Supplementary Material

Table S1. Discussion of eight factors possibly influencing transmission and bioavailability of drug-resistant bacteria.

Possible transmission influencing factors	**Key messages discussing the influence on transmission and bioavailability of resistant bacteria**	**First author, year**
• *The previously high prophylactic and current therapeutic usage of antibiotics has led to an increased number of multidrug-resistant bacteria in the intestinal flora of animals* [1-5]. • *The frequency of drug-resistance in bacterial populations may increase as a result of selective advantage under the pressure of antimicrobial use in human and veterinary medicine* [6,7].	• The analyses of Smith et al., 2002 [8] suggest that "agricultural antibiotic use hastens the appearance of antibiotic-resistant bacteria in humans." • "Use of an antimicrobial agent selects for overgrowth of bacterial strain that has a gene expressing resistance of the agent. It also selects for the assembly and evolution of complex genetic vectors encoding, expressing, linking, and spreading that and other resistance genes" [9]. • "The time scale for emergence of resistance under a constant selective pressure is typically much shorter than the decay time after cessation or decline in the volume of drug use" [10].	Aarestrupe and Wegener, 1999 [4]; Lammers [2]; Pohl [3]; Wegener [5]; Acar and Röstel [6]; Tenover [7]; Smith et al., 2002 [8]; O´Brien, 2002 [9]; Austin et al. 1999 [10].
• *Bacterial resistance via plasmid transfer has also been acquired against substances that are not actively administered* [1,11].	"Resistance is influenced by a number of other factors: • the availability of pre-existing resistance genes • the exchangeability of the resistance genes and their functional activity in different bacterial hosts, and the selective pressure" [12].	Messing 1986 [11]; Schwarz et al. 2001 [12].
• *Clonal spread disseminates resistance* [13,14].	• "Clonal lineages disseminate in Europe and worldwide. Regardless of their geographical or clonal origin, isolates display resistance to the major classes of antibiotics used in veterinary medicine" [118].	Robinson and Enright [13,14]; Petersen et al., 2010 [118].
• *The non-pathogenic flora is a possible reservoir for resistance plasmids* [15].	• "In the stable environment both commensal and environmental bacteria serve as reservoirs for the transfer of antimicrobial resistance genes to pathogenic bacteria" [16,17]. • "After the introduction of an antibiotic not only the level of resistance of pathogenic bacteria, but also of commensal bacteria increases. Commensal bacteria constitute a reservoir of resistance genes for (potentially) pathogenic bacteria. Their level of resistance is considered to be a good indicator for selection pressure by	Tschäpe and Rische, 1974 [15]; Blake et al., 2003 [16]; Martinez et al., 2009 [19]; van den Bogaard and Stobberingh, 2000 [18].

	antibiotic use and for resistance problems to be expected in pathogens" [18].	
• *The higher the occurrence of resistance transfer in non-pathogenic bacteria, the greater the risk of an increase in the resistance rate of pathogenic bacteria of the same family* [15,20].	• "The normal bacterial flora contains antibiotic resistance genes to various degrees, even in individuals with no history of exposure to commercially prepared antibiotics. Several factors seem to increase the number of antibiotic-resistant bacteria in feces" [21].	Lebek, 1970 [20]; Tschäpe and Rische, 1974 [15]; Sørum and Sunde, 2001 [21].
• *The most important factor for the persistence of resistance is probably selection pressure from antibiotics* [22].	• "Natural selection exerted by antibiotics favors the spread and maintenance of antibiotic resistance in the environment." • Exposure to sub-lethal concentrations of certain antimicrobials may contribute to the emerging problem of antibiotic resistance not only through selection of certain resistance phenotypes but also by means of stimulating transfer of antimicrobial resistance traits directly" [123].	Bengtsson-Palme et al., 2018 [22]; Jutkina et al. 2018 [123].
• *One decisive factor for the persistence and spread of resistance plasmids in a bacterial population is the density of bacteria in a medium (feces, urine, air, manure, dust, saliva, feeds, drinking water), the viability of the bacterial strain, and the so-called "turn-over" (natural change of bacteria) [23,24].*	• "The size and the type of farms (fattening or nursery/farrowing units) have no significant effects on the quantity of bioaerosols" [25]. • "None of the pigs from the large-scale pig production farms showed LA-MRSA positivity" [26].	Norpoth and Petersen, 1990 [24]; Rolle and Mayr, 1984 [23] Masclaux et al., 2013 [25]; Larsen et al., 2012 [26].
• *The spread of resistance depends on space (e.g. the spatial separation of animals) and time* [11].	• "A bacterial isolate at any place may be resistant—not only because nearby use had caused the construct or its components to evolve in the first place and spread there. The levels of resistance at any time and place may therefore reflect in part the total number of bacteria in the world exposed to antimicrobials up until then" [9].	Messing, 1986 [11]; O´Brien, 2002 [9].

Table S2. Overview over LA-MRSA and ESBL-E in humans in the stable biotope.
Abbreviations for the transmission pathways: HH = Human to Human, AA = Animal to Animal, HA = Human to Animal, AH = Animal to Human, HE = Human to Environment, EH = Environment to Human, AE = Animal to Environment, EA = Environment to Animal, EE = Environment to Environment, FH = Food to Human, HF = Human to Food, EF = Environment to Food, AF = Animal to Food.
Abbreviations for the countries: NL = Netherlands, ESP = Spain, IT =Italy, EU = Europe, DEN = Denmark, UK = United Kingdom, GER = Germany, BEL = Belgium, FR = France, USA = United States of America, CHE = Switzerland, HKG =Hongkong.

Organism	**Transmission pathways**	**Key message**	**Country**	**First author, year**
Humans – Biotope Community				
LA-MRSA	AH, EH	A case–control study showed that carriers of NT-MRSA were more often pig or cattle farmers. MRSA from an animal reservoir has entered the human population and is responsible for >20% of all MRSA in the Netherlands.	NL	Loo et al., 2007 [27]
ESBL-E	HH, AH, EH	Within the community ingestion of coliform bacteria (even with animal origin) can also happen via person to person contact. 6.6% rate of human fecal ESBL carriers in the community. The community could act as a reservoir and food could contribute to the spread of these strains.	ESP	Mesa et al., 2006 [28]
ESBL-E	HH, AH, EH	The most common variants in Europe are CTX-M-15 and CTX-M-1. Unsanitary conditions in households (rare hand washing and insufficient cleaning of surfaces), as well as living with care-dependent ESBL-E-carrying relatives, may support oral ingestion of fecal bacteria.	IT	Mugnaioli et al, 2006 [29]
ESBL-E	HA, AH, HH, EH, HE	Close human-animal ESBL/AmpC gene similarity between human farming communities and their animals (broilers and pigs) (PSIs from 0.8 to 0.9). Isolates from people in the general population had higher similarities to those from human clinical settings, surface and sewage water and wild birds (0.7-0.8), while similarities to livestock or food reservoirs were lower (0.3-0.6). Based on rarefaction curves, people in the general population had more diversity in ESBL/AmpC genes and plasmid replicon types than those in other reservoirs.	NL	Dorado-Garcia et al., 2018 [30]
LA-MRSA	HA, AH	The MRSA bacteraemia rates ranging from less than 1% to more than 50%. LA-MRSA strains have recently emerged as community and livestock-associated human pathogens in most EU Member States.	EU	Köck et al., 2010 [31]
LA-MRSA	HH, AH, EH	La-MRSA has been discovered in animals, livestock farmers and retail meat. This cross-sectional study aimed to determine the spread to persons not in direct contact with livestock in areas with a high density of pig farms. Of the 534 persons without livestock-contact, one was positive for MRSA (0.2%; 95% confidence interval, <0.01-1.2). Of the 49 persons who did indicate to be working at or living on a livestock farm, 13 were positive for MRSA (26.5%; 95% confidence interval, 16.1-40.4). All spa-types belonged to CC398. Livestock-associated MRSA has a	NL	van Cleef et al., 2010 [32]

		high prevalence in people with direct contact with animals. At this moment, it has not spread from the farms into the community.		
LA-MRSA	AH, EH	Epidemiology of methicillin-resistant Staphylococcus aureus carrying the novel mecC gene in Denmark corroborates a zoonotic reservoir with transmission to humans.	DEN	Petersen et al., 2013 [33]
LA-MRSA, ESBL-E	HA, AH, EH	*Enterobacteriaceae* can be spread by fecal-oral transmission via contact from human to livestock and/or companion animals. There is a concern that the numbers of MRSA or other antimicrobial-resistant bacteria might increase further when human isolates become established in animals, as this can amplify the numbers of such bacteria by dissemination within animal groups with subsequent spread back to humans.	UK	Cantas and Suer, 2014; Hunter et al., 2010 [34,35]
ESBL-E	HH, AH, EH, HA	Most ESBLgenes were found in both, human and non-human populations but quantitative differences for distinct ESBL-types were detectable. Same subtypes were detected in isolates from the human and livestock and companion animal populations. The enzymes CTX-M-1 (63.3% of all animal isolates, 29.3% of all human isolates), CTX-M-15 (17.7% vs. 48.0%) and CTX-M-14 (5.3% vs. 8.7%) were the most common ones. More than 70% of the animal isolates and more than 50% of the human isolates contained the broadly distributed ESBL genes.	GER	Valentin et al., 2014 [36]
ESBL-E	HH	Human-to-human contact is a key factor in the dissemination of ESBL-producing bacteria among humans.		Wu et al., 2013
ESBL-E	FH, EH, AH	It is assumed that foodborne exposure has an impact on the probability of human colonization and/or infection caused by ESBL-producing bacteria.	NL, DEN	Leverstein-van Hall et al., 2011; Overdevest et al., 2011 [37,38]
LA-MRSA	HA, AH, EH	LA-MRSA is primarily an occupational health risk to farm workers and veterinarians.	IT	Guardabassi et al. 2013 [39]
Humans – Biotope Farm / Stable (Farmers, Veterinarians, Household Members)				
LA-MRSA	HH, AH, EH	Transmission of MRSA CC398 from livestock veterinarians to their household members possible. ean MRSA CC398 prevalence over the study period was 44% (range 41.6–46.0%) in veterinarians and 4.0% (range 2.8–4.7%) in their household members. The MRSA CC398 prevalence in household members of veterinarians was significantly lower than the MRSA non-CC398 prevalence in household members of control patients (PRR 6.0; 95% CI 2.4–15.5),	NL	Verkade et al., 2014 [40]
LA-MRSA	AH, HH	The prevalence of MRSA carriage in pig and veal calf farmers in the Netherlands is estimated at 25 to 35%. But in most cases the strain is lost again after 24 h.	NL	Van Cleef et al., 2011 [41]
LA-	HH,	During a 6-month period in 2009-2010, 4 pig farms in Denmark, Belgium, and the Netherlands, respectively,	DEN	Garcia-Graells et

MRSA	AH, HA, EH, HE	were studied for the presence of MRSA. The proportion of persistent carriers was significantly higher among farmers than among household members (87% vs. 11%) and significantly higher in household members from Belgium compared to those from Denmark and the Netherlands (29% vs. 0% vs. 6%).	, BEL, NL	al., 2013 [42]
LA-MRSA	AH, AA, HH, EH, HE	Doubling pig, cattle, and veal calf densities per municipality increased the odds of LA-MRSA carriage over carriage of other types of MRSA by 24.7% (95% CI 0.9%-54.2%), 76.9% (95% CI 11.3%-81.3%), and 24.1% (95% CI 5.5%-45.9%), respectively, after adjusting for direct animal contact, living in a rural area, and the probable source of MRSA carriage. Controlling the spread of LA-MRSA thus requires giving attention to community members in animal-dense regions who are unaffiliated with livestock farming.	NL	Feingold et al., 2012 [43]
ESBL-E	AH, HA, EH, HE	The same ESBL genes, ESBL gene carrying plasmids or even the same ESBL-producing *E. coli* isolates could be detected in animals and the farmers taking care for them.	NL, IT, DEN	Dierikx et al., 2013a, Moodley and Guardabassi, 2009, Hammerum et al., 2014 [44-46]
LA-MRSA	HA	MRSA CC398 appears to be its capacity to spread to humans.	NL	Vanderhaeghen et al., 2010 [47]
ESBL-E	AH, HA, EH, HE	Fluoroquinolone-resistant CTX-M-15-producing Escherichia coli from human and animal populations were studied. ST410 is the most frequent sequence type, harbouring five different clades. Two clades (B and C) harbour chromosomally inserted CTX-M-15. ST410 clones circulate in animals, humans and the environment in Germany.	GER	Falgenhauer et al., 2016 [48]
ESBL-E	AH, HA, EH, HE	Livestock and animal-derived foods are considered relevant sources for the colonization of humans with ESBL-*E. coli*	GER	Hille et al., 2014 [49]
ESBL-E	AH, HA, EH, HE	Of 114 pig-exposed persons tested, Enterobacteriaceae were detected in the nares of 76 (66·7%) participants. ESBL-E were not detected.	GER	Fischer et al., 2016; Fischer et al, 2017 [50,51]
LA-MRSA	HH, AH, EH	MRSA rates of 4.5% for pig farmers in France. we showed that overcolonization of farmers was caused by a few bacterial strains that were not present in nonfarmers but often caused swine infections. This finding suggests a high rate of strain exchange between pigs and farmers.	FR	Armand-Lefevre et al., 2005 [52]

LA-MRSA	AH, AA, AH, EH	Persistence of livestock associated MRSA CC398 in humans is dependent on intensity of animal contact. Presence of MRSA in farmers was strongly related to duration of animal contact and was strongly reduced in periods with absence of animal contact (-58%). Family members, especially children, were more often carriers when the farmer was a carrier (OR=2, $P<0.05$). Only 7% (n=11) of the participants appeared to be persistent carriers.	NL	Graveland et al., 2011 [53]
LA-MRSA	AH, EH	international study among pig veterinarians revealed an overall MRSA-prevalence of 12.5%.	NL	Wulf et al., 2008 [54]
LA-MRSA	AH	45% LA-MRSA-positive swine workers with nasal carriage in the U.S.A.	USA	Smith et al., 2009 [55]
LA-MRSA	AA, HA, AH, EH, AE	Among the occupationally exposed persons (veterinarians, laboratory personnel and meat inspection personnel), 20 persons (23%) showed a nasal colonisation with MRSA ST398. A quite strong association between the intensity of the contact to pigs with the frequency of nasal colonisation in the occupationally exposed persons was detected.	NL	Meemken et al., 2008 [56]
LA-MRSA	AH, HE, EA, EE	A strong association between nasal ST398 MRSA carriage in people working in the farms for >20 h per week and MRSA air levels was confirmed. In people working in the barns < 20 h per week there was a strong association between nasal carriage and number of working hours. This study showed that working in the lairage area or scalding and dehairing area were the major risk factors for MRSA carriage in pig slaughterhouse workers, while the overall prevalence of MRSA carriage is low. Occupational exposure to MRSA decreased along the slaughterline, and the risk of carriage showed a parallel decrease.	NL	Bos et al., 2016, Gilbert et al., 2012 [57]
ESBL-E	AH, EH, HA	Farmers may come in contact with more antimicrobial-resistant bacteria from pigs. A significant association between pig farming and isolation of resistant commensal bacteria was determined.	FR	Aubry-Damon et al., 2004 [58]
LA-MRSA ESBL-E	AH, EH	MRSA (31%) and ESBL-E (24%) were found in the investigated farms. Results showed that ESBL-E was present in both pigs and farm workers and that the proportion of farms with MRSA had increased fourfold in seven years (from 7% to 31%). Associations between antibiotic use and resistant bacteria carriage were shown.	CHE	Kraemer et al., 2017 [59]
LA-MRSA	AH, EH	Heinemann et al. [238] showed, that a working time of 3 to 6 hours could be enough for positive findings of nasal colonization with MRSA.	GER	Heinemann et al., 2017 [60,61]
LA-MRSA	AH, EH	case report one farm worker with clinical symptoms was infected with MRSA CC398 Methicillin-resistant Staphylococcus aureus sequence type 398 (ST398 MRSA) was identified in Dutch pigs and pig farmers. ST398 methicillin-susceptible S. aureus circulates among humans at low frequency.	NL	Van Belkum et al., 2008 [62]

LA-MRSA ESBL-E	AH, HA	verified a genetic relationship of MRSA and ESBL-producing *Enterobacteriaceae* strains from human and companion animal origins, implicating the original source in animal-to-human transmission and vice versa.	GER	Wieler et al., 2011 [63]
ESBL-E	AH	(2009) identified the same ESBL strains (CTX-M-1-positive *E. coli*) in farm workers and pigs, assuming that the farm workers acquired the drug-resistant strains from the pigs.	IT	Moodley and Guardabassi, 2009 [45]
ESBL-E	AH, EH	In total, 70.6% (24/36) of the tested farms were ESBL positive. Furthermore, 9 out of 60 cloacal swabs turned out to be ESBL positive. One human isolate shared an identical MLST sequence type (ST) 3891. In summary, the study shows the high prevalence of ESBL-producing *E.coli* in livestock in Mecklenburg- Western Pomerania and provides the risk of transfer between livestock and farm workers.	GER	Dahms et al., 2015 [64]
Humans – Biotope Abattoir (Abattoir workers, Butchers)				
LA-MRSA	HH, AH	Carriage of MRSA was higher in butchers than in the general community. Although five strains were probably of healthcare origin, the high incidence of t899 (CC9) suggests that cross-contamination from pork occurs frequently.	HKG	Boost et al., 2012 [65]
LA-MRSA	HH, AH	Although the prevalence of *S. aureus* and MRSA was similar in hog slaughter/processing plant workers and their household and community members, *S. aureus* isolates from workers were resistant to a greater number of antimicrobial classes.	USA	Neyra et al., 2014 [66]
LA-MRSA	AH, HE, EH	The overall prevalence of nasal MRSA carriage in employees of pig slaughterhouses was 5.6% (14/249) (95% CI 3.4-9.2) and working with live pigs was the single most important factor for being MRSA positive (OR 38.2, P<0.0001). At the start of the day MRSA was only found in environmental samples from the lairages (10/12), whereas at the end of the day MRSA was found in the lairages (11/12), the dirty (5/12) and clean (3/12) areas and green offal (1/3). The MRSA status of the environmental samples correlated well with the MRSA status of humans working in these sections (r=0.75).	NL	Van Cleef et al., 2013 [67]
LA-MRSA	AF, AA, AH	39% of pigs and 81% of the slaughter batches at Dutch slaughterhouses were MRSA positive.	NL	Dierikx et al., 2016 [44]

Table S3. Overview over several studies describing the different possibilities of the transmission of antibiotic-resistant bacteria (MRSA and ESBL-E) between pigs.
Abbreviations for the transmission pathways: HH = Human to Human, AA = Animal to Animal, HA = Human to Animal, AH = Animal to Human, HE = Human to Environment, EH = Environment to Human, AE = Animal to Environment, EA = Environment to Animal, EE = Environment to Environment, FH = Food to Human, HF = Human to Food, EF = Environment to Food, AF = Animal to Food.

Abbreviations for the countries: NL = Netherlands, ESP = Spain, IT =Italy, EU = Europe, DEN = Denmark, UK = United Kingdom, GER = Germany, BEL = Belgium, FR = France, USA = United States of America, CHE = Switzerland, INT = international (worldwide).

Organism	**Transmission pathways**	**Key message**	**Country**	**First author, year**
Animals – Biotope Stable (Livestock)				
LA-MRSA	HH, AH, AA, EH, EA, AE	Transmission routes are "trading" and "reherding" along the food production chain. The MRSA status of a pig supplier highly affects the MRSA status of the receiving herd. The prevalence of methicillin resistant Staphylococcus aureus (MRSA) in pigs at abattoirs is higher than in pigs sampled on farms. MRSA negative pigs can become MRSA positive during transportation from the farm to the abattoir after exposure to other pigs and environmental sources of MRSA. Pigs (n=117) were tested MRSA negative before transportation. On arrival at the abattoir, 12/117 (10.3%) pigs in two batches tested MRSA positive.	NL	Broens et al., 2011; Broens et al., 2012 [68,69]
LA-MRSA	HA, AH, EH, HE, AA, AE	trading of pigs, prevalence of LA-MRSA varies on farm level and in pigs tested in the Netherlands. Closed groups can also be MRSA positive. different kinds of pig farms, like farrowing farms and rearing farms, play a role in the transmission of MRSA to Dutch finishing farms. Screening of 310 pigs from these 31 farms showed 35 pigs (11%) to carry MRSA in their nares. On 7 of the 31 (23%) investigated farms colonized pigs were found, including 3 finishing farms, 3 farrowing farms and 1 farrow-to-finish farm. The use of standard antimicrobial medication of the pigs seemed to be a risk factor for MRSA carriage. Screening of the pigs on six farms supplying pigs for the MRSA positive farms revealed that the pigs on all but one farm were MRSA positive.	NL	van Duijkeren et al., 2008 [70]
LA-MRSA	HA, AH, AA, HH, EA, AE	All reported cases of livestock-associated MRSA (CC398) in humans and pigs in Norway between 2008 and 2014 were included. Three outbreak clusters were identified, including 26 pig farms, 2 slaughterhouses, and 36 humans. This study identified preventable routes of MRSA CC398 introduction and transmission: human occupational exposure, trade of pigs and livestock transport vehicles.	NOR	Grøntvedt et al., 2016 [71]
LA-MRSA	HA, AA, HH, EA	The VIM-1 carbapenemase most likely originated from humans and was isolated on a pig farm in Germany.	GER	Fischer et al., 2012 [72]
LA-MRSA	AA, AH,	In order to assess the dissemination of MRSA in the Dutch pig population, we screened 540 pigs in 9 slaughterhouses, where a representative portion of Dutch pigs (63%) was slaughtered in 2005. We found 209	NL	de Neeling et al., 2007 [73]

	AE, EA	(39%) of the pigs to carry MRSA in their nares. Forty-four of 54 groups of 10 consecutive pigs (81%), each group from a different farm, and all slaughterhouses were affected. The percentage of MRSA positive pigs was significantly different among slaughterhouses and among groups within slaughterhouses, indicating a high prevalence of MRSA in pigs delivered from the farms as well as cross contamination in the slaughterhouses.		
LA-MRSA	AA, AH, AE, EA	prevalence of LA-MRSA varies on farm level from 23 to 81% in the Netherlands, prevalence of LA-MRSA varies in pigs tested from 11 to 39 % in Europe.	NL, EU	Broens et al., 2011 [74]
LA-MRSA	AA, AE, EA	In Denmark 46% of pigs tested positive for MRSA CC398 on 80% of farms.	DEN	Lewis et al., 2008 [75]
LA-MRSA	AA, AE, EA, AH	In Germany, MRSA was isolated on 70% of pig farms.	GER	Köck et al., 2009 [76]
LA-MRSA	AA, AE, EA, AH	52% finishing pigs were MRSA-positive with a prevalence from 39% to 59% from east to south-west of the country.	GER	Alt et al., 2011 [77]
LA-MRSA	AA	The MRSA-carrying pigs differ depending on their breed	ESP	Porrero et al., 2012 [78]
LA-MRSA	AA, EA, AE, HA, AH	Although direct contact is probably the main route for MRSA transmission between pigs, also environmental contamination, the presence of other livestock, the herd size, and farm management are factors that may be involved in the dissemination of MRSA CC398.	BEL	Crombé et al., 2013 [79]
LA-MRSA	AE, EA, AH, AA	The dissemination of MRSA between pigs within a farm by air is based on a positive association of samples from pigs and environment.	GER	Friese et al., 2012 [80]
ESBL-E	AE, EA, AH, AA	Fischer et al. (2017) detected ESBL-*Enterobacteriaceae* on 61% of German pig farms.	GER	Fischer et al., 2017 [51]
ESBL-E	AE, EA, AH, AA	The presence of *Enterobacteriaceae* producing broad-spectrum betalactamase in food-producing animals range from 0.2 to 40.7% worldwide.	INT	Smet et al., 2009 [81]
ESBL-E	AE, EA, AH, AA	Particular investigations on *E. coli* in Swiss pigs detected ESBL-E in 15.3% of fecal samples. Five detected ESBLs (5.5%) belonged to the SHV group and 2 isolates (2.2%) contained a TEM-type enzyme. The relatively high rates of ESBL producers in food animals and the high genetic diversity among these isolates are worrisome and indicate an established reservoir in farm animals.	CHE	Geser et al., 2012 [82]
ESBL-E	AA, EA	Pig fecal samples were contaminated with ESBL-E in 11.0% in Denmark.	DEN	Agerso et al., 2011 [83]

ESBL-E	AA, EA	Pig fecal samples were contaminated with ESBL-E in 3.7% in the Netherlands.	NL	Bondt et al., 2013 [84]
ESBL-E	AA, EA	In Spain 72.0% (n = 29) of the *E. coli* isolates were positive for ESBL.	ESP	Escudero et al., 2010 [85]
ESBL-E	AE, EA, AH, AA	In Germany, on the level of the farm, up to 88.0% of the examined pig herds (in pigs and environmental samples) were suspicious for ESBL-E.	GER	Hering et al., 2014 [86]
ESBL-E	AA, EA	The most common ESBL genes detected from animal *E. coli* isolates were blaCTX-M-1 and M-14-blaCTX.	IT	Carattoli et al., 2008 [87]
ESBL-E	AA, EA	First isolation of CTX-M-1 from food-producing animals in Denmark.	DEN	Aarestrup et al., 2006 [88]
ESBL-E	AA, EA	First isolation of CTX-M-1 from food-producing animals in Spain.	ESP	Brinas et al., 2003 [89]

Table S4. Overview over LA-MRSA and ESBL-E in air and dust in the stable environment.
Abbreviations for the transmission pathways: HH = Human to Human, AA = Animal to Animal, HA = Human to Animal, AH = Animal to Human, HE = Human to Environment, EH = Environment to Human, AE = Animal to Environment, EA = Environment to Animal, EE = Environment to Environment, FH = Food to Human, HF = Human to Food, EF = Environment to Food, AF = Animal to Food.
Abbreviations for the countries: HUN = Hungary, NL = Netherlands, ESP = Spain, IT =Italy, EU = Europe, CHN = China, NOR =Norway, DEN = Denmark, UK = United Kingdom, GER = Germany, BEL = Belgium, FR = France, USA = United States of America, CHE = Switzerland.

Organism	**Transmission pathways**	**Key message**	**Country**	**First author, year**
Air and Dust – Biotope Stable (stable environment)				
LA-MRSA ESBL-E	EH, AE, EA, EE	The level of contamination of stable air by both airborne and coliform bacteria depends on both the animal and stable environment, including density, age, and activity of animals, the ventilation system, the quantity of dust.	HUN	Venglovský et al., 2011 [90]
LA-MRSA ESBL-E	AE, EA, EE	Survival rates of coliforms are best in the immediate vicinity of the animal and, therefore, in feces and fecal contaminated surfaces, whereas the detection rate in air immediately decreases.	GER	Gundermann, 1972 [91]; Müller, 1977 [92]
LA-	EH, AE,	As part of the EFSA study from 2009, pooled dust samples were investigated from pig breeding farms in	EU	EFSA study, 2009

MRSA	EA, EE	Germany: Contamination with MRSA CC398 was found on 41.8% of the farms with almost no differences on the breed level (43.5%) or the production level (41.3%). The distribution in Europe ranged from 11.7% MRSA CC398-positive pig breeding holdings to 25.5% pig production holdings.		[93]
LA-MRSA	EH, AE, EA, EE	On Chinese pig farms, MRSA was isolated from 59% of dust samples.	CHN	Wagenaar et al., 2009 [94]
LA-MRSA	EH, AE, EA, EE	Danish pig farms with 68% MRSA CC398-positive dust samples.	DEN	Espinosa-Gongora et al., 2012 [95]
LA-MRSA	AA, EH, AE, EA, EE	air, MRSA. indicate a high sensitivity of air samples equal to the within-herd prevalence. Therefore, they recommend air sampling for initial testing or even screening of herds.	NOR	Agersø et al., 2014 [96]
LA-MRSA	AH, EH	The presence of cultivable airborne methicillin-resistant S. aureus (MRSA) CC398 in a pig farm in Switzerland was reported for the first time. Total mean airborne concentrations of endotoxins (1298 units of endotoxin m–3) and fungi (5707 colony-forming units m–3) exceeded the Swiss recommended values and were higher in winter than in summer.	CHE	Masclaux et a., 2013 [25]
LA-MRSA	AA, EH, AE, EA, EE	The results show that there is regular airborne LA-MRSA transmission and deposition, which are strongly influenced by wind direction and season, of up to at least 300 m around positive pig barns.	GER	Schulz et al., 2012 [97]
LA-MRSA	AA, EH, AE, EA, EE	Dust is an important factor for the occurrence of MRSA in the air. The dissemination of MRSA between pigs within a farm by air is based on a positive association of samples from pigs and environment.	GER	Friese et al., 2012 [80]
LA-MRSA	EE, AE, EA	No evidence of MRSA-positive isolates in animal drinking water on pig and poultry farms, while environmental samples (dust, animal feed, manure) and samples from pigs and farmers were contaminated with MRSA	NL	Pletinckx et al., 2011 [98]
LA-MRSA	EH, AE, EA, EE	85.2% of pig stables in Germany are LA-MRSA positive in the air. They also identified dust as an important factor for the occurrence of MRSA in the air. Drug-resistant S. aureus could be identified inside and outside the pig stables and originated from contaminated dust.	GER	Gibbs et al., 2004 [99]
LA-MRSA ESBL-E	EH, AE, EA, EE	The imbalance between gram-positive and gram-negative bacteria is attributed to the lower survival time of gram-negative bacteria in their airborne condition. *S. aureus* can disperse in the air as directly suspendable airborne particles. Coliform bacteria, which are excreted in feces, are mechanically bound to stable surfaces and/or litter and feed.	GER	Hartung et al., 1998 [100]
LA-MRSA	EH, AE, EA, EE	Hoffmann (2014) proved the association of CTX-M-1-positive dust samples obtained from pig farms with positive fecal samples from farm workers. On the other hand, the positivity of CTX-M-1 in pig and human feces	GER	Hoffmann, 2014 [101]

ESBL-E		was significantly associated. Therefore, he hypothesizes a possible transmission of CTX-M-1 subtypes to humans via inhalation of contaminated dust particles during exposure in the stable environment.		
ESBL-E	EH, AE, EA, EE, AA	In the vicinity of the pig barns these resistant bacteria were detected in 14/87 (16.1%) boot swabs taken from various ground surfaces and in 2/36 (6%) ambient air samples. Inside the pig barns, 6/63 (9.5%) barn air samples and a small proportion of flies and mice feces samples were ESBL/AmpC-positive.	GER	von Salviati et al. 2015 [102]
ESBL-E	HH, AA, HA, AH, EH, AE, EA, EE	saying that CTX-M-1 carriage in pig farmers and the presence of CTX-M-1 in dust are associated, indicating that air transmission of CTX-M 1 might be possible on pig farms.	GER	Dohmen et al., 2017 [103]
ESBL-E	EH, AE, EA, EE	the emissions of ESBL-producing E. coli from pig farms to the surrounding environment, fecal and environmental samples from six pig farms were collected. In total, 119 ESBL-producing E. coli were isolated from feces, air samples, water, sludge and soil samples. Antibiotic susceptibility testing showed that the ESBL-producing isolates were resistant to multiple antibiotics and isolates of different origin within the same farm showed similar resistance phenotypes.	CHN	Gao et al., 2015 [104]
LA-MRSA ESBL-E	AA, AH, EH, AE, EA, EE	MRSA and ESBl-E was detected in air and dust.	GER	Schmithausen et al., 2015 [105]
LA-MRSA ESBL-E	AA, HA, AH, EH, AE, EA, EE	The transmission pathway of ESBL-*Enterobacteriaceae* via air and/or dust a spread via the airborne route or via different vectors seems possible.	GER	Schmithausen et al., 2015 [106]
LA-MRSA	AH, EH	Exposure to ST398 MRSA in barn air seems to be an important determinant for nasal carriage, especially in the highly exposed group of farmers, next to duration of contact with animals.	NL	Bos et al., 2016 [57]
LA-MRSA	AH, EH, AE, EA, EE	MRSA was detected in air and dust.	GER	Heinemann et al., 2017 [60]
LA-MRSA	EH, AE, EA, EE	Isolation of antibiotic-resistant bacteria from the air plume downwind of a swine confined or concentrated animal feeding operation. Bacterial concentrations with multiple antibiotic resistances or multidrug resistance were recovered inside and outside to (at least) 150 m downwind of this facility.	GER	Gibbs et al., 2006 [99]

LA-MRSA	EH, AE, EA, EE	Bacterial plume are emanating from the air surrounding swine confinement operations.	UK	Green et al., 2006 [107]

Table S5. Table overview over LA-MRSA and ESBL-E in Water, Wastewater and Manure of pig production facilities.
Abbreviations for the transmission pathways: HH = Human to Human, AA = Animal to Animal, HA = Human to Animal, AH = Animal to Human, HE = Human to Environment, EH = Environment to Human, AE = Animal to Environment, EA = Environment to Animal, EE = Environment to Environment, FH = Food to Human, HF = Human to Food, EF = Environment to Food, AF = Animal to Food.
Abbreviations for the countries: NL = Netherlands, ESP = Spain, IT =Italy, EU = Europe, CHN = China, NOR =Norway, DEN = Denmark, UK = United Kingdom, GER = Germany, BEL = Belgium, FR = France, USA = United States of America, CHE = Switzerland, PHL = Philippines.

Organism	**Transmission pathways**	**Key message**	**Country**	**First author, year**
Drinking water – Biotope Stable (stable environment)				
LA-MRSA	EH, AE, EA, EE	The authors did not find any evidence of MRSA-positive isolates in animal drinking water on pig and poultry farms, while environmental samples (dust, animal feed, manure) and samples from pigs and farmers were contaminated with MRSA	NL	Pletinckx, 2011 [98]
LA-MRSA	EH, AE, EA, EE	spa types t011 (35.3%, 6/17) and t2011 (70.6%, 12/17) were found in all samples (human, pig, air, dust, drinking water and troughs).	GER	Schmithausen et al., 2015 [105]
LA-MRSA ESBL-E	EH, AE, EA, EE	Presently there are no specific legal regulations which define the quality of the drinking water for animals in Germany. However, some rules and criteria exist which help to survey and secure the water supply of animals on farm level.	GER	Hartung, 2000 [108]
LA-MRSA ESBL-E	EH, AE, EA, EE	Only an integrated vision of these two aspects can provide elements to assess the risk of spread of antibiotic resistances via water bodies and suggest, in this context, solutions for this urgent health issue.	GER	Lupo, 2012 [109]
LA-MRSA ESBL-E	EH, AE, EA, EE	The authors found high bacterial loads in animal drinkers after cleaning and disinfection, which could lead to a vertical transfer of pathogens to newly arriving pigs. They evaluate methods for cleaning performances in pig stables.	GER	Heinemann et al., 2017 [61]
Wastewater – Biotope environment (stable environment/agricultural influence)				
ESBL-E	AE, EE, HE, EH,	The reservoir of resistance genes in the environment is due to a mix of naturally occurring resistance and those present in animal and human waste and the selective effects of pollutants, which can co-select for mobile	UK	Wellington et al., 2013 [110]

	AH	genetic elements carrying multiple resistant gene.		
ESBL-E	HA, EA, AE	ESBL-producing *Enterobacteriaceae* were detected in the five samples of human sewage, in samples from 8 of 10 pig farms.	ESP	Mesa, 2006 [28]
ESBL-E	EH, AE, EA, EE	The authors proved that multidrug-resistant isolates were observed in irrigation water, soil, and vegetables in urban farms were most prevalent in water (25.3%) compared to soil (2.8%) and vegetable (8.4%) isolates, indicating that water serves as a possible route for a wide distribution across all kinds of borders.	PHL	Vital et al., 2018 [111]
MRSA	AE, AH, HE, EE	MRSA was isolated with a higher percentage from swine wastewater samples (62.8%) than from municipal WWTPs (3.7%). In swine slaughterhouse wastewater were antiseptic-resistant MRSA strains detected.	CHN	Wan and Chou et al., 2015 [112]
ESBL-E	AE, AH, HE, EE, EH	Diallo et al. (2013) identified a significantly higher prevalence of ESBL-producing *E. coli* from municipal wastewater (8.4%), compared to slaughterhouse wastewater (1.2%).	GER	Diallo et al., 2013 [113]
ESBL-E	AE, AH, HE, EE, EH	This is confirmed by Müller et al. (2016), who found identical ESBL CTX-M-15 clones in surface water and healthy humans.	GER	Müller et al., 2016 [114]
ESBL-E	EE, HE, AE	More highly resistant gramnegative strains were found in wastewater treatment plants with urban/clinical influence than in wastewaters with rural influence.	GER	Müller et al., 2018 [115]
ESBL-E	AE, EH, EA, EE	Animals may defecate onto surface waters directly, or animal faeces may reach surface waters by runoff. Exposure of humans to ESBL-producing bacteria in the aquatic environment may occur.	RA	Schijven et al., 2015 [116]
ESBL-E	AE, AH, HE, EE, EH	Hu et al. (2013) discovered CTX-M-1 in both human and water-environmental *E. coli* isolates, suggesting frequent and continuous inter-compartment transmission between human and water-environment.	CHN	Hu et al., 2013 [117]
ESBL-E	AE, AH, HE, EE, EH	Zurfluh et al. (2015a) isolated CTX-M-15 ESBL-*Enterobacteriaceae* in the environment, livestock and humans.	CHE	Zurfluh et al., 2015 [118]
Manure – Biotope environment (stable environment)				
MRSA	EH, AH	Casey et al. (2013) assume that 11% of MRSA and skin and soft tissue infections in humans may be caused by the application of pig manure to soil.	USA	Casey et al., 2013 [119]
LA-	EE, AE,	Gompel (2014) identified minute quantities of MRSA CC398 in manure and lesser amounts in soil and air.	GER	Gompel, 2014

MRSA	HE, EH			[120]
LA-MRSA ESBL-E	EE, AE, HE, EH	Even more, ESBL and AmpC resistance genes encoding betalactamase activity originating from livestock have been found in wastewater, surface water, and even in drinking water biofilms.	GER	Schwartz et al., 2003 [121]
LA-MRSA ESBL-E	EE, AE, HE, EH,	The prevalence of antibiotic residues and antibiotic resistance is significantly influenced by the inputs from agricultural animal husbandry.	GER	Westphal-Settele et al., 2018 [122]
ESBL-E	HE, AE, EE	The author indicates that the coliform bacteria residing in the intestinal flora of humans and animals can be distributed to soil by manure.	GER	Witte, 2000 [123]
ESBL-E	HE, AE, EE	*E. coli* producing SHV, TEM, and CTX-M enzymes have been isolated from manure and fertilized soil.	GER	Friese et al., 2013 [124]
ESBL-E	HE, AE, EE	Hartmann (2012) has proven long-term survival of CTX-M isolates in soil; isolates were from soil that had been treated with manure one year before sampling.	GER	Hartmann, 2012 [125]
ESBL-E	AE, HE, EE, EA, EH	High rates of (multi-) resistant bacteria in pig manure emphasize the need for a prudent use of antibiotics in farm animals in Europe. Heavy metals might select antibiotic resistant bacteria. Hölzel et al. (2010) report the prevalence of ESBL-E isolates below 2% for both pig manure and sludge.	EU	Hölzel, 2010; Hölzel et al., 2012 [126]
ESBL-E	EH, EA, EE	Manure has become a reservoir of resistant bacteria and antibiotic compounds, and its application to agricultural soils is assumed to significantly increase antibiotic resistance genes and selection of resistant bacterial populations in soil. The human exposure to soil-borne resistance has yet to be determined, but is likely to be underestimated.	GER	Heuer et al., 2011; Heuer et al., 2007 [127,128]
ESBL-E	EE, AE, HE, EH	Results obtained in this study thus indicate that tetracycline resistance levels in soil are temporarily influenced by the addition of pig manure slurry. The results indicate also that increased amount of pig manure slurry amendment may result in increased levels of tetracycline resistance in the soil.	NOR	Agersø et al., 2006 [88]
ESBL-E	EE, AE, HE, EH	ESBL producers from feces and environmental samples within the same farm carried similar CTX-M types. The results indicated that the ESBL-producing E. coli carrying multidrug resistance could readily disseminate to the surrounding environment.	CHN	Gao et al., 2015 [104]
LA-MRSA	HE, AE, EE, EH, EA	Environmental samples (dust, animal feed, manure) and samples from pigs and farmers were contaminated with MRSA.	NL	Pletinckx et al., 2011 [98]
ESBL-E	EH, EA, EE	Manure antibiotic residues synergistically increase the bacterial antibiotic resistance in soil over months (Heuer and Smalla, 2007).	GER	Heuer and Smalla, 2007 [128]
ESBL-E	HE, AE, EE, EH,	Von Salviati et al. (2015) detected high prevalences of ESBL-E in manure and proofed the emission potential via manure and transmission via flies in pig farms and their surroundings. In the vicinity of the pig barns	GER	von Salviati et al., 2015 [102]

	EA	ESBL/AmpC-producing E. coli were detected in 16.1% (14/87) of the examined boot swab samples taken from various ground surfaces and in 6% (2/36) of ambient air samples. The majority of slurry samples (82.4%; 14/17) and three of four samples of digestate from biogas plants were also tested positive for these resistant bacteria. In total 274 E. coli isolates were further analysed by phenotypical and genotypical methods. The present study provides novel information about amounts and dynamics of ESBL/AmpC-producing E. coli in the German pig production. Moreover, this is the first systematic study on a potential emission and transmission of ESBL/AmpC-producing bacteria between pig fattening farms and their surroundings. Contaminated slurry presented the major emission source for ESBL/AmpC-producing E. coli in the pig fattening farms (von Salviati et al., 2015).		

Table S6. Table overview over LA-MRSA and ESBL-E in the Food Chain: Abattoir Biotope and Human vectors in Pig Meat Processing.
Abbreviations for the transmission pathways: HH = Human to Human, AA = Animal to Animal, HA = Human to Animal, AH = Animal to Human, HE = Human to Environment, EH = Environment to Human, AE = Animal to Environment, EA = Environment to Animal, EE = Environment to Environment, FH = Food to Human, HF = Human to Food, EF = Environment to Food, AF = Animal to Food.
Abbreviations for the countries: CAN =Canada, NL = Netherlands, ESP = Spain, IT =Italy, EU = Europe, CHN = China, NOR =Norway, DEN = Denmark, UK = United Kingdom, GER = Germany, BEL = Belgium, FR = France, USA = United States of America, CHE = Switzerland, JAP = Japan, AUS = Austria.

Organism	**Transmission pathways**	**Key message**	**Country**	**First author, year**
Food – Biotope Abattoir (Meat)				
LA-MRSA ESBL-E	FH, HF, AH	The exposure of consumers to antibiotic-resistant bacteria depends on a variety of factors in the food chain, such as antibiotic usage in food animals, the level of excretion at the time of slaughter, hygiene related to the slaughter processes, meat processing hygiene, and retail handling.	CAN	Vincent et al., 2010 [129]
LA-MRSA	AH, AF, FF, FH, AA	Several studies in European abattoir biotopes report a very high prevalence of nasal MRSA carriage in slaughter pigs, of the slaughter pigs or even 70% [286] were found to be MRSA-positive. The study of Normanno et al. shows the great genetic diversity of MRSA strains in slaughtered pigs and in abattoir employees in Italy. The main path of contamination is caused by smear infections due to improper removal of the intestines, especially the intestinal package. In Italy, the prevalence among pigs at slaughter was (38%).	IT	Normanno et al., 2015 [130]
LA-MRSA	AF, AA, AH	Abattoirs are possible sources of drug-resistant bacteria, In Italy, the prevalence among pigs at slaughter was (38%)	IT	Ikegbunam et al., 2014 [131]

LA-MRSA	AF, AA	Several studies in abattoirs report from 1% of slaughter pigs are colonized with MRSA.	IT	Guardabassi et al., 2007 [132]
LA-MRSA	AA, AH, EA, EE	The transmission of MRSA to slaughter pigs (39%) is assumed to be prior to their arrival at the abattoir. Nevertheless, the high prevalence of MRSA in abattoirs may be assumed to have been caused by cross contamination in the waiting areas.	NL	de Neeling et al., 2007 [73]
LA-MRSA	AA, EE, AE, EA, AF, FF	All pigs (n=117) tested MRSA negative before transportation. On arrival at the abattoir, 12/117 (10.3%) pigs in two batches tested MRSA positive. In lorries that tested positive after transportation, the prevalence of MRSA positive pigs was 21.1%, whereas no MRSA was detected in pigs that had been transported in lorries that tested negative after transportation. At stunning, all batches and 70/117 (59.8%) pigs tested MRSA positive. Pigs can become MRSA positive in the short period of time during transportation from the farm to stunning at the abattoir.	NL	Broens et al., 2011 [68]
LA-MRSA	AA, AF	were found to be MRSA-positive. In Germany slaughter pigs were determined to be MRSA-positive up to *70.8% [287], of 99% slaughter batches found to be positive for MRSA in the Netherlands.*	NL	Dierikx et al., 2016 [44]
LA-MRSA ESBL-E	AA, AH, AF, HF, AE, EA	In Germany slaughter pigs were determined to be MRSA-positive up to 21% at the Dutch-German border. Statistically significant acquisition of MRSA or ESBL-E in pigs tested negative before arrival at the abattoirs was observed in 29.7% and 29.4%. All pig carcasses were negative for MRSA and ESBL-E.	GER	Schmithausen et al., 2015 [106]
LA-MRSA ESBL-E	AA, AE, EA, AF	This epidemiological study indicates the importance of horizontal approaches: (i. pigs sampled on the farm before transport to the abattoir, ii. in the waiting area at the abattoir, iii. on the carcasses, iv. and on the retail pork.	GER	Tenhagen et al., 2009 [133]
ESBL-E	AA, AH, AF, HF, AE, EA	ESBL-E in slaughter pigs in Switzerland (15.2%), Furthermore, it has been shown that retail samples reflect the presence of antibiotic resistance on farms.	CHE	Geser et al., 2011 [134]
ESBL-E	AA, AE, EA, AF	ESBL-E in slaughter pigs in Denmark (11 %). However, the processing of food in meat production facilities may also contribute to the spread of antibiotic-resistant bacteria to the consumer at the endpoint of the food chain.	NOR	Agersø et al., 2014 [96]
ESBL-E	AA, AE, EA, AF	ESBL-E in slaughter pigs in the UK (23.4%).	UK	Randall et al., 2014 [135]
ESBL-E	AA, AE,	The level of ESBL-E shedding in pigs has been studied and shows levels in piglets of 107 CFU/g, with a drop to	GER	Hansen et al.,

	EA, AF	103 CFU/g in animals at slaughter.		2013 [136]
LA-MRSA	AF	the isolation of MRSA from samples derived from post-mortem examinations at the Animal Health Service in The Netherlands in the period from 2003 through October 2008.The proportion of pigs from which MRSA was isolated from, did not increase over the years.	NL	Van der Wolf et al., 2012 [137]
LA-MRSA	AA, AH, AF, HF, AE, EA	Samples of raw beef, pork, veal, lamb/mutton, chicken, turkey, fowl and game were collected from the retail trade. MRSA strains were isolated from 264 (11.9%) of 2217 samples analyzed: 6.2% in pork. At present the high prevalence of MRSA in meat has not been shown to contribute significantly to the dissemination of MRSA to humans and the possible health hazard for consumers of the presence of MRSA in foods should be further elucidated. De Boer et al. isolated the CC398 MRSA strain on 10.7% of pork in the Netherlands. Furthermore, it has been shown that retail samples reflect the presence of antibiotic resistance on farms.	NL	De Boer et al., 2009 [138]
LA-MRSA	HH, HA, HE, FH, HF, EF	presented a horizontal approach that shows 3% of pigs sampled on the farm before transport to the abattoir, 1% in the waiting area at the abattoir, 2% of carcasses, and 4% of retail pork samples were MRSA positive.		Molla et al., 2012 [139]
Human vectors in Pig Meat Processing				
ESBL-E	HH, HA, HE, FH, HF, EF	Humans involved in food processing need to be considered as very important intermediate reservoirs and vectors for ESBL genes remain food retailers contaminated with ESBL-producing bacteria. Food dealers especially may represent a reservoir for ESBL genes, because while working with contaminated food they are at a greater risk for infection with ESBL-producing bacteria [306]. Lavilla et al. [306] found that 27.5% of food retailers (372 tested persons) are colonized with ESBL-producing microorganisms. Therefore, the food retailer is considered to be an intermediate vector for the transmission of antibiotic-resistant bacteria.	IT	Lavilla, 2008 [140]
ESBL-E	AH, AE, EF, AF, HF	Bacteria from the intestinal tract of slaughter pigs can be transferred to the carcass during processing in abattoirs by the staff, contaminated tools, or other contact surfaces.	GER	Teuber, 1999 [141]
ESBL-E	FH, HF	determined that retail foods may be an important vehicle for the community-wide dissemination of antimicrobial-resistant *E. coli*. Furthermore, studies in Denmark comparing *E. coli* from meat and urinary tract infections suggest that *E. coli* strains obtained from meat and production animals pose a zoonotic risk for humans.	UK	Johnson, 2005 [142]
ESBL-E	FH	The findings of López-Cerero et al., 2011 showed the possibility of lateral gene transfer of blaCTX-M-15 as well as other antibiotic resistance determinants between low-virulence food and clinical isolates.	ESP	López-Cerero et al., 2011 [143]
ESBL-E	HF, FH,	Pietsch et al. 2015 found isolates of distinct *E. coli* clonal lineages in all three reservoirs human, animal and	GER	Pietsch et al., 2015

	AF	food.		[144]
ESBL-E	HF, FH	Data have shown reduced survival of zoonotic bacteria in meat processing facilities.	USA	Erickson et al., 2012 [145]
ESBL-E	AF, HF, FH	Antibiotic-resistant *Enterobacteriaceae* can contaminate foods during the processes of packing and storage.	PRT	Fornazari et al., 2010 [146]
ESBL-E	HF, FH, AF	ESBL *E.coli* in farm animals and raw retail meat in Japan.	JAP	Hiroi et al., 2011 [147]
LA-MRSA ESBL-E	AF, HF, FH	A contamination of meat with ESBL-producing E. coli and MRSA was confirmed in this study. The large diversity of ESBL producing *E. coli* could indicate a growing dissemination of ESBL genes in *E. coli* found in meat products from porcine and bovine origin.	AUS	Petternel et al., 2014 [148]

Supplementary Table References

1. Norpoth, A. Resistenzdynamik der E.Coli Population der Darmflora von Schweinen unter Einfluß von Sulfamidin. University of Bonn, Bonn, 1989.
2. Lammers, J. Methodische Untersuchungen zur Erfassung der Keimflora in Schweineställen und Bestimmung der Resistenz von Indikatorkeimen. University of Bonn, 1983.
3. Pohl, P. Effects et consequences de l´antibiosupplémentation sur la résistance des entéro bactéries du bétail. *Schweiz. Arch. Tierheilkde* 1983.
4. Aarestrup, F.M.; Wegener, H.C. The effects of antibiotic usage in food animals on the development of antimicrobial resistance of importance for humans in Campylobacter and Escherichia coli. *Microbes Infect* **1999**, *1*, 639-644.
5. Wegener, H.C. Antibiotics in animal feed and their role in resistance development. *Curr Opin Microbiol* **2003**, *6*, 439-445.
6. Acar, J.; Röstel, B. Antimicrobial resistance: an overview. *Rev Sci Tech* **2001**, *20*, 797-810.
7. Tenover, F.C. Mechanisms of antimicrobial resistance in bacteria. *Am J Med* **2006**, *119*, S3-10; discussion S62-70, doi:10.1016/j.amjmed.2006.03.011.
8. Smith, D.L.; Harris, A.D.; Johnson, J.A.; Silbergeld, E.K.; Morris, J.G. Animal antibiotic use has an early but important impact on the emergence of antibiotic resistance in human commensal bacteria. *Proc Natl Acad Sci U S A* **2002**, *99*, 6434-6439, doi:10.1073/pnas.082188899.
9. O'Brien, T.F. Emergence, spread, and environmental effect of antimicrobial resistance: how use of an antimicrobial anywhere can increase resistance to any antimicrobial anywhere else. *Clin Infect Dis* **2002**, *34 Suppl 3*, S78-84, doi:10.1086/340244.
10. Austin, D.J.; Kristinsson, K.G.; Anderson, R.M. The relationship between the volume of antimicrobial consumption in human communities and the frequency of resistance. *Proc Natl Acad Sci U S A* **1999**, *96*, 1152-1156.

11. Messing, F.-J. Persistenz von Resistenzdeterminanten bei E.Coli- und Staphylokokken Aureus-Isolaten aus den Medien Kot, Urin, Oberflächen und Luft gegenüber antibakteriell wirksamen Substanzen. University of Bonn, Bonn, 1986.
12. Schwarz, S.; Kehrenberg, C.; Walsh, T.R. Use of antimicrobial agents in veterinary medicine and food animal production. *Int J Antimicrob Agents* **2001**, *17*, 431-437.
13. Robinson, D.A.; Enright, M.C. Multilocus sequence typing and the evolution of methicillin-resistant Staphylococcus aureus. *Clin Microbiol Infect* **2004**, *10*, 92-97.
14. Robinson, D.A.; Enright, M.C. Evolution of Staphylococcus aureus by large chromosomal replacements. *J Bacteriol* **2004**, *186*, 1060-1064.
15. Tschäpe, H.; Rische, H. *Ökologie und epidemiologische Bedeutung der infektiösen Chemotherapeutikaresistenz*; 1974; Vol. 22.
16. Blake, D.P.; Hillman, K.; Fenlon, D.R.; Low, J.C. Transfer of antibiotic resistance between commensal and pathogenic members of the Enterobacteriaceae under ileal conditions. *J Appl Microbiol* **2003**, *95*, 428-436.
17. Martinez, J.L. The role of natural environments in the evolution of resistance traits in pathogenic bacteria. *Proc Biol Sci* **2009**, *276*, 2521-2530, doi:10.1098/rspb.2009.0320.
18. van den Bogaard, A.E.; Stobberingh, E.E. Epidemiology of resistance to antibiotics. Links between animals and humans. *Int J Antimicrob Agents* **2000**, *14*, 327-335.
19. Martinez, J.L. Environmental pollution by antibiotics and by antibiotic resistance determinants. *Environ Pollut* **2009**, *157*, 2893-2902, doi:10.1016/j.envpol.2009.05.051.
20. Lebek, G. Einflüsse der antibakteriellen Arzneimittel im Tierfutter auf das Auftreten von antibiotika- und chemoresistenten Pathogenese Bakterien. *Zbl.Vet.Med.B.* 1970, pp 103-115.
21. Sørum, H.; Sunde, M. Resistance to antibiotics in the normal flora of animals. *Vet Res* **2001**, *32*, 227-241, doi:10.1051/vetres:2001121.
22. Bengtsson-Palme, J.; Kristiansson, E.; Larsson, D.G.J. Environmental factors influencing the development and spread of antibiotic resistance. *FEMS Microbiol Rev* **2018**, *42*, doi:10.1093/femsre/fux053.
23. Rolle, M.; Mayr, A. *Mikrobiologie, Infektions- und Seuchenlehre*, 5 ed.; Stuttgart, 1984.
24. Norpoth, A.; Petersen, B. Epidemiologische Bedeutung der infektiösen Arzneimittelresistenz bei Bakterien (E.Coli) aus Schweinebeständen. *ZAU* 1990 pp 75-87.
25. Masclaux, F.G.; Sakwinska, O.; Charrière, N.; Semaani, E.; Oppliger, A. Concentration of airborne Staphylococcus aureus (MRSA and MSSA), total bacteria, and endotoxins in pig farms. *Ann Occup Hyg* **2013**, *57*, 550-557, doi:10.1093/annhyg/mes098.
26. Larsen, J.; Imanishi, M.; Hinjoy, S.; Tharavichitkul, P.; Duangsong, K.; Davis, M.F.; Nelson, K.E.; Larsen, A.R.; Skov, R.L. Methicillin-resistant Staphylococcus aureus ST9 in pigs in Thailand. *PLoS One* **2012**, *7*, e31245, doi:10.1371/journal.pone.0031245.
27. van Loo, I.; Huijsdens, X.; Tiemersma, E.; de Neeling, A.; van de Sande-Bruinsma, N.; Beaujean, D.; Voss, A.; Kluytmans, J. Emergence of methicillin-resistant Staphylococcus aureus of animal origin in humans. *Emerg Infect Dis* **2007**, *13*, 1834-1839, doi:10.3201/eid1312.070384.

28. Mesa, R.J.; Blanc, V.; Blanch, A.R.; Cortés, P.; González, J.J.; Lavilla, S.; Miró, E.; Muniesa, M.; Saco, M.; Tórtola, M.T., et al. Extended-spectrum beta-lactamase-producing Enterobacteriaceae in different environments (humans, food, animal farms and sewage). *J Antimicrob Chemother* **2006**, *58*, 211-215, doi:10.1093/jac/dkl211.
29. Mugnaioli, C.; Luzzaro, F.; De Luca, F.; Brigante, G.; Perilli, M.; Amicosante, G.; Stefani, S.; Toniolo, A.; Rossolini, G.M. CTX-M-type extended-spectrum beta-lactamases in Italy: molecular epidemiology of an emerging countrywide problem. *Antimicrob Agents Chemother* **2006**, *50*, 2700-2706, doi:10.1128/AAC.00068-06.
30. Dorado-García, A.; Smid, J.H.; van Pelt, W.; Bonten, M.J.M.; Fluit, A.C.; van den Bunt, G.; Wagenaar, J.A.; Hordijk, J.; Dierikx, C.M.; Veldman, K.T., et al. Molecular relatedness of ESBL/AmpC-producing Escherichia coli from humans, animals, food and the environment: a pooled analysis. *J Antimicrob Chemother* **2018**, *73*, 339-347, doi:10.1093/jac/dkx397.
31. Köck, R.; Becker, K.; Cookson, B.; van Gemert-Pijnen, J.E.; Harbarth, S.; Kluytmans, J.; Mielke, M.; Peters, G.; Skov, R.L.; Struelens, M.J., et al. Methicillin-resistant Staphylococcus aureus (MRSA): burden of disease and control challenges in Europe. *Euro Surveill* **2010**, *15*, 19688.
32. van Cleef, B.A.; Verkade, E.J.; Wulf, M.W.; Buiting, A.G.; Voss, A.; Huijsdens, X.W.; van Pelt, W.; Mulders, M.N.; Kluytmans, J.A. Prevalence of livestock-associated MRSA in communities with high pig-densities in The Netherlands. *PLoS One* **2010**, *5*, e9385, doi:10.1371/journal.pone.0009385.
33. Petersen, A.; Stegger, M.; Heltberg, O.; Christensen, J.; Zeuthen, A.; Knudsen, L.K.; Urth, T.; Sorum, M.; Schouls, L.; Larsen, J., et al. Epidemiology of methicillin-resistant Staphylococcus aureus carrying the novel mecC gene in Denmark corroborates a zoonotic reservoir with transmission to humans. *Clin Microbiol Infect* **2013**, *19*, E16-22, doi:10.1111/1469-0691.12036.
34. Hunter, P.A.; Dawson, S.; French, G.L.; Goossens, H.; Hawkey, P.M.; Kuijper, E.J.; Nathwani, D.; Taylor, D.J.; Teale, C.J.; Warren, R.E., et al. Antimicrobial-resistant pathogens in animals and man: prescribing, practices and policies. *J Antimicrob Chemother* **2010**, *65 Suppl 1*, i3-17, doi:10.1093/jac/dkp433.
35. Cantas, L.; Suer, K. Review: the important bacterial zoonoses in "one health" concept. *Front Public Health* **2014**, *2*, 144, doi:10.3389/fpubh.2014.00144.
36. Valentin, L.; Sharp, H.; Hille, K.; Seibt, U.; Fischer, J.; Pfeifer, Y.; Michael, G.B.; Nickel, S.; Schmiedel, J.; Falgenhauer, L., et al. Subgrouping of ESBL-producing Escherichia coli from animal and human sources: an approach to quantify the distribution of ESBL types between different reservoirs. *Int J Med Microbiol* **2014**, *304*, 805-816, doi:10.1016/j.ijmm.2014.07.015.
37. Leverstein-van Hall, M.A.; Dierikx, C.M.; Cohen Stuart, J.; Voets, G.M.; van den Munckhof, M.P.; van Essen-Zandbergen, A.; Platteel, T.; Fluit, A.C.; van de Sande-Bruinsma, N.; Scharinga, J., et al. Dutch patients, retail chicken meat and poultry share the same ESBL genes, plasmids and strains. *Clin Microbiol Infect* **2011**, *17*, 873-880, doi:10.1111/j.1469-0691.2011.03497.x.

38. Overdevest, I.; Willemsen, I.; Rijnsburger, M.; Eustace, A.; Xu, L.; Hawkey, P.; Heck, M.; Savelkoul, P.; Vandenbroucke-Grauls, C.; van der Zwaluw, K., et al. Extended-spectrum β-lactamase genes of Escherichia coli in chicken meat and humans, The Netherlands. *Emerg Infect Dis* **2011**, *17*, 1216-1222, doi:10.3201/eid1707.110209.
39. Guardabassi, L.; Larsen, J.; Weese, J.S.; Butaye, P.; Battisti, A.; Kluytmans, J.; Lloyd, D.H.; Skov, R.L. Public health impact and antimicrobial selection of meticillin-resistant staphylococci in animals. *J Glob Antimicrob Resist* **2013**, *1*, 55-62, doi:10.1016/j.jgar.2013.03.011.
40. Verkade, E.; van Benthem, B.; den Bergh, M.K.; van Cleef, B.; van Rijen, M.; Bosch, T.; Kluytmans, J. Dynamics and determinants of Staphylococcus aureus carriage in livestock veterinarians: a prospective cohort study. *Clin Infect Dis* **2013**, *57*, e11-17, doi:10.1093/cid/cit228.
41. van Cleef, B.A.; Graveland, H.; Haenen, A.P.; van de Giessen, A.W.; Heederik, D.; Wagenaar, J.A.; Kluytmans, J.A. Persistence of livestock-associated methicillin-resistant Staphylococcus aureus in field workers after short-term occupational exposure to pigs and veal calves. *J Clin Microbiol* **2011**, *49*, 1030-1033, doi:10.1128/JCM.00493-10.
42. Garcia-Graells, C.; van Cleef, B.A.; Larsen, J.; Denis, O.; Skov, R.; Voss, A. Dynamic of livestock-associated methicillin-resistant Staphylococcus aureus CC398 in pig farm households: a pilot study. *PLoS One* **2013**, *8*, e65512, doi:10.1371/journal.pone.0065512.
43. Feingold, B.J.; Silbergeld, E.K.; Curriero, F.C.; van Cleef, B.A.; Heck, M.E.; Kluytmans, J.A. Livestock density as risk factor for livestock-associated methicillin-resistant Staphylococcus aureus, the Netherlands. *Emerg Infect Dis* **2012**, *18*, 1841-1849, doi:10.3201/eid1811.111850.
44. Dierikx, C.M.; Hengeveld, P.D.; Veldman, K.T.; de Haan, A.; van der Voorde, S.; Dop, P.Y.; Bosch, T.; van Duijkeren, E. Ten years later: still a high prevalence of MRSA in slaughter pigs despite a significant reduction in antimicrobial usage in pigs the Netherlands. *J Antimicrob Chemother* **2016**, *71*, 2414-2418, doi:10.1093/jac/dkw190.
45. 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**, *53*, 1709-1711, doi:10.1128/AAC.01014-08.
46. Hammerum, A.M.; Larsen, J.; Andersen, V.D.; Lester, C.H.; Skovgaard Skytte, T.S.; Hansen, F.; Olsen, S.S.; Mordhorst, H.; Skov, R.L.; Aarestrup, F.M., et al. Characterization of extended-spectrum β-lactamase (ESBL)-producing Escherichia coli obtained from Danish pigs, pig farmers and their families from farms with high or no consumption of third- or fourth-generation cephalosporins. *J Antimicrob Chemother* **2014**, doi:10.1093/jac/dku180.
47. Vanderhaeghen, W.; Hermans, K.; Haesebrouck, F.; Butaye, P. Methicillin-resistant Staphylococcus aureus (MRSA) in food production animals. *Epidemiol Infect* **2010**, *138*, 606-625, doi:10.1017/S0950268809991567.
48. Falgenhauer, L.; Imirzalioglu, C.; Ghosh, H.; Gwozdzinski, K.; Schmiedel, J.; Gentil, K.; Bauerfeind, R.; Kämpfer, P.; Seifert, H.; Michael, G.B., et al. Circulation of clonal populations of fluoroquinolone-resistant CTX-M-15-producing Escherichia coli ST410 in humans and animals in Germany. *Int J Antimicrob Agents* **2016**, *47*, 457-465, doi:10.1016/j.ijantimicag.2016.03.019.

49. Hille, K.; Fischer, J.; Falgenhauer, L.; Sharp, H.; Brenner, G.M.; Kadlec, K.; Friese, A.; Schwarz, S.; Imirzalioglu, C.; Kietzmann, M., et al. [On the occurence of extended-spectrum- and AmpC-beta-lactamase-producing Escherichia coli in livestock: results of selected European studies]. *Berl Munch Tierarztl Wochenschr* **2014**, *127*, 403-411.
50. Fischer, J.; Hille, K.; Mellmann, A.; Schaumburg, F.; Kreienbrock, L.; Köck, R. Low-level antimicrobial resistance of Enterobacteriaceae isolated from the nares of pig-exposed persons. *Epidemiol Infect* **2016**, *144*, 686-690, doi:10.1017/S0950268815001776.
51. Fischer, J.; Hille, K.; Ruddat, I.; Mellmann, A.; Köck, R.; Kreienbrock, L. Simultaneous occurrence of MRSA and ESBL-producing Enterobacteriaceae on pig farms and in nasal and stool samples from farmers. *Vet Microbiol* **2017**, *200*, 107-113, doi:10.1016/j.vetmic.2016.05.021.
52. Armand-Lefevre, L.; Ruimy, R.; Andremont, A. Clonal comparison of Staphylococcus aureus isolates from healthy pig farmers, human controls, and pigs. *Emerg Infect Dis* **2005**, *11*, 711-714, doi:10.3201/eid1105.040866.
53. Graveland, H.; Wagenaar, J.A.; Bergs, K.; Heesterbeek, H.; Heederik, D. Persistence of livestock associated MRSA CC398 in humans is dependent on intensity of animal contact. *PLoS One* **2011**, *6*, e16830, doi:10.1371/journal.pone.0016830.
54. Wulf, M.W.; Sørum, M.; van Nes, A.; Skov, R.; Melchers, W.J.; Klaassen, C.H.; Voss, A. Prevalence of methicillin-resistant Staphylococcus aureus among veterinarians: an international study. *Clin Microbiol Infect* **2008**, *14*, 29-34, doi:10.1111/j.1469-0691.2007.01873.x.
55. Smith, T.C.; Male, M.J.; Harper, A.L.; Kroeger, J.S.; Tinkler, G.P.; Moritz, E.D.; Capuano, A.W.; Herwaldt, L.A.; Diekema, D.J. Methicillin-resistant Staphylococcus aureus (MRSA) strain ST398 is present in midwestern U.S. swine and swine workers. *PLoS One* **2009**, *4*, e4258, doi:10.1371/journal.pone.0004258.
56. Meemken, D.; Cuny, C.; Witte, W.; Eichler, U.; Staudt, R.; Blaha, T. [Occurrence of MRSA in pigs and in humans involved in pig production--preliminary results of a study in the northwest of Germany]. *Dtsch Tierarztl Wochenschr* **2008**, *115*, 132-139.
57. Bos, M.E.; Verstappen, K.M.; van Cleef, B.A.; Dohmen, W.; Dorado-García, A.; Graveland, H.; Duim, B.; Wagenaar, J.A.; Kluytmans, J.A.; Heederik, D.J. Transmission through air as a possible route of exposure for MRSA. *J Expo Sci Environ Epidemiol* **2016**, *26*, 263-269, doi:10.1038/jes.2014.85.
58. Aubry-Damon, H.; Grenet, K.; Sall-Ndiaye, P.; Che, D.; Cordeiro, E.; Bougnoux, M.E.; Rigaud, E.; Le Strat, Y.; Lemanissier, V.; Armand-Lefèvre, L., et al. Antimicrobial resistance in commensal flora of pig farmers. *Emerg Infect Dis* **2004**, *10*, 873-879, doi:10.3201/eid1005.030735.
59. Kraemer, J.G.; Pires, J.; Kueffer, M.; Semaani, E.; Endimiani, A.; Hilty, M.; Oppliger, A. Prevalence of extended-spectrum β-lactamase-producing Enterobacteriaceae and Methicillin-Resistant Staphylococcus aureus in pig farms in Switzerland. *Sci Total Environ* **2017**, *603-604*, 401-405, doi:10.1016/j.scitotenv.2017.06.110.
60. Heinemann, C.; Schmithausen, R.M.; Sib, E.; Meyer, I.; Petersen, B.; Steinhoff-Wagner, J. Preventive effect of nasal lavage with physiologic

saline on the colonization with MRSA after working in porcine stable. *Journal of Animal Science* **2017**, *95*, 250.

61. Heinemann, C.; Steinhoff-Wagner, J.; Petersen, B. Evaluation of methods for determining cleaning performances in pig stables. *Journal of Animal Science* **2017**, *95*, 48.
62. van Belkum, A.; Melles, D.C.; Peeters, J.K.; van Leeuwen, W.B.; van Duijkeren, E.; Huijsdens, X.W.; Spalburg, E.; de Neeling, A.J.; Verbrugh, H.A.; MRSA-SOM, D.W.P.o.S.a.R.o. Methicillin-resistant and -susceptible Staphylococcus aureus sequence type 398 in pigs and humans. *Emerg Infect Dis* **2008**, *14*, 479-483, doi:10.3201/eid1403.070760.
63. Wieler, L.H.; Ewers, C.; Guenther, S.; Walther, B.; Lübke-Becker, A. Methicillin-resistant staphylococci (MRS) and extended-spectrum beta-lactamases (ESBL)-producing Enterobacteriaceae in companion animals: nosocomial infections as one reason for the rising prevalence of these potential zoonotic pathogens in clinical samples. *Int J Med Microbiol* **2011**, *301*, 635-641, doi:10.1016/j.ijmm.2011.09.009.
64. Dahms, C.; Hübner, N.O.; Kossow, A.; Mellmann, A.; Dittmann, K.; Kramer, A. Occurrence of ESBL-Producing Escherichia coli in Livestock and Farm Workers in Mecklenburg-Western Pomerania, Germany. *PLoS One* **2015**, *10*, e0143326, doi:10.1371/journal.pone.0143326.
65. Boost, M.; Ho, J.; Guardabassi, L.; O'Donoghue, M. Colonization of butchers with livestock-associated methicillin-resistant Staphylococcus aureus. *Zoonoses Public Health* **2013**, *60*, 572-576, doi:10.1111/zph.12034.
66. Neyra, R.C.; Frisancho, J.A.; Rinsky, J.L.; Resnick, C.; Carroll, K.C.; Rule, A.M.; Ross, T.; You, Y.; Price, L.B.; Silbergeld, E.K. 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**, *122*, 471-477, doi:10.1289/ehp.1306741.
67. Van Cleef, B.A.; Broens, E.M.; Voss, A.; Huijsdens, X.W.; Züchner, L.; Van Benthem, B.H.; Kluytmans, J.A.; Mulders, M.N.; Van De Giessen, A.W. High prevalence of nasal MRSA carriage in slaughterhouse workers in contact with live pigs in The Netherlands. *Epidemiol Infect* **2010**, *138*, 756-763, doi:10.1017/S0950268810000245.
68. Broens, E.M.; Graat, E.A.; Van der Wolf, P.J.; Van de Giessen, A.W.; De Jong, M.C. Transmission of methicillin resistant Staphylococcus aureus among pigs during transportation from farm to abattoir. *Vet J* **2011**, *189*, 302-305, doi:10.1016/j.tvjl.2010.08.003.
69. Broens, E.M.; Graat, E.A.; van de Giessen, A.W.; Broekhuizen-Stins, M.J.; de Jong, M.C. Quantification of transmission of livestock-associated methicillin resistant Staphylococcus aureus in pigs. *Vet Microbiol* **2012**, *155*, 381-388, doi:10.1016/j.vetmic.2011.09.010.
70. van Duijkeren, E.; Ikawaty, R.; Broekhuizen-Stins, M.J.; Jansen, M.D.; Spalburg, E.C.; de Neeling, A.J.; Allaart, J.G.; van Nes, A.; Wagenaar, J.A.; Fluit, A.C. Transmission of methicillin-resistant Staphylococcus aureus strains between different kinds of pig farms. *Vet Microbiol* **2008**, *126*, 383-389, doi:10.1016/j.vetmic.2007.07.021.
71. Grøntvedt, C.A.; Elstrøm, P.; Stegger, M.; Skov, R.L.; Skytt Andersen, P.; Larssen, K.W.; Urdahl, A.M.; Angen, Ø.; Larsen, J.; Åmdal, S., et al. Methicillin-Resistant Staphylococcus aureus CC398 in Humans and Pigs in Norway: A "One Health" Perspective on Introduction and Transmission. *Clin Infect Dis* **2016**, *63*, 1431-1438, doi:10.1093/cid/ciw552.

72. Fischer, J.; Rodríguez, I.; Schmoger, S.; Friese, A.; Roesler, U.; Helmuth, R.; Guerra, B. Escherichia coli producing VIM-1 carbapenemase isolated on a pig farm. *J Antimicrob Chemother* **2012**, *67*, 1793-1795, doi:10.1093/jac/dks108.
73. de Neeling, A.J.; van den Broek, M.J.; Spalburg, E.C.; van Santen-Verheuvel, M.G.; Dam-Deisz, W.D.; Boshuizen, H.C.; van de Giessen, A.W.; van Duijkeren, E.; Huijsdens, X.W. High prevalence of methicillin resistant Staphylococcus aureus in pigs. *Vet Microbiol* **2007**, *122*, 366-372, doi:10.1016/j.vetmic.2007.01.027.
74. Broens, E.M.; Graat, E.A.; Van der Wolf, P.J.; Van de Giessen, A.W.; De Jong, M.C. Prevalence and risk factor analysis of livestock associated MRSA-positive pig herds in The Netherlands. *Prev Vet Med* **2011**, *102*, 41-49, doi:10.1016/j.prevetmed.2011.06.005.
75. Lewis, H.C.; Mølbak, K.; Reese, C.; Aarestrup, F.M.; Selchau, M.; Sørum, M.; Skov, R.L. Pigs as source of methicillin-resistant Staphylococcus aureus CC398 infections in humans, Denmark. *Emerg Infect Dis* **2008**, *14*, 1383-1389, doi:10.3201/eid1409.071576.
76. Köck, R.; Harlizius, J.; Bressan, N.; Laerberg, R.; Wieler, L.H.; Witte, W.; Deurenberg, R.H.; Voss, A.; Becker, K.; Friedrich, A.W. Prevalence and molecular characteristics of methicillin-resistant Staphylococcus aureus (MRSA) among pigs on German farms and import of livestock-related MRSA into hospitals. *Eur J Clin Microbiol Infect Dis* **2009**, *28*, 1375-1382, doi:10.1007/s10096-009-0795-4.
77. Alt, K.; Fetsch, A.; Schroeter, A.; Guerra, B.; Hammerl, J.A.; Hertwig, S.; Senkov, N.; Geinets, A.; Mueller-Graf, C.; Braeunig, J., et al. Factors associated with the occurrence of MRSA CC398 in herds of fattening pigs in Germany. *BMC Vet Res* **2011**, *7*, 69, doi:10.1186/1746-6148-7-69.
78. Porrero, M.C.; Wassenaar, T.M.; Gómez-Barrero, S.; García, M.; Bárcena, C.; Alvarez, J.; Sáez-Llorente, J.L.; Fernández-Garayzábal, J.F.; Moreno, M.A.; Domínguez, L. Detection of methicillin-resistant Staphylococcus aureus in Iberian pigs. *Lett Appl Microbiol* **2012**, *54*, 280-285, doi:10.1111/j.1472-765X.2012.03207.x.
79. Crombé, F.; Argudín, M.A.; Vanderhaeghen, W.; Hermans, K.; Haesebrouck, F.; Butaye, P. Transmission Dynamics of Methicillin-Resistant Staphylococcus aureus in Pigs. *Front Microbiol* **2013**, *4*, 57, doi:10.3389/fmicb.2013.00057.
80. Friese, A.; Schulz, J.; Hoehle, L.; Fetsch, A.; Tenhagen, B.A.; Hartung, J.; Roesler, U. Occurrence of MRSA in air and housing environment of pig barns. *Vet Microbiol* **2012**, *158*, 129-135, doi:10.1016/j.vetmic.2012.01.019.
81. Smet, A.; Martel, A.; Persoons, D.; Dewulf, J.; Heyndrickx, M.; Cloeckaert, A.; Praud, K.; Claeys, G.; Catry, B.; Herman, L., et al. Comparative analysis of extended-spectrum-{beta}-lactamase-carrying plasmids from different members of Enterobacteriaceae isolated from poultry, pigs and humans: evidence for a shared {beta}-lactam resistance gene pool? *J Antimicrob Chemother* **2009**, *63*, 1286-1288, doi:10.1093/jac/dkp101.
82. Geser, N.; Stephan, R.; Hächler, H. Occurrence and characteristics of extended-spectrum β-lactamase (ESBL) producing Enterobacteriaceae in food producing animals, minced meat and raw milk. *BMC Vet Res* **2012**, *8*, 21, doi:10.1186/1746-6148-8-21.
83. Agersø, Y.; Hald, T.; Helwigh, B.; Brock Høg, B.; Jensen, B., Lars. *DANMAP 2011*; 2011.
84. Bondt, N.; Jensen, V.F.; Puister-Jansen, L.F.; van Geijlswijk, I.M. Comparing antimicrobial exposure based on sales data. *Prev Vet Med* **2013**, *108*, 10-20, doi:10.1016/j.prevetmed.2012.07.009.

85. Escudero, E.; Vinué, L.; Teshager, T.; Torres, C.; Moreno, M.A. Resistance mechanisms and farm-level distribution of fecal Escherichia coli isolates resistant to extended-spectrum cephalosporins in pigs in Spain. *Res Vet Sci* **2010**, *88*, 83-87, doi:10.1016/j.rvsc.2009.05.021.
86. Hering, J.; Hille, K.; Frömke, C.; von Münchhausen, C.; Hartmann, M.; Schneider, B.; Friese, A.; Roesler, U.; Merle, R.; Kreienbrock, L. Prevalence and potential risk factors for the occurrence of cefotaxime resistant Escherichia coli in German fattening pig farms--a cross-sectional study. *Prev Vet Med* **2014**, *116*, 129-137, doi:10.1016/j.prevetmed.2014.06.014.
87. Carattoli, A. Animal reservoirs for extended spectrum beta-lactamase producers. *Clin Microbiol Infect* **2008**, *14 Suppl 1*, 117-123, doi:10.1111/j.1469-0691.2007.01851.x.
88. Aarestrup, F.M.; Hasman, H.; Agersø, Y.; Jensen, L.B.; Harksen, S.; Svensmark, B. First description of blaCTX-M-1-carrying Escherichia coli isolates in Danish primary food production. *J Antimicrob Chemother* **2006**, *57*, 1258-1259, doi:10.1093/jac/dkl109.
89. Briñas, L.; Moreno, M.A.; Teshager, T.; Zarazaga, M.; Sáenz, Y.; Porrero, C.; Dominguez, L.; Torres, C. Beta-lactamase characterization in Escherichia coli isolates with diminished susceptibility or resistance to extended-spectrum cephalosporins recovered from sick animals in Spain. *Microb Drug Resist* **2003**, *9*, 201-209, doi:10.1089/107662903765826804.
90. Venglovský, J.; Gregová, G.; Kmeť, V.; Sasáková, N. Detection of airborne microorganisms and antibiotic resistance from animal housing facilities. In Proceedings of Animal hygiene and sustainable livestock production. Proceedings of the XVth International Congress of the International Society for Animal Hygiene, Vienna, Austria; pp. 813-815.
91. Gundermann, K.O. [Life-span of bacterial strains in dust as influenced by various degrees of air humidity]. *Zentralbl Bakteriol Orig B* **1972**, *156*, 422-429.
92. Müller, W.; Wieser, P.; Woiwode, J. Zur Größe koloniebildender Einheiten in der Stallluft. *Berl. Münch. Tierärztl. Wschr.* **1977**, *90*, 6-11.
93. EFSA. Assessment of the Public Health significance of methicillin resistant *Staphylococcus aureus* (MRSA) in animals and foods. (EFSA), E.F.S.A., Ed. 2009.
94. Wagenaar, J.A.; Yue, H.; Pritchard, J.; Broekhuizen-Stins, M.; Huijsdens, X.; Mevius, D.J.; Bosch, T.; Van Duijkeren, E. Unexpected sequence types in livestock associated methicillin-resistant Staphylococcus aureus (MRSA): MRSA ST9 and a single locus variant of ST9 in pig farming in China. *Vet Microbiol* **2009**, *139*, 405-409, doi:10.1016/j.vetmic.2009.06.014.
95. Espinosa-Gongora, C.; Broens, E.M.; Moodley, A.; Nielsen, J.P.; Guardabassi, L. Transmission of MRSA CC398 strains between pig farms related by trade of animals. *Vet Rec* **2012**, *170*, 564, doi:10.1136/vr.100704.
96. Agersø, Y.; Vigre, H.; Cavaco, L.M.; Josefsen, M.H. Comparison of air samples, nasal swabs, ear-skin swabs and environmental dust samples for detection of methicillin-resistant Staphylococcus aureus (MRSA) in pig herds. *Epidemiol Infect* **2014**, *142*, 1727-1736, doi:10.1017/S095026881300280X.

97. Schulz, J.; Friese, A.; Klees, S.; Tenhagen, B.A.; Fetsch, A.; Rösler, U.; Hartung, J. Longitudinal study of the contamination of air and of soil surfaces in the vicinity of pig barns by livestock-associated methicillin-resistant Staphylococcus aureus. *Appl Environ Microbiol* **2012**, *78*, 5666-5671, doi:10.1128/AEM.00550-12.
98. Pletinckx, L.J.; Verhegghe, M.; Dewulf, J.; Crombé, F.; De Bleecker, Y.; Rasschaert, G.; Goddeeris, B.M.; De Man, I. Screening of poultry-pig farms for methicillin-resistant Staphylococcus aureus: sampling methodology and within herd prevalence in broiler flocks and pigs. *Infect Genet Evol* **2011**, *11*, 2133-2137, doi:10.1016/j.meegid.2011.07.008.
99. Gibbs, S.G.; Green, C.F.; Tarwater, P.M.; Scarpino, P.V. Airborne antibiotic resistant and nonresistant bacteria and fungi recovered from two swine herd confined animal feeding operations. *J Occup Environ Hyg* **2004**, *1*, 699-706, doi:10.1080/15459620490515824.
100. Hartung, J.; Seedorf, J.; Trickl, T.; Gronauer, H. [Emission of particulates from a pig farm with central air exhaust in the pig stall]. *Dtsch Tierarztl Wochenschr* **1998**, *105*, 244-245.
101. Hoffmann, A. Presence of CTX-M-1 group extended-spectrum-ß-lactamase in dust from Dutch pig farms. In Proceedings of Faculty of Veterinary Medicine, Utrecht.
102. von Salviati, C.; Laube, H.; Guerra, B.; Roesler, U.; Friese, A. Emission of ESBL/AmpC-producing Escherichia coli from pig fattening farms to surrounding areas. *Vet Microbiol* **2015**, *175*, 77-84, doi:10.1016/j.vetmic.2014.10.010.
103. Dohmen, W.; Schmitt, H.; Bonten, M.; Heederik, D. Air exposure as a possible route for ESBL in pig farmers. *Environ Res* **2017**, *155*, 359-364, doi:10.1016/j.envres.2017.03.002.
104. Gao, P.; Munir, M.; Xagoraraki, I. Correlation of tetracycline and sulfonamide antibiotics with corresponding resistance genes and resistant bacteria in a conventional municipal wastewater treatment plant. *Sci Total Environ* **2012**, *421-422*, 173-183, doi:10.1016/j.scitotenv.2012.01.061.
105. Schmithausen, R.M.; Kellner, S.R.; Schulze-Geisthoevel, S.V.; Hack, S.; Engelhart, S.; Bodenstein, I.; Al-Sabti, N.; Reif, M.; Fimmers, R.; Körber-Irrgang, B., et al. Eradication of methicillin-resistant Staphylococcus aureus and of Enterobacteriaceae expressing extended-spectrum beta-lactamases on a model pig farm. *Appl Environ Microbiol* **2015**, *81*, 7633-7643, doi:10.1128/AEM.01713-15.
106. Schmithausen, R.M.; Schulze-Geisthoevel, S.V.; Stemmer, F.; El-Jade, M.; Reif, M.; Hack, S.; Meilaender, A.; Montabauer, G.; Fimmers, R.; Parcina, M., et al. Analysis of Transmission of MRSA and ESBL-E among Pigs and Farm Personnel. *PLoS One* **2015**, *10*, e0138173, doi:10.1371/journal.pone.0138173.
107. Zhang, X.; Wu, B.; Zhang, Y.; Zhang, T.; Yang, L.; Fang, H.H.; Ford, T.; Cheng, S. Class 1 integronase gene and tetracycline resistance genes tetA and tetC in different water environments of Jiangsu Province, China. *Ecotoxicology* **2009**, *18*, 652-660, doi:10.1007/s10646-009-0332-3.
108. Hartung, J. [Rules to control ddrinking water supply systems in livestock farming]. *Dtsch Tierarztl Wochenschr* **2000**, *107*, 302-304.
109. Lupo, A.; Coyne, S.; Berendonk, T.U. Origin and evolution of antibiotic resistance: the common mechanisms of emergence and spread in water bodies. *Front Microbiol* **2012**, *3*, 18, doi:10.3389/fmicb.2012.00018.

110. Wellington, E.M.; Boxall, A.B.; Cross, P.; Feil, E.J.; Gaze, W.H.; Hawkey, P.M.; Johnson-Rollings, A.S.; Jones, D.L.; Lee, N.M.; Otten, W., et al. The role of the natural environment in the emergence of antibiotic resistance in gram-negative bacteria. *Lancet Infect Dis* **2013**, *13*, 155-165, doi:10.1016/S1473-3099(12)70317-1.
111. Vital, P.G.; Zara, E.S.; Paraoan, C.E.M.; Dimasupil, A.Z.; Abello, J.J.M.; Santos, I.T.G.; Rivera, W.L. Antibiotic Resistance and Extended-Spectrum Beta-Lactamase Production of Escherichia coli isolated from Irrigation Waters in Selected Urban Farms in Metro Manila, Philippines. *Water* **2018**, *10*.
112. Wan, M.T.; Chou, C.C. Class 1 Integrons and the Antiseptic Resistance Gene (qacEΔ1) in Municipal and Swine Slaughterhouse Wastewater Treatment Plants and Wastewater-Associated Methicillin-Resistant Staphylococcus aureus. *Int J Environ Res Public Health* **2015**, *12*, 6249-6260, doi:10.3390/ijerph120606249.
113. Diallo, A.A.; Brugère, H.; Kérourédan, M.; Dupouy, V.; Toutain, P.L.; Bousquet-Mélou, A.; Oswald, E.; Bibbal, D. Persistence and prevalence of pathogenic and extended-spectrum beta-lactamase-producing Escherichia coli in municipal wastewater treatment plant receiving slaughterhouse wastewater. *Water Res* **2013**, *47*, 4719-4729, doi:10.1016/j.watres.2013.04.047.
114. Müller, A.; Stephan, R.; Nüesch-Inderbinen, M. Distribution of virulence factors in ESBL-producing Escherichia coli isolated from the environment, livestock, food and humans. *Sci Total Environ* **2016**, *541*, 667-672, doi:10.1016/j.scitotenv.2015.09.135.
115. Müller, H.; Sib, E.; Gajdiss, M.; Klanke, U.; Lenz-Plet, F.; Barabasch, V.; Albert, C.; Schallenberg, A.; Timm, C.; Zacharias, N., et al. Dissemination of multi-resistant Gram-negative bacteria into German wastewater and surface waters. *FEMS Microbiol Ecol* **2018**, doi:10.1093/femsec/fiy057.
116. Schijven, J.F.; Blaak, H.; Schets, F.M.; de Roda Husman, A.M. Fate of Extended-Spectrum β-Lactamase-Producing Escherichia coli from Faecal Sources in Surface Water and Probability of Human Exposure through Swimming. *Environ Sci Technol* **2015**, *49*, 11825-11833, doi:10.1021/acs.est.5b01888.
117. Hu, Y.Y.; Cai, J.C.; Zhou, H.W.; Chi, D.; Zhang, X.F.; Chen, W.L.; Zhang, R.; Chen, G.X. Molecular typing of CTX-M-producing escherichia coli isolates from environmental water, swine feces, specimens from healthy humans, and human patients. *Appl Environ Microbiol* **2013**, *79*, 5988-5996, doi:10.1128/AEM.01740-13.
118. Zurfluh, K.; Power, K.A.; Klumpp, J.; Wang, J.; Fanning, S.; Stephan, R. A novel Tn3-like composite transposon harboring blaVIM-1 in Klebsiella pneumoniae spp. pneumoniae isolated from river water. *Microb Drug Resist* **2015**, *21*, 43-49, doi:10.1089/mdr.2014.0055.
119. Casey, J.A.; Curriero, F.C.; Cosgrove, S.E.; Nachman, K.E.; Schwartz, B.S. High-density livestock operations, crop field application of manure, and risk of community-associated methicillin-resistant Staphylococcus aureus infection in Pennsylvania. *JAMA Intern Med* **2013**, *173*, 1980-1990, doi:10.1001/jamainternmed.2013.10408.
120. Gompel, L.V. Quantification and detection of Methicillin Resistant Staphylococcus aureus (MRSA) in manure, soil and air by means of a mega specific qPCR. 2014.

121. Schwartz, T.; Kohnen, W.; Jansen, B.; Obst, U. Detection of antibiotic-resistant bacteria and their resistance genes in wastewater, surface water, and drinking water biofilms. *FEMS Microbiol Ecol* **2003**, *43*, 325-335, doi:10.1111/j.1574-6941.2003.tb01073.x.
122. Westphal-Settele, K.; Konradi, S.; Balzer, F.; Schönfeld, J.; Schmithausen, R. [The environment as a reservoir for antimicrobial resistance : A growing problem for public health?]. *Bundesgesundheitsblatt Gesundheitsforschung Gesundheitsschutz* **2018**, *61*, 533-542, doi:10.1007/s00103-018-2729-8.
123. Witte, W. Ecological impact of antibiotic use in animals on different complex microflora: environment. *Int J Antimicrob Agents* **2000**, *14*, 321-325.
124. Friese, A.; Schulz, J.; Laube, H.; von Salviati, C.; Hartung, J.; Roesler, U. Faecal occurrence and emissions of livestock-associated methicillin-resistant Staphylococcus aureus (laMRSA) and ESbl/AmpC-producing E. coli from animal farms in Germany. *Berl Munch Tierarztl Wochenschr* **2013**, *126*, 175-180.
125. Hartmann, A.; Locatelli, A.; Amoureux, L.; Depret, G.; Jolivet, C.; Gueneau, E.; Neuwirth, C. Occurrence of CTX-M Producing Escherichia coli in Soils, Cattle, and Farm Environment in France (Burgundy Region). *Front Microbiol* **2012**, *3*, 83, doi:10.3389/fmicb.2012.00083.
126. Hölzel, C.S.; Schwaiger, K.; Harms, K.; Küchenhoff, H.; Kunz, A.; Meyer, K.; Müller, C.; Bauer, J. Sewage sludge and liquid pig manure as possible sources of antibiotic resistant bacteria. *Environ Res* **2010**, *110*, 318-326, doi:10.1016/j.envres.2010.02.009.
127. Heuer, H.; Schmitt, H.; Smalla, K. Antibiotic resistance gene spread due to manure application on agricultural fields. *Curr Opin Microbiol* **2011**, *14*, 236-243, doi:10.1016/j.mib.2011.04.009.
128. Heuer, H.; Smalla, K. Manure and sulfadiazine synergistically increased bacterial antibiotic resistance in soil over at least two months. *Environ Microbiol* **2007**, *9*, 657-666, doi:10.1111/j.1462-2920.2006.01185.x.
129. Vincent, C.; Boerlin, P.; Daignault, D.; Dozois, C.M.; Dutil, L.; Galanakis, C.; Reid-Smith, R.J.; Tellier, P.P.; Tellis, P.A.; Ziebell, K., et al. Food reservoir for Escherichia coli causing urinary tract infections. *Emerg Infect Dis* **2010**, *16*, 88-95, doi:10.3201/eid1601.091118.
130. Normanno, G.; Dambrosio, A.; Lorusso, V.; Samoilis, G.; Di Taranto, P.; Parisi, A. Methicillin-resistant Staphylococcus aureus (MRSA) in slaughtered pigs and abattoir workers in Italy. *Food Microbiol* **2015**, *51*, 51-56, doi:10.1016/j.fm.2015.04.007.
131. Ikegbunam, M.N.; Anagu, L.O.; Iroha, I.R.; Ejikeugwu, C.E.; Esimone, C.O. Abattoirs as non-hospital source of extended spectrum beta lactamase producers: confirmed by the double disc synergy test and characterized by matrix-assisted laser desorption/ionization time of flight mass spectrometry. *PLoS One* **2014**, *9*, e94461, doi:10.1371/journal.pone.0094461.
132. Guardabassi, L.; Stegger, M.; Skov, R. Retrospective detection of methicillin resistant and susceptible Staphylococcus aureus ST398 in Danish slaughter pigs. *Vet Microbiol* **2007**, *122*, 384-386, doi:10.1016/j.vetmic.2007.03.021.
133. Tenhagen, B.A.; Fetsch, A.; Stührenberg, B.; Schleuter, G.; Guerra, B.; Hammerl, J.A.; Hertwig, S.; Kowall, J.; Kämpe, U.; Schroeter, A., et al. Prevalence of MRSA types in slaughter pigs in different German abattoirs. *Vet Rec* **2009**, *165*, 589-593.

134. Geser, N.; Stephan, R.; Kuhnert, P.; Zbinden, R.; Kaeppeli, U.; Cernela, N.; Haechler, H. Fecal carriage of extended-spectrum β-lactamase-producing Enterobacteriaceae in swine and cattle at slaughter in Switzerland. *J Food Prot* **2011**, *74*, 446-449, doi:10.4315/0362-028X.JFP-10-372.
135. Randall, L.P.; Lemma, F.; Rogers, J.P.; Cheney, T.E.; Powell, L.F.; Teale, C.J. Prevalence of extended-spectrum-β-lactamase-producing Escherichia coli from pigs at slaughter in the UK in 2013. *J Antimicrob Chemother* **2014**, *69*, 2947-2950, doi:10.1093/jac/dku258.
136. Hansen, K.H.; Damborg, P.; Andreasen, M.; Nielsen, S.S.; Guardabassi, L. Carriage and fecal counts of cefotaxime M-producing Escherichia coli in pigs: a longitudinal study. *Appl Environ Microbiol* **2013**, *79*, 794-798, doi:10.1128/AEM.02399-12.
137. van der Wolf, P.J.; Rothkamp, A.; Junker, K.; de Neeling, A.J. Staphylococcus aureus (MSSA) and MRSA (CC398) isolated from post-mortem samples from pigs. *Vet Microbiol* **2012**, *158*, 136-141, doi:10.1016/j.vetmic.2012.01.025.
138. de Boer, E.; Zwartkruis-Nahuis, J.T.; Wit, B.; Huijsdens, X.W.; de Neeling, A.J.; Bosch, T.; van Oosterom, R.A.; Vila, A.; Heuvelink, A.E. Prevalence of methicillin-resistant Staphylococcus aureus in meat. *Int J Food Microbiol* **2009**, *134*, 52-56, doi:10.1016/j.ijfoodmicro.2008.12.007.
139. Molla, B.; Byrne, M.; Abley, M.; Mathews, J.; Jackson, C.R.; Fedorka-Cray, P.; Sreevatsan, S.; Wang, P.; Gebreyes, W.A. Epidemiology and genotypic characteristics of methicillin-resistant Staphylococcus aureus strains of porcine origin. *J Clin Microbiol* **2012**, *50*, 3687-3693, doi:10.1128/JCM.01971-12.
140. Lavilla, S.; González-López, J.J.; Miró, E.; Domínguez, A.; Llagostera, M.; Bartolomé, R.M.; Mirelis, B.; Navarro, F.; Prats, G. Dissemination of extended-spectrum beta-lactamase-producing bacteria: the food-borne outbreak lesson. *J Antimicrob Chemother* **2008**, *61*, 1244-1251, doi:10.1093/jac/dkn093.
141. Teuber, M. Spread of antibiotic resistance with food-borne pathogens. *Cell Mol Life Sci* **1999**, *56*, 755-763.
142. Johnson, J.R.; Kuskowski, M.A.; Smith, K.; O'Bryan, T.T.; Tatini, S. Antimicrobial-resistant and extraintestinal pathogenic Escherichia coli in retail foods. *J Infect Dis* **2005**, *191*, 1040-1049, doi:10.1086/428451.
143. López-Cerero, L.; Egea, P.; Serrano, L.; Navarro, D.; Mora, A.; Blanco, J.; Doi, Y.; Paterson, D.L.; Rodríguez-Baño, J.; Pascual, A. Characterisation of clinical and food animal Escherichia coli isolates producing CTX-M-15 extended-spectrum β-lactamase belonging to ST410 phylogroup A. *Int J Antimicrob Agents* **2011**, *37*, 365-367, doi:10.1016/j.ijantimicag.2011.01.001.
144. Pietsch, M.; Irrgang, A.; Roschanski, N.; Brenner Michael, G.; Hamprecht, A.; Rieber, H.; Käsbohrer, A.; Schwarz, S.; Rösler, U.; Kreienbrock, L., et al. Whole genome analyses of CMY-2-producing Escherichia coli isolates from humans, animals and food in Germany. *BMC Genomics* **2018**, *19*, 601, doi:10.1186/s12864-018-4976-3.
145. Erickson, M.; Doyle, M. PLANT FOOD SAFETY ISSUES: LINKING PRODUCTION AGRICULTURE WITH ONE HEALTH. *Institute of Medicine (US). Improving Food Safety Through a One Health Approach: Workshop Summary*. 2012.
146. Fornazari, A.C.Z.; M.L.H., M.; C.J.C., C.; V.C.A., e.J. Enterobacteria determination in vacuum-packed refrigerated meat with blown pack type spoilage International conference of food innovation. In Proceedings of Food Innova 2010; pp. 25-29.

147. Hiroi, M.; Harada, T.; Kawamori, F.; Takahashi, N.; Kanda, T.; Sugiyama, K.; Masuda, T.; Yoshikawa, Y.; Ohashi, N. A survey of β-lactamase-producing Escherichia coli in farm animals and raw retail meat in Shizuoka Prefecture, Japan. *Jpn J Infect Dis* **2011**, *64*, 153-155.
148. Petternel, C.; Galler, H.; Zarfel, G.; Luxner, J.; Haas, D.; Grisold, A.J.; Reinthaler, F.F.; Feierl, G. Isolation and characterization of multidrug-resistant bacteria from minced meat in Austria. *Food Microbiol* **2014**, *44*, 41-46, doi:10.1016/j.fm.2014.04.013.