterobacteriaceae	OR
Koliou	(75)	Risk factors for carriage of Streptococcus pneumoniae in children.	Breast feeding	Streptococcus pneumoniae	OR

Nakamura	(76)	Outbreak of extended-spectrum β-lactamase-producing Escherichia coli transmitted through breast milk sharing in a neonatal intensive care unit	Breast feeding	*E. coli*	OR, genes
Nordberg	(77)	High Proportion of Intestinal Colonization with Successful Epidemic Clones of ESBL-Producing Enterobacteriaceae in a Neonatal Intensive Care Unit in Ecuador	Breast feeding	*E. coli*	OR
Ciftçi	(78)	Investigation of risk factors for penicillin-resistant Streptococcus pneumoniae carriage in Turkish children.	Breast feeding, other crowding	Streptococcus pneumoniae	OR
Gastelum	(21)	Transmission of community-associated methicillin-resistant Staphylococcus aureus from breast milk in the neonatal intensive care unit.	Breast feeding, contact with infected person	*S. aureus*	Risk, genes
Benito	(79)	Characterization of Staphylococcus aureus strains isolated from faeces of healthy neonates and potential mother-to-infant microbial transmission through breastfeeding	Breast feeding	*S. aureus*	Genes
Gueimonde	(80)	Presence of specific antibiotic (tet) resistance genes in infant faecal microbiota.	Breast feeding	Genes	Genes
Morgan	(25)	Frequent Multidrug-Resistant Acinetobacter baumannii Contamination of Gloves, Gowns, and Hands of Healthcare Workers	Contact with infected person, space sharing	*Acinetobacter baumannii*	OR, risk
Schwartz-Neiderman	(81)	Risk Factors for Carbapenemase-Producing Carbapenem-Resistant Enterobacteriaceae (CP-CRE) Acquisition Among Contacts of Newly Diagnosed CP-CRE Patients	Contact with infected person, space sharing	Enterobacteriaceae	OR
Nerby	(15)	Risk factors for household transmission of community-associated methicillin-resistant Staphylococcus aureus	Contact with infected person, space sharing, other soap, fomites, family member colonized,	*S. aureus*, VRE	OR, genes
Grabsch	(82)	Risk of Environmental and Healthcare Worker Contamination With Vancomycin-Resistant Enterococci During Outpatient Procedures and Hemodialysis	Contact with infected person, human to nearby environment	VRE	Risk
Snyder	(17)	Detection of methicillin-resistant Staphylococcus aureus and vancomycin-resistant enterococci on the gowns and gloves of healthcare workers.	Contact with infected person	*S. aureus*, VRE	Risk
El Shafie	(83)	Investigation of an outbreak of multidrug-resistant *Acinetobacter baumannii* in trauma intensive care unit	Contact with infected person, human to nearby environment	*Acinetobacter baumannii*	Risk

Senn	(18)	The Stealthy Superbug: the Role of Asymptomatic Enteric Carriage in Maintaining a Long-Term Hospital Outbreak of ST228 Methicillin-Resistant Staphylococcus aureus.	Contact with infected person	*S. aureus*	Risk
Rydberg	(84)	Intrafamilial spreading of Escherichia coli resistant to trimethoprim	Contact with infected person	*E. coli*	Risk, genes
Frénay	(19)	Long-term carriage, and transmission of methicillin-resistant Staphylococcus aureus after discharge from hospital.	Contact with infected person	*S. aureus*	Risk
McBryde	(20)	An investigation of contact transmission of methicillin-resistant Staphylococcus aureus	Contact with infected person	*S. aureus*	Risk
Jackson	(85)	Bacterial burden is associated with increased transmission to health care workers from patients colonized with vancomycin-resistant Enterococcus	Contact with infected person	VRE	Risk
Mutters	(52)	Low risk of apparent transmission of vancomycin-resistant Enterococci from bacteraemicpatients to hospitalized contacts.	Contact with infected person	VRE	Risk, genes
Schaumburg	(34)	Transmission of Staphylococcus aureus between mothers and infants in an African setting	Family member colonized, mother to child	*S. aureus*	Risk^{rs}, OR^{rs}
Tandé	(30)	Intrafamilial transmission of extended-spectrum-beta-lactamase-producing Escherichia coli and Salmonella enterica Babelsberg among the families of internationally adopted children.	Family member colonized	Enterobacteriaceae	Risk, genes
Torres	(86)	Prevalence and transmission dynamics of Escherichia coli ST131 among contacts of infected community and hospitalized patients.	Contact with infected person	*E. coli*	Risk
Zhou	(87)	Factors Associated with acquisition of vancomycin-resistant Enterococci(VRE) in roommate contacts of patients colonized or infected with VRE in a tertiary care hospital	Contact with infected person	VRE	Risk
Hedin	(88)	Multiply antibiotic-resistant *Staphylococcus epidermidis* in patients, staff and environment- a one-week survey in a bone marrow transplant unit.	Contact with infected person, human to air	*Staphylococcus epidermidis*	Risk
Pierce	(22)	Methicillin-resistant *Staphyloccus areus* (MRSA) acquisition risk in an endemic neonatal intensive care unit with an active surveillance culture and decolonization programme	Contact with infected person	*S. aureus*	RR
Calfee	(23)	Spread of methicillin-resistant Staphylococcus aureus (MRSA) among household contacts of individuals with nosocomially acquired MRSA.	Contact with infected person	*S. aureus*	RR

Domenech de Cellès	(89)	Identifying more epidemic clones during a hospital outbreak of multidrug-resistant *Acinetobacter baumannii*	Contact with infected person	*Acinetobacter baumannii*	R0
Christopher	(90)	Transmission dynamics of methicillin-resistant *Staphylococcus aureus* in a medical intensive care unit in India	Contact with infected person	*S. aureus*	R0
Austin	(91)	Vancomycin-resistant enterococci in intensive-care hospital settings: transmission dynamics, persistence, and the impact of infection control programs.	Contact with infected person	VRE	R0
Plipat	(92)	The dynamics of methicillin-resistant Staphylococcus aureus exposure in a hospital model and the potential for environmental intervention.	Contact with infected person, Nearby environment to human	*S. aureus*	Importance of Route
Mikolajczyk	(93)	Mixture model to assess the extent of cross-transmission of multidrug-resistant pathogens in hospitals	Contact with infected person	*S. aureus*, *Acinetobacter baumannii*, Pseudomonas aeruginosa	Importance of Route
Cheah	(94)	Mathematical modelling of vancomycin-resistant enterococci transmission during passive surveillance and active surveillance with contact isolation highlights the need to identify and address the source of acquisition	Contact with infected person	VRE	Importance of Route
Cooper	(95)	Quantifying type-specific reproduction numbers for nosocomial pathogens: evidence for heightened transmission of an Asian sequence type 239 MRSA clone	Contact with infected person	*S. aureus*	acquisition rate
Domenech de Cellès	(96)	Intrinsic epidemicity of Streptococcus pneumoniae depends on strain serotype and antibiotic susceptibility pattern	Contact with infected person	Streptococcus pneumoniae	transmission rate
Forrester	(97)	Use of stochastic epidemic modeling to quantify transmission rates of colonization with methicillin-resistant Staphylococcus aureus in an intensive care unit	Contact with infected person, nearby environment to human	*S. aureus*	cases per day
Forrester	(98)	Bayesian inference of hospital-acquired infections and control measures given imperfect surveillance data	Contact with infected person	*S. aureus*	cases per day
Hetem	(99)	Nosocomial transmission of community-associated methicillin-resistant Staphylococcus aureus in Danish Hospitals	Contact with infected person, nearby environment to human	*S. aureus*	R0
Mikolajczyk	(100)	A statistical method for estimating the proportion of cases resulting from cross-transmission of multi-resistant pathogens in an intensive care unit.	Contact with infected person	*S. aureus*, Pseudomonas aeruginosa	Importance of Route

Simon	(101)	Modeling bacterial colonization and infection routes in health care settings: analytic and numerical approaches.	Contact with infected person	*S. aureus*	R0
López-García	(102)	A unified stochastic modelling framework for the spread of nosocomial infections	Contact with infected person, human to nearby environment	*S. aureus*, VRE	R0
McBryde	(103)	A stochastic mathematical model of methicillin resistant Stap hylococcus aureus transmission in an intensive care unit: predicting the impact of interventions	Contact with infected person	*S. aureus*	R0, transmission rate
Pelupessy	(2)	How to assess the relative importance of different colonization routes of pathogens within hospital settings	Contact with infected person	VRE, Pseudomonas aeruginosa	transmission rate
Wang	(104)	Modeling nosocomial infections of methicillin-resistant *Staphylococcus aureus* with environment contamination	Contact with infected person	*S. aureus*	R0, transmission rate
Lo	(8)	Fecal carriage of CTXM type extended-spectrum beta-lactamase-producing organisms by children and their household contacts.	Family member colonize, contact with infected person	Enterobacteriaceae	Genes
Givon-Lavi	(105)	Spread of Streptococcus pneumoniae and antibiotic-resistant S. pneumoniae from day-care center attendees to their younger siblings	Family member colonized	Streptococcus pneumoniae	Genes^{rs}
Alam	(37)	Transmission and Microevolution of USA300 MRSA in U.S. Households: Evidence from Whole-Genome Sequencing	Family member colonized	*S. aureus*	Genes
Alves	(9)	Extended-spectrum beta-lactamase-producing Enterobacteriaceae in the intensive care unit: acquisition does not mean cross-transmission	Contact with infected person	Enterobacteriaceae	Genes
Chidekel	(36)	Nasopharyngeal colonization in children with cystic fibrosis: Antibiotic resistance and intrafamilial spread	Family member colonized	*S. aureus*, Streptococcus pneumoniae, other	Genes^{rs}
Cochard	(10)	Extended-spectrum β-lactamase-producing Enterobacteriaceae in French nursing homes: an association between high carriage rate among residents, environmental contamination, poor conformity with good hygiene practice, and putative resident-to-resident trans	Contact with infected person, human to nearby environment	Enterobacteriaceae	Genes
Crombach	(24)	Control of an epidemic spread of a multi-resistant strain of *Acinetobacter calcoaceticus* in a hospital	Contact with infected person, human to air, human to nearby environment	Acinetobacter calcoaceticus	Genes

Davis	(38)	Genome sequencing reveals strain dynamics of methicillin-resistant *Staphylococcus aureus* in the same household in the context of clinical disease in a person and a dog	Family member colonized, pet to human, nearby environment to animal	*S. aureus*	Genes
Cuny	(11)	Nasal colonization of humans with methicillin-resistant *Staphylococcus aureus* (MRSA) CC398 with and without exposure to pigs	Contact with infected person	*S. aureus*	Genes
Eveillard	(39)	Carriage of methicillin-resistant *Staphylococcus aureus* among hospital employees: prevalence, duration, and transmission to households	Family member colonized	*S. aureus*	Genes
Griffith	(26)	The epidemiology of *Pseudomonas aeruginosa* in oncology patients in a general hospital	Contact with infected person, environment to human	*Pseudomonas aeruginosa*	Genes
Gustafsson	(12)	MRSA in children from foreign countries adopted to Swedish families	Family member colonized	*S. aureus*	Genes
Henriqus Normark	(106)	Clonal analysis of *Streptococcus pneumoniae* nonsusceptible to penicillin at day-care centers with index cases, in a region with low incidence of resistance: emergence of an invasive type 35B clone among carriers	Contact with infected person	Streptococcus pneumoniae	Genes
Johansson	(13)	High prevalence of MRSA in household contacts.	Family member colonized	*S. aureus*	Genes
Johnson	(107)	The role of patient-to-patient transmission in the acquisition of imipenem-resistant *Pseudomonas aeruginosa* colonization in the intensive care unit	Contact with infected person	Pseudomonas aeruginosa	Genes
Kojima	(108)	Spread of CTX-M-15 Extended-Spectrum-Lactamase-Producing *Escherichia coli* isolates through household contact and plasmid transfer	Contact with infected person	*E. coli*	Genes
Maataoui	(109)	High acquisition rate of extended-spectrum β-lactamase-producing Enterobacteriaceae among French military personnel on mission abroad, without evidence of inter-individual transmission.	Contact with infected person, travelling $^{+}$	*E. coli*	Genes, OR, risk
McCallum	(42)	Spread of an epidemic *Pseudomonas aeruginosa* strain from a patient with cystic fibrosis (CF) to non-CF relatives	Family member colonized	Pseudomonas aeruginosa	Genes
Mitsuda	(14)	The influence of methicillin-resistant *Staphylococcus aureus* (MRSA) carriers in a nursery and transmission of MRSA to their households	Contact with infected person, family member colonized	*S. aureus*	Genes

Ozaki	(40)	Genotypes, intrafamilial transmission, and virulence potential of nasal methicillin-resistant *Staphylococcus aureus* from children in the community.	Contact with infected person, family member colonized	*S. aureus*	Genes
Stone	(110)	Methicillin-resistant *Staphylococcus aureus* (MRSA) nasal carriage in residents of Veterans Affairs long-term care facilities: role of antimicrobial exposure and MRSA acquisition.	Contact with infected person	*S. aureus*	Genes
Toleman	(41)	Systematic surveillance detects multiple silent introductions and household transmission of methicillin-resistant *Staphylococcus aureus* USA300 in the east of England.	Family member colonized	*S. aureus*	Genes
Kariuki	(111)	Invasive multidrug-resistant non-typhoidal Salmonella infections in Africa: zoonotic or anthroponotic transmission?	Contact with infected person, Environment to human	Salmonella	Genes
Geffers	(112)	Risk of Transmission of Nosocomial Methicillin-Resistant Staphylococcus aureus (MRSA) From Patients Colonized With MRSA	Contact with infected person	*S. aureus*	transmission rate
Martínez	(113)	Role of environmental contamination as a risk factor for acquisition of vancomycin-resistant enterococci in patients treated in a medical intensive care unit	Contaminated room	VRE	OR
Salm	(114)	Prolonged outbreak of clonal MDR *Pseudomonas aeruginosa* on an intensive care unit: contaminated sinks and contamination of ultra-filtrate bags as possible route of transmission?	Contaminated room	*Pseudomonas aeruginosa*	OR
Leistner	(115)	Risk factors associated with the community-acquired colonization of extended-spectrum beta-lactamase (ESBL) positive *Escherichia Coli*. an exploratory case-control study.	Eating Meat to human	*E. coli*	OR
Lietzau	(29)	Clustering of antibiotic resistance of *E. coli* in couples: suggestion for a major role of conjugal transmission	Eating Meat to human, family member colonized	*E. coli*	OR
Nadimpalli	(116)	Meat and fish as sources of Extended-Spectrum β-Lactamase–Producing *Escherichia coli*, Cambodia	Eating meat to human, pet to human, vegetables to human	*E. coli*	OR
Samore	(117)	Impact of outpatient antibiotic use on carriage of ampicillin-resistant *Escherichia coli*?	Eating Meat to human, travelling $^{-}$, occupational exposure	*E. coli*	PR

Börjesson	(118)	Limited dissemination of Extended-Spectrum β-Lactamase- and Plasmid-Encoded AmpC-Producing *Escherichia coli* from food and farm animals, Sweden	Eating Meat to human, occupational exposure	*E. coli*	Genes
Sørensen	(119)	Transient intestinal carriage after ingestion of antibiotic-resistant Enterococcus faecium from chicken and pork.	Eating Meat to human	Enterococcus faecium	Bacteria intake
Duckro	(120)	Transfer of vancomycin-resistant enterococci via health care worker hands	Environment to environment, human to nearby environment	VRE	Risk
Kotay	(121)	Spread from the sink to the patient: In situ study using green fluorescent protein (GFP)- expressing *Escherichia coli* to model bacterial dispersion from hand-washing sink-trap reservoirs	Environment to environment	*E. coli*	Bacteria intake
Habteselassie	(122)	Understanding the role of agricultural practices in the potential colonization and contamination by *Escherichia coli* in the rhizospheres of fresh produce	Environment to Plant, water to Plant	*E. coli*	Bacteria intake
Ferreira	(31)	Transmission of MRSA between companion animals and infected human patients presenting to outpatient medical care facilities	Family member colonized	*S. aureus*	OR
Fornasini	(28)	Trimethoprim-resistant *Escherichia coli* in households of children attending day care centers.	Family member colonized	*E. coli*	OR
Samore	(123)	High rates of multiple antibiotic resistance in Streptococcus pneumoniae from healthy children living in isolated rural communities: association with cephalosporin use and intrafamilial transmission.	Family member colonized	Streptococcus pneumoniae	OR
Cluzet	(32)	Risk factors for recurrent colonization with methicillin-resistant *Staphylococcus aureus* in community-dwelling adults and children	Family member colonized	*S. aureus*	OR
Stewardson	(124)	Effect of outpatient antibiotics for urinary tract infections on antimicrobial resistance among commensal Enterobacteriaceae: a multinational prospective cohort study.	Family member colonized, travelling $^-$	Enterobacteriaceae	PR
Paltansing	(125)	Extended-spectrum β-lactamase-producing Enterobacteriaceae among travelers from the Netherlands.	Family member colonized, travelling $^+$	*E. coli*	Risk
Zetsma	(35)	Carrier state and spread of methicillin resistant *Staphylococcus aureus* following hospital discharge	Family member colonized, pet to human	*S. aureus*	Risk

Garcia-Graells	(126)	Livestock veterinarians at high risk of acquiring methicillin-resistant *Staphylococcus aureus* ST398	Family member occupational exposure, occupational exposure	*S. aureus*	OR
Lo	(127)	Dissemination of methicillin-resistant *Staphylococcus aureus* among healthy children in Northern Taiwan	Family member occupational exposure	*S. aureus*	OR
Lu	(128)	Methicillin-resistant *Staphylococcus aureus* carriage, infection and transmission in dialysispatients, healthcare workers and their family members	Family member occupational exposure	*S. aureus*	OR
Neyra	(129)	Multidrug-resistant and methicillin-resistant *Staphylococcus aureus* (MRSA) in hog slaughter and processing plant workers and their community in North Carolina (USA)	Family member occupational exposure, occupational Exposure	*S. aureus*	PR
Würtz	(130)	No apparent transmission of livestock-associated methicillin-resistant *Staphylococcus aureus* CC398 in a survey of staff at a regional Danish hospital	Family member occupational exposure	*S. aureus*	Risk
Baran	(131)	Stool colonization with vancomycin-resistant Enterococci in healthcare workers and their households	Family member occupational exposure	VRE	Risk
Maree	(132)	Risk factors for infection and colonization with community-associated methicillin-resistant *Staphylococcus aureus* in the Los Angeles county jail: A case-control study	Fomites, other Bathing/Showering	*S. aureus*	OR
Nilsson	(133)	Carriage of penicillin-resistant *Streptococcus pneumoniae* by children in day-care centers during an intervention program in Malmo, Sweden	Fomites	Streptococcus pneumoniae	OR
Rackham	(134)	Community-associated methicillin-resistant *Staphylococcus aureus* nasal carriage in a college student athlete population	Fomites	*S. aureus*	Risk
Groat	(135)	Canine raw meat diets and antimicrobial resistant *E. coli*: is there a link?	Food to animal	*E. coli*	OR
Olkkola	(136)	Population genetics and antimicrobial susceptibility of canine Campylobacter isolates collected before and after a raw feeding experiment.	Food to animal	Campylobacter	Risk
Fukuda	(137)	Role of flies in the maintenance of antimicrobial resistance in farm environments	Food to animal	*E. coli*	Bacteria Intake
Barbarin	(138)	Colonization of Cimex lectularius with methicillin-resistant *Staphylococcus aureus*.	Human to animal	*S. aureus*	

Lis	(139)	Methicillin resistance of airborne coagulase-negative staphylococci in homes of persons having contact with a hospital environment.	Human to air	*Staphylococcus epidermidis*, other	Risk difference
Kennedy	(140)	Face mask sampling reveals antimicrobial resistance genes in exhaled aerosols from patients with chronic obstructive pulmonary disease and healthy volunteer	Human to air	Genes	Risk
Thom	(141)	Environmental contamination due to multidrug-resistant *Acinetobacter baumannii* surrounding colonized or infected patients	Human to nearby environment	Enterobacteriaceae	Risk
Bures	(142)	Computer keyboards and faucet handles as reservoirs of nosocomial pathogens in the intensive care unit.	Human to nearby environment	*S. aureus*	Risk
Shahbazian	(143)	Multidrug and mupirocin resistance in environmental methicillin-resistant *Staphylococcus aureus* (MRSA) isolates from homes of people diagnosed with community-onset MRSA infection.	Human to nearby environment	*S. aureus*	Risk
Levin	(144)	Environmental contamination by multidrug-resistant *Acinetobacter baumannii* in an intensive care unit.	Human to nearby environment	*Acinetobacter baumannii*	Risk
Zimbudzi	(145)	Contamination of renal patients' hospital chart covers with vancomycin-resistant enterococci: Handle with care	Human to nearby environment	VRE	Risk, genes
Chalfine	(146)	Ten-year decrease of acquired methicillin-resistant *Staphylococcus aureus* (MRSA) bacteremia at a single institution: the result of a multifaceted program combining cross-transmission prevention and antimicrobial stewardship.	Intervention	*S. aureus*	Risk
Duggal	(147)	An investigation of MRSA from the burns ward the importance of hand hygiene	Intervention	*S. aureus*	Risk
Batra	(148)	Efficacy and limitation of a chlorhexidine-based decolonization strategy in preventing transmission of methicillin-resistant *Staphylococcus aureus* in an intensive care unit	Intervention	*S. aureus*	Incidence rate ratios
D'Agata	(149)	The impact of persistent gastrointestinal colonization on the transmission dynamics of vancomycin-resistant enterococci.	Intervention	VRE	Importance of Route
Perencevich	(150)	Projected benefits of active surveillance for vancomycin-resistant enterococci in intensive care units	Intervention	VRE	Incidence
Montecalvo	(151)	Infection-control measures reduce transmission of vancomycin-resistant enterococci in an endemic setting.	Intervention	VRE	Incidence transmission rate

Coleman	(152)	Contamination of Canadian private drinking water sources with antimicrobial resistant *Escherichia coli*.	Livestock to drinking water, occupational Exposure	*E. coli*	OR
Caudell	(153)	Identification of risk factors associated with carriage of resistant Escherichia coli in three culturally diverse ethnic groups in Tanzania: a biological and socioeconomic analysis	Milk to human, non - commercial animal keeping, sharing water with animal	*E. coli*	OR
Moodley	(154)	Experimental colonization of pigs with methicillin-resistant Staphylococcus aureus (MRSA): insights into the colonization and transmission of livestock-associated MRSA.	Mother (animal) to child	*S. aureus*	Risk
Corrò	(155)	Occurrence and characterization of methicillin-resistant *Staphylococcus pseudintermedius* in successive parturitions of bitches and their puppies in two kennels in Italy.	Mother (animal) to child	*Staphylococcus pseudintermedius*	Genes
Tamelienė	(156)	*Escherichia coli* colonization in neonates: prevalence. perinatal transmission. antimicrobial susceptibility. and risk factors.	Mother to child	*E. coli*	OR[rs]
Denkel	(157)	The mother as most important risk factor for colonization of very low birth weight (VLBW) infants with extended-spectrum β-lactamase-producing Enterobacteriaceae (ESBL-E).	Mother to child	Enterobacteriaceae, *S. aureus*	OR, risk[rs]
Kunze	(43)	Colonization, serotypes and transmission rates of group B streptococci in pregnant women and their infants born at a single University Center in Germany.	Mother to child	Group B streptococci	Risk
Bourgeois-Nicolaos	(158)	Maternal vaginal colonisation by *Staphylococcus aureus* and newborn acquisition at delivery.	Mother to child	*S. aureus*	Risk
Chua	(159)	Ureaplasma urealyticum and Mycoplasma hominis isolation from cervical secretions of pregnant women and nasopharyngeal secretions of their babies at delivery	Mother to child	Other	Risk[rs]
Eren	(47)	The carriage of group B streptococci in Turkish pregnant women and its transmission rate in newborns and serotype distribution	Mother to child	Group B streptococci	Risk[rs]
Facchinetti	(45)	Chlorhexidine vaginal flushings versus systemic ampicillin in the prevention of vertical transmission of neonatal group B streptococcus, at term	Mother to child	Group B streptococci	Risk[rs]

Jiménez-Rámila	(160)	Vagino-rectal colonization and maternal-neonatal transmission of Enterobacteriaceae producing extended-spectrum β-lactamases or carbapenemases: a cross-sectional study.	Mother to child	Enterobacteriaceae	Risk
Kadanali	(46)	Maternal carriage and neonatal colonisation of group B streptococcus in eastern Turkey: prevalence, risk factors and antimicrobial resistance	Mother to child	Group B streptococci	Risk^{rs}
Kunze	(44)	Comparison of pre- and intrapartum screening of group B streptococci and adherence to screening guidelines: a cohort study.	Mother to child	Group B streptococci	Risk^{rs}
Strus	(48)	Group B streptococcus colonization of pregnant women and their children observed on obstetric and neonatal wards of the University Hospital in Krakow, Poland.	Mother to child	Group B streptococci	Risk
Kothari	(161)	Community acquisition of beta-lactamase producing Enterobacteriaceae in neonatal gut	Mother to child	Enterobacteriaceae	Risk
Morel	(162)	Nosocomial transmission of methicillin-resistant *Staphylococcus aureus* from a mother to her preterm quadruplet infants	Mother to child	*S. aureus*	Genes
Peretz	(163)	Peripartum maternal transmission of extended-spectrum β-lactamase organism to newborn infants	Mother to child	Enterobacteriaceae	Genes
Kurita	(164)	Nosocomial transmission of methicillin-resistant *Staphylococcus aureus* via the surfaces of the dental operatory.	Nearby environment to human	*S. aureus*	Genes
Zhou	(165)	Sources of sporadic *Pseudomonas aeruginosa* colonizations/infections in surgical ICUs: Association with contaminated sink trap.	Nearby environment to human	*Pseudomonas aeruginosa*	Genes^{rs}
Rubini	(166)	Prevalence of Salmonella strains in wild animals from a highly populated area of north-eastern Italy	Nearby farm to Animal	Salmonella	OR
Wielders	(167)	Extended-spectrum β-lactamase- and pAmpC-producing Enterobacteriaceae among the general population in a livestock-dense area	Nearby farm to human, non-commercial animal keeping, occupational exposure, pet to human, travelling^{-}	Enterobacteriaceae	OR
Reynaga	(168)	Clinical impact and prevalence of MRSA CC398 and differences between MRSA-TetR and MRSA-TetS in an area	Occupational Exposure	*S. aureus*	OR

		of Spain with a high density of pig farming: a prospective cohort study.			
Diercke	(169)	Livestock-associated methicillin-resistant Staphylococcus aureus in patients admitted to hospitals in the Ems-Dollart-Region, 2011	Occupational Exposure	*S. aureus*	OR, genes
Founou	(170)	Mannitol-fermenting methicillin-resistant staphylococci (MRS) in pig abatoirs in Cameroon and South Africa: A serious foodsafety threat.	Occupational Exposure	*S. aureus*, Staphylococci	OR, risk
Ho	(50)	Occupational exposure to raw meat: a newly-recognized risk factor for *Staphylococcus aureus* nasal colonization amongst food handlers	Occupational Exposure	*S. aureus*	OR, OR^{rs}
Jayaweera	(171)	Antibiotic resistance patterns of methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from livestock and associated farmers in Anuradhapura, Sri Lanka	Occupational Exposure	*S. aureus*	OR
Dohmen	(172)	Carriage of extended-spectrum β-lactamases in pig farmers is associated with occurrence in pigs	Occupational Exposure	Enterobacteriaceae	OR, risk, genes
Mascaro	(173)	Prevalence of livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) among farm and slaughterhouse workers in Italy	Occupational Exposure	*S. aureus*	OR, risk
Moodley	(174)	High risk for nasal carriage of methicillin-resistant Staphylococcus aureus among Danish veterinary practitioners	Occupational Exposure	*S. aureus*	OR
Rasamiravaka	(49)	Evaluation of methicillin-resistant Staphylococcus aureus nasal carriage in Malagasy pig and poultry non-industrial farmers	Occupational Exposure	*S. aureus*	OR^{rs}
Rasamiravaka	(175)	Evaluation of methicillin-resistant staphylococcus aureus nasal carriage in Malagasy veterinary students	Occupational Exposure	*S. aureus*	OR
Rosenberg Goldstein	(176)	Occupational exposure to *Staphylococcus aureus* and Enterococcus spp. among spray irrigation workers using reclaimed water.	Occupational Exposure	*S. aureus*	OR
van Rijen	(177)	Increase in a Dutch hospital of methicillin-resistant Staphylococcus aureus related to animal farming	Occupational Exposure, travelling (healthcare system contact) $^{-}$	*S. aureus*	OR
Ye	(178)	Livestock-associated methicillin and multidrug resistant *S. aureus* in humans is associated with occupational pig contact, not pet contact	Occupational Exposure, pet to human	*S. aureus*	OR, PR

Ye	(179)	Genotypic and phenotypic markers of livestock-associated methicillin-resistant *Staphylococcus aureus* CC9 in humans	Occupational Exposure	*S. aureus*	OR
Price	(180)	Elevated risk of carrying gentamicin-resistant *Escherichia coli* among U.S. poultry workers	Occupational Exposure	*E. coli*	OR
Trung	(181)	Zoonotic transmission of mcr-1 colistin resistance gene from small-scale poultry Farms, Vietnam	Occupational Exposure	*E. coli*	OR
Moser	(182)	The role of mobile genetic elements in the spread of antimicrobial-resistant *Escherichia coli* From chickens to humans in small-scale production poultry operations in rural Ecuador	Occupational Exposure	*E. coli*	OR
Wardyn	(183)	Swine farming Is a risk factor for infection with and high prevalence of carriage of multidrug-resistant *Staphylococcus aureus*	Occupational exposure, family member occupational exposure	*S. aureus*	PR, OR
Rinsky	(184)	Livestock-associated methicillin and multidrug resistant *Staphylococcus aureus* is present among industrial, not antibiotic-free livestock operation workers in North Carolina	Occupational Exposure	*S. aureus*	PR
Hatcher	(185)	The prevalence of antibiotic-resistant *Staphylococcus aureus* nasal carriage among industrial hog operation workers, community residents, and children living in their households: North Carolina, USA.	Occupational Exposure	*S. aureus*	PR
Li	(186)	Nasal carriage of methicillin-resistant coagulase-negative staphylococci in healthy humans is associated with occupational pig contact in a dose-response manner	Occupational exposure	Staphylococci, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*	PR
Borgen	(187)	Continuing high prevalence of VanA-type vancomycin-resistant enterococci on Norwegian poultry farms three years after avoparcin was banned	Occupational exposure	VRE	PR
Fischer	(188)	Nasal colonization of pig-exposed persons with Enterobacteriaceae and associated microbial resistance	Occupational exposure	Enterobacteriaceae	Risk
Frana	(189)	Isolation and characterization of methicillin-resistant *Staphylococcus aureus* from pork farms and visiting veterinary students	Occupational exposure	*S. aureus*	Risk
Wulf	(190)	Prevalence of methicillin-resistant *Staphylococcus aureus* among veterinarians: an international study.	Occupational exposure	*S. aureus*	OR

Fang	(191)	Livestock-associated methicillin-resistant *Staphylococcus aureus* ST9 in pigs and related personnel in Taiwan.	Occupational exposure	*S. aureus*	Risk, genes
Khanna	(192)	Methicillin resistant *Staphylococcus aureus* colonization in pigs and pig farmers.	Occupational exposure	*S. aureus*	Risk
Witte	(193)	Emergence of caMRSA infections in humans caused by MRSA CC398 which has its main reservoir in animals	Occupational exposure	*S. aureus*	Risk
Cuny	(194)	Methicillin-resistant *Staphylococcus aureus* from infections in horses in Germany are frequent colonizers of veterinarians but rare among MRSA from infections in humans	Occupational exposure, pet to human	*S. aureus*	Risk, genes
Drougka	(195)	Interspecies spread of *Staphylococcus aureus* clones among companion animals and human close contacts in a veterinary teaching hospital. Across-sectional study in Greece	Occupational Exposure, pet to human	*S. aureus*	Risk
Graells	(126)	Livestock veterinarians at high risk of acquiring methicillin-resistant *Staphylococcus aureus* ST398.	Occupational Exposure	*S. aureus*	Risk
Oppliger	(196)	Antimicrobial resistance of *Staphylococcus aureus* strains acquired by pig farmers from pigs	Occupational Exposure	*S. aureus*	Risk
Nakane	(197)	Long-term colonization by blaCTX-M-harboring *Escherichia coli* in healthy Japanese people engaged in food handling	Occupational Exposure	*E. coli*	Risk
Castro	(198)	Food handlers as potential sources of dissemination of virulent strains of *Staphylococcus aureus* in the community.	Occupational Exposure	*S. aureus*	Risk
Zurfluh	(199)	Screening for fecal carriage of MCR-producing Enterobacteriaceae in healthy humans and primary care patients	Occupational Exposure	Enterobacteriaceae	Risk
Cuny	(200)	Occurrence of cfr-mediated multiresistance in staphylococci from veal calves and pigs, from humans at the corresponding farms, and from veterinarians and their family members	Occupational Exposure	Staphylococci	Risk
Gràinne	(201)	The emergence and spread of multiple livestock-associated clonal complex 398 methicillin-resistant and methicillin-susceptible *Staphylococcus aureus* strains among animals and humans in the Republic of Ireland, 2010–2014	Occupational Exposure, Pet to human	*S. aureus*	Genes
Knetsch	(202)	Whole genome sequencing reveals potential spread of Clostridium difficile between humans and farm animals in the Netherlands, 2002 to 2011.	Occupational Exposure	*S. aureus*	Genes

Lozano	(203)	Dynamic of nasal colonization by methicillin-resistant Staphylococcus aureus ST398 and ST1after mupirocin treatment in a family in close contact with pigs.	Occupational Exposure	*S. aureus*	Genes
Tzavaras	(204)	Diversity of vanA-type vancomycin-resistant Enterococcus faecium isolated from broilers, poultry slaughterers and hospitalized humans in Greece.	Occupational Exposure	Enterococcus faecium	Genes
Köck	(205)	Livestock-associated methicillin-resistant Staphylococcus aureus (MRSA) as causes of human infection and colonization in Germany	Occupational Exposure	*S. aureus*	Genes
Wang	(206)	Distribution of the multidrug resistance gene cfr in Staphylococcus isolates from pigs, workers, and the environment of a hog market and a slaughterhouse in Guangzhou, China	Occupational Exposure	Staphylococci	Genes
Mularoni	(207)	Outcome of Transplantation Using Organs From Donors Infected or Colonized With Carbapenem-Resistant Gram-Negative Bacteria.	Organ	Enterobacteriaceae	Risk
Goldberg	(208)	Organ transplantation from a donor colonized with a multidrug-resistant organism: A case report	Organ	Other	Risk
Mingquan	(209)	Distinct mechanisms of acquisition of mcr-1 –bearing plasmid by Salmonella strains recovered from animals and food samples	Other (animal to meat of animal)	Salmonella	Genes
Mork	(210)	Comprehensive modeling reveals proximity, seasonality, and hygiene practices as keydeterminants of MRSA colonization in exposed households.	Other Bathing/Showering, space sharing, other Soap	*S. aureus*	OR
Gandolfi-Decristophoris	(211)	Evaluation of pet contact as a risk factor for carriage of multidrug-resistant staphylococci in nursing home residents	Pet to human	Staphylococci	OR
Morita	(212)	Survey of Methicillin–Resistant *Staphylococcus aureus* (MRSA) Carriage in Healthy College Students, Hawaii	Pet to human, water(exposure)to human	*S. aureus*	Risk
De Martino	(213)	Methicillin-resistant staphylococci isolated from healthy horses and horse personnel in Italy.	Pet to human	Staphylococci	Risk, genes
Loncaric	(214)	Suspected goat-to-human transmission of methicillin-resistant *Staphylococcus aureus* sequence type 398	Pet to human	*S. aureus*	Risk

Morris	(215)	Potential for pet animals to harbour methicillin-resistant *Staphylococcus aureus* when residing with human MRSA patients	Pet to human	*S. aureus*	Risk, genes
Boost	(51)	Prevalence of Staphylococcus aureus carriage among dogs and their owners	Pet to human	*S. aureus*	Genes^{rs}
Boehmer	(216)	Phenotypic characterization and whole genome analysis of extended-spectrum beta-lactamase-producing bacteria isolated from dogs in Germany	Pet to human	*E. coli*	Genes
Damborg	(217)	Dogs are a reservoir of ampicillin-resistant Enterococcus faecium lineages associated with human infections	Pet to human	Enterococcus faecium	Genes
Gordoncillo	(218)	Detection of methicillin-resistant *Staphylococcus aureus* (MRSA) in backyard pigs and their owners, Michigan, USA.	Pet to human	*S. aureus*	Genes
van den Eede	(219)	MRSA carriage in the equine community: an investigation of horse-caretaker couples	Pet to human	*S. aureus*	Genes
Walther	(220)	Sharing more than friendship - nasal colonization with coagulase-positive staphylococci (CPS) and co-habitation aspects of dogs and their owners	Pet to human	*Staphylococcus pseudintermedius*	Genes^{rs}
Shorman	(221)	Risk factors associated with vancomycin-resistant enterococcus in intensive care unit settings in Saudi Arabia	Prior colonised patient in room	Other	OR
Nseir	(222)	Risk of acquiring multidrug-resistant Gram-negative bacilli from prior room occupants in the intensive care unit	Prior colonised patient in room	*Pseudomonas aeruginosa, Acinetobacter baumannii*	OR
Morales Barroso	(223)	Intestinal colonization due to *Escherichia coli* ST131: Risk factors and prevalence	Space sharing	*E. coli*	OR
Torres-Gonzalez	(224)	Factors associated to prevalence and incidence of carbapenem-resistant Enterobacteriaceae fecal carriage: A cohort study in a Mexican tertiary care hospital	Space sharing	Enterobacteriaceae	OR
Ben-David	(225)	Carbapenem-resistant *Klebsiella pneumoniae* in post-acute-care facilities in Israel	Space sharing	Enterobacteriaceae	OR
Papadimitriou-Olivgeris	(226)	Risk factors for enterococcal infection and colonization by vancomycin-resistant enterococci in critically ill patients	Space sharing	VRE	OR
Jiménez-Truque	(227)	Association Between Contact Sports and Colonization with Staphylococcus aureus in a Prospective Cohort of Collegiate Athletes	Space sharing	*S. aureus*	OR

Fossi Djembi	(228)	Factors associated with Vancomycin-resistant Enterococcus acquisition during a large outbreak	Space sharing	VRE	PR
Ulstad	(229)	Carriage of ESBL/AmpC-producing or ciprofloxacin non-susceptible *Escherichia coli* and *Klebsiella spp*. in healthy people in Norway	Travelling $^{-}$	Enterobacteriaceae	OR
Vading	(230)	Frequent acquisition of low-virulence strains of ESBL-producing *Escherichia coli* in travellers	Travelling $^{+}$	Enterobacteriaceae	OR
Peirano	(231)	Rates of colonization with extended-spectrum β-lactamase-producing Escherichia coli in Canadian travellers returning from South Asia: a cross-sectional assessment	Travelling $^{+}$, travelling (eating food) $^{+}$	*E. coli*	OR
MacFadden	(232)	A passage from India: Association between air traffic and reported cases of New Delhi Metallo-beta-lactamase 1 from 2007 to 2012	Travelling $^{-}$	Enterobacteriaceae	OR
Epelboin	(233)	High rate of multidrug-resistant gram-negative bacilli carriage and infection in hospitalized returning travelers: A cross-sectional cohort study	Travelling $^{+}$	*E. coli*	OR
Lorme	(234)	Acquisition of plasmid-mediated cephalosporinase producing Enterobacteriaceae after a travel to the tropics	Travelling $^{+}$	Enterobacteriaceae	OR, risk
Nurjadi	(235)	Skin and soft tissue infections in intercontinental travellers and the import of multi-resistant Staphylococcus aureus to Europe	Travelling $^{-}$	*S. aureus*	OR
Ostholm-Balkhed	(236)	Travel-associated faecal colonization with ESBL-producing Enterobacteriaceae: incidence and risk factors	Travelling $^{+}$	Enterobacteriaceae	OR
Yaita	(237)	Epidemiology of extended-spectrum β-lactamase producing *Escherichia coli* in the stools of returning Japanese travelers, and the risk factors for colonization	Travelling $^{+}$	*E. coli*	OR
Sannes	(238)	Predictors of antimicrobial-resistant *Escherichia coli* in the feces of vegetarians and newly hospitalized adults in Minnesota and Wisconsin	Travelling $^{-}$	*E. coli*	PR
Islam	(239)	Intestinal carriage of third-generation cephalosporin-resistant and extended-spectrum β-lactamase-producing Enterobacteriaceae in healthy US children	Travelling $^{-}$	Enterobacteriaceae	OR

Coleman	(27)	The role of drinking water in the transmission of antimicrobial-resistant *E. coli*	Travelling $^{-}$, drinking water to human, eating meat to human	*E. coli*	PR
Tängdén	(240)	Foreign travel is a major risk factor for colonization with Escherichia coli producing CTX-M-type extended-spectrum beta-lactamases: a prospective study with Swedish volunteers	Travelling $^{+}$	Enterobacteriaceae	Risk
Pires	(241)	Polyclonal intestinal colonization with Extended-Spectrum Cephalosporin-Resistant Enterobacteriaceae upon traveling to India	Travelling $^{+}$	Enterobacteriaceae	Risk
Lausch	(242)	Colonisation with multi-resistant Enterobacteriaceae in hospitalised Danish patients with a history of recent travel: a cross-sectional study	Travelling $^{-}$	*E. coli*	Risk
Arcilla	(243)	Import and spread of extended-spectrum β-lactamase-producing Enterobacteriaceae by international travellers (COMBAT study): a prospective, multicentre cohort study	Travelling $^{+}$	Enterobacteriaceae	Risk
Blyth	(244)	Antimicrobial resistance acquisition after international travel in U.S. travelers	Travelling $^{+}$	*E. coli*	Risk
Bevan	(245)	Acquisition and loss of CTX-M-producing and non-producing *Escherichia coli* in the fecal microbiome of travelers to South Asia	Travelling $^{+}$	*E. coli*	Risk
Lübbert	(246)	Colonization with extended-spectrum beta-lactamase-producing and carbapenemase-producing Enterobacteriaceae in international travelers returning to Germany	Travelling $^{+}$	Enterobacteriaceae	Risk
Nakayama	(247)	Carriage of colistin-resistant, extended-spectrum β-lactamase-producing Escherichia coli harboring the mcr-1 resistance gene after short-term international travel to Vietnam	Travelling $^{+}$	*E. coli*	Risk
Valverde	(248)	Intestinal Colonisation with multidrug-resistant Enterobacteriaceae in travellers, immigrants and 'visiting friends and relatives': Dominance of E. coli producing CTX-M enzymes	Travelling $^{-}$	Enterobacteriaceae	Risk
Johnning	(249)	Quinolone resistance mutations in the faecal microbiota of Swedish travellers to India	Travelling $^{+}$	*E. coli*	Risk difference
Sun	(250)	Varying High Levels of faecal carriage of Extended-Spectrum Beta-Lactamase producing Enterobacteriaceae in	Vegetables to human, drinking water to human,	*E. coli*	OR

		rural villages in Shandong, China: Implications for global health	pet to human, nearby farm to human		
O'Flaherty	(251)	Human exposure to antibiotic resistant-*Escherichia coli* through irrigated lettuce.	Vegetables to human	*E. coli*	Bacteria intake
Dekić	(252)	Emerging human pathogen *Acinetobacter baumannii* in the natural aquatic environment: a public health risk?	Water to Animal	*Acinetobacter baumannii*	Bacteria intake
Goldstein	(253)	Higher prevalence of coagulase-negative staphylococci carriage among reclaimed water spray irrigators.	Water(exposure)to human	Staphylococci	OR
Leonard	(254)	Exposure to and colonisation by antibiotic-resistant *E. coli* in UK coastal water users: Environmental surveillance, exposure assessment, and epidemiological study (Beach Bum Survey).	Water(exposure)to human	*E. coli*	OR
Yang	(255)	Discharge of KPC-2 genes from the WWTPs contributed to their enriched abundance in the receiving river	Water(exposure)to human	Enterobacteriaceae	Genes