SCIENTIFIC REPORT

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The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2015

European Food Safety Authority
European Centre for Disease Prevention and Control

Abstract

The data on antimicrobial resistance in zoonotic and indicator bacteria in 2015, submitted by 28 EU Member States (MSs), were jointly analysed by EFSA and ECDC. Resistance in zoonotic *Salmonella* and *Campylobacter* from humans, animals and food, and resistance in indicator *Escherichia coli* as well as meticillin-resistant *Staphylococcus aureus* in animals and food were addressed. 'Microbiological' resistance was assessed using epidemiological cut-off (ECOFF) values; for some countries, qualitative data on human isolates were interpreted in a way which corresponds closely to the ECOFF-defined 'microbiological' resistance. In *Salmonella* from humans, high proportions of isolates were resistant to ampicillin, sulfonamides and tetracyclines, whereas resistance to third-generation cephalosporins was low. In *Salmonella* and *Escherichia coli* isolates from fattening pigs and calves under one year of age, resistance to ampicillin, tetracyclines and sulfonamides was frequently detected, whereas resistance to third-generation cephalosporins was uncommon. For the first time, presumptive extended-spectrum beta-lactamase (ESBL)-/AmpC-/carbapenemase-production in *Salmonella* and *Escherichia coli* was monitored in humans (*Salmonella*), meat (pork and beef), fattening pigs and calves. Varying occurrence/prevalence rates of ESBL-/AmpC-producers were observed between countries, and carbapenemase-producing *Escherichia coli* were detected in single samples of pig meat and from fattening pigs from two MSs. Resistance to colistin was observed at low levels in *Salmonella* and *Escherichia coli* from fattening pigs and calves under one year of age and meat thereof. In *Campylobacter* from humans, high to extremely high proportions of isolates were resistant to ciprofloxacin and tetracyclines, particularly in *C. coli*. In a few countries, a third to half of *C. coli* in humans were resistant also to erythromycin, leaving few options for treatment of severe *Campylobacter* infections. High resistance to ciprofloxacin and tetracyclines was observed in *C. coli* isolates from fattening pigs, whereas much lower levels were recorded for erythromycin. Co-resistance to critically important antimicrobials in both human and animal isolates was generally uncommon.

Keywords: antimicrobial resistance, zoonotic bacteria, indicator bacteria, ESBL

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Correspondence: zoonoses@efsa.europa.eu (EFSA); FWD@ecdc.europa.eu (ECDC)

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Summary

Highlights

Zoonoses are infections that are transmissible between animals and humans. Infections can be acquired directly from animals, via environmental exposure or through the ingestion of contaminated foodstuffs. The severity of these diseases in humans can vary from mild symptoms to life-threatening conditions. Zoonotic bacteria that are resistant to antimicrobials are of particular concern, as they might compromise the effective treatment of infections in humans. Data from the EU Member States (MSs) are collected and analysed in order to monitor the occurrence of antimicrobial resistance (AMR) in zoonotic bacteria isolated from humans, animals and food in the European Union (EU).

For 2015, 28 MSs reported data on AMR in zoonotic bacteria to the European Food Safety Authority (EFSA), and 22 MSs reported data to the European Centre for Disease Prevention and Control (ECDC). In addition, three other European countries reported data; Iceland and Norway reported to ECDC, while Iceland, Norway and Switzerland reported to EFSA. The enhanced monitoring of AMR in bacteria from food and food-producing animals set out in the Commission Implementing Decision 2013/652/EU was successfully implemented in reporting MSs and non-MSs in the EU during 2015. In accordance with the legislation, the 2015 AMR data on food and food-producing animals specifically targeted fattening pigs and calves under one year of age and meat derived thereof. EFSA and ECDC performed the analyses of the data, the results of which are published in this EU Summary Report on AMR. Data on resistance were reported regarding *Salmonella* and *Campylobacter* isolates from humans and fattening pigs, whereas data on indicator *Escherichia coli* isolates were related only to fattening pigs and calves under one year of age and meat derived thereof. Some MSs also reported data on the occurrence of meticillin-resistant *Staphylococcus aureus* (MRSA) in animals and food; the antimicrobial susceptibility of MRSA isolates was additionally reported by three countries.

For the first time, all MSs reported AMR data on fattening pigs and calves under one year of age and meat thereof at the isolate level. The information published in this report provides an overview of resistance in most MSs with detailed consideration of certain important aspects, such as multidrug resistance (MDR) and co-resistance patterns to critically important antimicrobials in both human and animal isolates at the EU level but also at country level. More specifically, reporting data at isolate level allowed characterisation of important patterns of resistance, enabling *Salmonella* serovars to be linked to particular resistance patterns and to identify high-level resistance to fluoroquinolones and important resistance phenotypes in both *Salmonella* and indicator *E. coli*.

Highlights of this report include the continued monitoring of the spread of certain highly resistant *Salmonella* serovars. Two serovars in particular, *S*. Typhimurium and monophasic *S*. Typhimurium, contribute significantly to the overall numbers of multidrug-resistant *Salmonella* in Europe. Only one *S.* Typhimurium isolate from calves under one year of age displayed high-level resistance to ciprofloxacin, while microbiological resistance was low in *Salmonella* spp. from pig meat (4.3%), from bovine meat (2.5%) and from fattening pigs (4.7%), important from a public health perspective because ciprofloxacin is a common first-line treatment for invasive salmonellosis in humans.

The introduction of Commission implementing Decision 2013/652/EU with revised panels of antimicrobials to be tested has been timely, preceding recent reports of emergence of transferable colistin and erythromycin resistance in Asia (Liu et al., 2015; Wang et al., 2015). The continually evolving threat from emerging resistance underlines the need to review the data collected, interpret the findings and assess trends. This report has attempted to highlight some of the most important findings in 2015, but space constraints mean that it is necessarily selective.

The inclusion within the harmonised monitoring scheme of a supplementary panel of antimicrobials, to be tested when certain resistances to an initial panel of antimicrobials are detected, enabled detailed screening of resistance to three carbapenem compounds. Carbapenemase-producing *E. coli* were detected in voluntary monitoring of indicator *E. coli* from pig meat in Belgium and in the mandatory, specific monitoring for extended-spectrum beta-lactamase (ESBL)/AmpC/carbapenemase-producing *E. coli* in fattening pigs in Germany. The isolate from fattening pigs in Germany produced the carbapenemase enzyme VIM-1 (Irrgang et al., 2016b) and genes encoding for this enzyme have been previously detected in isolates from pigs in Germany (EFSA BIOHAZ Panel, 2013; Irrgang et al., 2016b). The detection of carbapenemase-producing enterobacteriaceae in the environment of a swine farrow-to-finish operation in the United States was also recently reported (Mollenkopf et al., 2017). These findings are important, because carbapenems are critically important in human medicine Collignon et al., 2016; WHO, 2016).

The supplementary testing also allowed, for the first time, detailed characterisation of the beta-lactam resistance phenotypes occurring in *Salmonella* and indicator *E. coli* from fattening pigs and from calves under one year of age. It enabled further phenotypic characterisation of third-generation cephalosporin and carbapenem resistance in *Salmonella* and indicator *E. coli,* by inferring presumptive genotypes of ESBL-/AmpC-/carbapenemase-producers. The occurrence of ESBL-/AmpC-producers in *Salmonella* and indicator *E. coli* from fattening pigs and from calves under one year of age was assessed as being at low levels. ESBL- and AmpC-producing *Salmonella* was detected at low levels also in humans, but in a significant proportion of some serovars, although this could be affected by selective sampling.

For the first time in 2015, specific monitoring of ESBL-/AmpC-/carbapenemase-producing *E. coli*, which is able to detect very low numbers of resistant isolates present within a sample, was performed on caecal samples from fattening pigs, calves under one year of age and meat derived thereof from these animals. The occurrence and prevalence of *E. coli* showing an ESBL, AmpC and ESBL+AmpC profiles from these animal populations and kinds of meat were assessed at both the reporting MS-group level and the individual MS level. Overall and in most but not all countries, the detection of ESBL-producing *E. coli* exceeded that of AmpC-producing *E. coli* in fattening pigs, calves and meat derived thereof. Prevalence figures observed for the two kinds of meat studied were remarkably similar in all reporting countries and overall much lower than those observed in animals. The prevalence of *E. coli* with an ESBL phenotype in the animals tested varied widely, from low to very high levels, between reporting countries.

Main findings regarding *Salmonella*

The *Salmonella* spp. data presented in this report comprise all reported non-typhoidal *Salmonella* serovars and represent the overall occurrence of AMR in *Salmonella* in humans, fattening pigs and calves under one year of age and meat thereof. Differences in the prevalence of particular serovars and phage types of *Salmonella* in different countries and poultry populations, and their associated patterns of resistance, may explain some of the differences in the levels of AMR and MDR (reduced susceptibility to at least three of the nine antimicrobial classes tested according to epidemiological cut-off values, ECOFFs). The spread of particularly resistant clones and the occurrence of resistance genes within these clones can be exacerbated by the use of antimicrobials in human and animal populations and the associated selective pressure. Other factors, such as foreign travel by humans, international food trade, animal movements, farming systems, animal husbandry and the pyramidal structure of some types of animal primary production, may also influence the spread of resistant clones.

In addition to the aggregated data for *Salmonella* spp., resistance data for the most common *Salmonella* serovars in pigs and calves, *S.* Derby, *S.* Typhimurium, monophasic *S.* Typhimurium and *S.* Infantis, were analysed separately. In fattening pigs, calves under one year of age and meat derived thereof, resistance profiles of isolates belonging to these serovars were also considered when less than 10 isolates were recovered from a given animal/food category in a country, to account for the low prevalence of certain serovars, to prevent exclusion of emerging serovars and to ensure that the analysis included all relevant data.

In humans

For 2015, 22 MSs and 2 non-MSs reported data on AMR in *Salmonella* isolates from human cases of salmonellosis. Fourteen countries provided data as measured values (quantitative data), which is double compared to 2013 when this type of data collection was implemented. The reported data represented 15.9% of the confirmed salmonellosis cases reported in the EU/European Economic Area (EEA) in 2015.

High proportions of human *Salmonella* isolates were resistant to sulfonamides (32.1%), tetracyclines (28.1%), and ampicillin (27.8%). MDR was high overall (29.3%) in the EU. Among the investigated serovars, monophasic *S.* Typhimurium 1,4,[5],12:i:- exhibited extremely high MDR (81.1%). Multidrug resistance increased by more than 10% in both *S.* Typhimurium and monophasic *S.* Typhimurium from 2014 to 2015, with very large increases in a few MSs. One isolate of each of these two serotypes was reported as resistant to eight of the nine tested substances, only susceptible to meropenem.

The proportions of *Salmonella* isolates resistant to either of the clinically important antimicrobials ciprofloxacin and cefotaxime were relatively low overall (13.3% resistant to ciprofloxacin and 0.9% to cefotaxime). The increase in ciprofloxacin resistance observed from 2013 to 2015 is to a large extent due to a combination of the lowered European Committee on Antimicrobial Susceptibility Testing (EUCAST, 2014) CBP for ciprofloxacin in 2014 – now directly comparable with the ECOFF – and the gradual

implementation of a better marker (pefloxacin) than ciprofloxacin for screening with disk diffusion of low-level fluoroquinolone resistance in *Salmonella*. 'Clinical' and 'microbiological' co-resistance to ciprofloxacin and cefotaxime was overall very low in *Salmonella* spp. (0.4% and 0.3%, respectively).

Eight MSs performed testing for presence of ESBL- and AmpC-producing *Salmonella* in human isolates. ESBL-producing *Salmonella* were identified in seven of eight MSs in 0.5% of the isolates and encompassed 12 different serovars (Table 1). *S.* Infantis with ESBL was detected in half of the MSs in 5.3% tested isolates. ESBL-carrying monophasic *S.* Typhimurium 1,4,[5],12:i:- was detected in three MSs but their proportion was small in comparison to the total number of isolates. AmpC-producing *Salmonella* were detected in six MSs at a lower proportion than ESBL and in five different serovars.

In fattening pigs, calves under one year of age and meat thereof

For 2015, information on AMR in *Salmonella* isolates from fattening pigs, calves under one year of age and meat derived thereof was reported by 20 MSs and one non-MS.

Among the *Salmonella* spp. isolates from pig meat, the highest levels of resistance were noted to ampicillin, sulfamethoxazole and tetracyclines, where high to extremely high levels were recorded by most of the MSs included in the analysis (overall, 44.7%, 48.5% and 49.1%, respectively). In *Salmonella* spp. isolates from bovine meat, resistance to the majority of the antimicrobial tested were lower than those observed in pig meat with the exception of the resistance to sulfamethoxazole, tetracycline and tigecycline which were slightly higher than the values registered for pig meat. The countries reporting results for meat from pigs and cattle differed; the numbers of isolates available for testing in each reporting country was also variable and these factors introduce a source of variation into the results for all reporting countries. Conversely, 'microbiological' resistance to the third-generation cephalosporins (cefotaxime and ceftazidime) in *Salmonella* spp. from pig meat was either not discerned or detected at low levels in most of the reporting MSs and it was not reported in any of the reporting countries for bovine meat. Resistance to azithromycin in *Salmonella* spp. isolates from pig meat was generally low or not detected, with the exception of Portugal which reported high levels of resistance (37.5%) and Cyprus, which reported a 25% prevalence of resistance, although Cyprus reported results for a very low sample size. In bovine meat, resistance to azithromycin in *Salmonella* spp. isolates was reported only by one MS, but the sample size was very low. MDR (reduced susceptibility to at least three of the nine antimicrobial classes tested) was overall high and almost at the same level in pig and bovine meat (40.4% and 40.5%, respectively).

Among *Salmonella* spp. isolates from fattening pigs, most MSs reported moderate or high to extremely high resistance to tetracyclines and sulfonamides, and similar or slightly lower levels of ampicillin resistance. Resistance levels to these antimicrobials were generally higher in isolates from fattening pigs than in those from calves under one year of age. Overall, lower levels of resistance to ciprofloxacin and nalidixic acid were observed in *Salmonella* spp. isolates from fattening pigs compared with the levels recorded in *Salmonella* spp. isolates from calves, although only a low number of countries reported results which were strongly influenced by the individual contribution from particular MSs. No resistance to third-generation cephalosporins was detected in calves, consistent with the result obtained for *Salmonella* spp. from bovine meat.

One MS reported co-resistance to ciprofloxacin and cefotaxime in *Salmonella* spp. from fattening pigs at low levels of 'microbiological' resistance (2.2%). When the resistance to ciprofloxacin and cefotaxime was interpreted using clinical breakpoints (CBPs), no isolates displayed 'clinical' resistance.

The supplementary testing performed in 2015 allowed further phenotypic characterisation of those *Salmonella* isolates which were resistant to third-generation cephalosporins (Table 1).

Table 1: Summary of phenotypic characterisation of third generation cephalosporin resistance in *Salmonella* from humans, meat from pigs and fattening pigs in 2015

	Presumptive ESBL-producers[(a)] n (% R)	Presumptive AmpC-producers[(b)] n (% R)	ESBL + AmpC phenotype n (% R)
Humans (N = 5,567)	28 (0.5)	7 (0.1)	3 (0.1)
Meat from pig (N = 443)	4 (0.9)	3 (0.7)	1 (0.2)
Fattening pigs (N = 91)	2 (2.2)	0 (0)	0 (0)

N: number of isolates tested; n: number of resistant isolates; % R: percentage of resistant isolates.
(a): Isolates exhibiting an ESBL- and/or ESBL/AmpC-phenotype.
(b): Isolates exhibiting an AmpC and/or ESBL/AmpC-phenotype.

Salmonella spp. isolates with an ESBL phenotype were detected in meat from pigs in Germany (two *S.* Derby) and in Belgium (one *S.*, unspecified) and from fattening pigs in Italy (one *S.* Typhimurium and one monophasic *S.* Typhimurium isolate). *Salmonella* spp. isolates with an AmpC phenotype were detected in meat from pigs in Portugal (two *S.* Bredeney isolates) as well as in fattening pigs in Italy (one *S.* Typhimurium). *Salmonella* spp. isolates with an ESBL and AmpC phenotype were detected in meat from pigs in Czech Republic (*S.* Infantis).

Resistance to carbapenems in *Salmonella* from fattening pigs and calves under one year of age and meat thereof was not observed in any of the reporting countries.

Fattening pigs and calves under one year of age were the main focus of the monitoring in 2015 in accordance with Decision 2013/652/EU. The detailed reporting of results at the serovar level clearly demonstrated the major contribution of a few serovars to the observed prevalence of resistance in *Salmonella*. In fattening pigs, six serovars (Derby, monophasic Typhimurium, Typhimurium, Bredeney Rissen and Infantis) accounted for 87.6% of *Salmonella* spp. (Figure 1) and in meat from pigs, seven serovars (Derby, monophasic Typhimurium, Typhimurium, Rissen, Infantis, Bredeney and Livingstone) accounted for 85.6% of *Salmonella* spp. In meat from bovine animals, four serovars (Infantis, monophasic Typhimurium, Derby and Typhimurium) accounted for 72.2% of *Salmonella* spp. and in calves under one year of age, four serovars (Typhimurium, monophasic Typhimurium, Derby and Enteritidis) accounted for 53.3% of *Salmonella* spp. Patterns of resistance associated with these serovars, may therefore be expected to have a marked influence on the overall resistance levels in *Salmonella* from these types of fattening pigs (Figure 2).

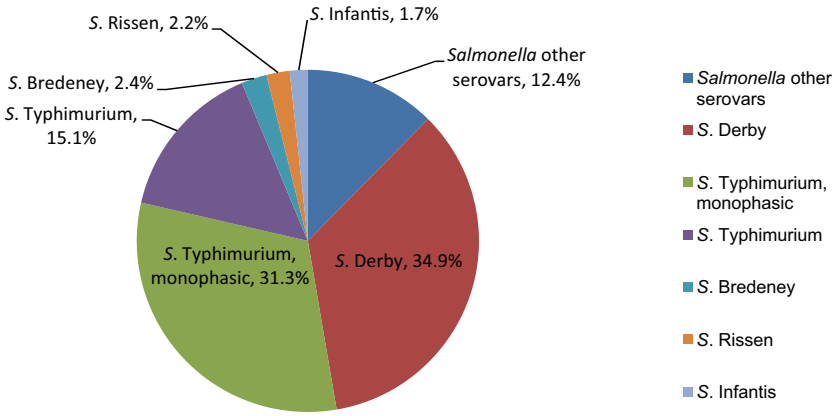
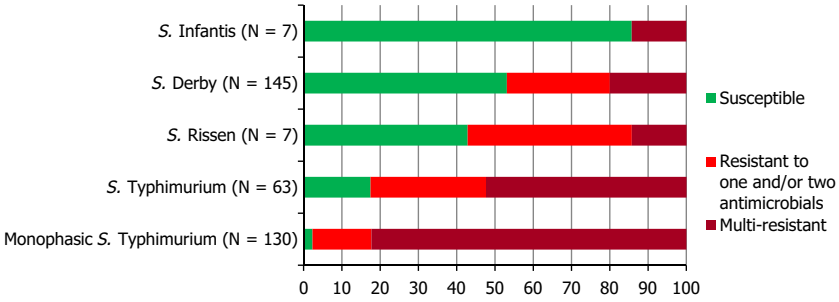


Figure 1: Breakdown of serovars in *Salmonella* isolates from fattening pigs tested for antimicrobial susceptibility in the EU, 2015



N: total number of isolates tested for susceptibility against the whole common antimicrobial.

Figure 2: Proportions of isolates fully susceptible, resistant to one to two classes of substances and multiresistant in the most commonly recovered *Salmonella* serovars in fattening pigs in the EU, 2015

S. Derby is a dominant serovar in fattening pigs, accounting for 34.9% of all *Salmonella* isolates examined from fattening pigs (145/416), and in which 46.9% showed resistance to one or more antimicrobials.

Monophasic *Salmonella* Typhimurium

Monophasic *S.* Typhimurium was the second most dominant serovar in fattening pigs, accounting for 31.3% of all *Salmonella* isolates examined from pigs (130/416), and commonly showing resistance. The proportion of all isolates showing MDR in fattening pigs was greatly influenced by the occurrence of multiresistant monophasic *S.* Typhimurium, this serovar accounting for 25.2% (107/424) of the multiresistant isolates in fattening pigs. Monophasic Typhimurium is currently the third most frequent serovar causing human infection in Europe, with 5,770 cases in 2015. Data from 1,437 human isolates were reported to ECDC in 2015, with 1.2% resistant to third generation cephalosporins. While resistance was not detected in monophasic Typhimurium isolates reported from pig (N = 187) or bovine carcases (N = 14), or from calves under one year of age (N = 7), it was detected in fattening pigs (N = 130), with a single isolate from Italy resistant to third generation cephalosporins. From the monitoring of human monophasic Typhimurium cases reported to ECDC, 6/1,043 isolates for which data were available had an ESBL phenotype and 1/1,043 had an AmpC phenotype, with the enzymes SHV-12, CTX-M-9 and CMY-2 detected; the isolate from fattening pigs in Italy also possessed SHV-12. Thus, in the case of monophasic Typhimurium, the monitoring has highlighted detection of ESBL-producing isolates with common characteristics (the production of SHV-12) in both human and animal monophasic Typhimurium isolates and indicates where further more detailed comparison of isolates may be useful. A number of reasons may account for the differences between the other types of beta-lactamase enzyme encountered in monophasic Typhimurium isolates recovered from man (CMY-2, CTX-M-9) which were not encountered in those animal and meat/carcase types monitored in 2015, not least that other animal species, other food sources or sources outside Europe are responsible or because resistant isolates were present, but were not detected in the monitoring which was performed.

S. Typhimurium was the third most dominant serovar in fattening pigs, accounting for 15.1% of all *Salmonella* isolates examined from fattening pigs (63/416), and commonly showing resistance. Resistance to third-generation cephalosporins was detected in 2/5 *S.* Typhimurium isolates from fattening pigs in Italy (with a presumptive ESBL phenotype).

S. Rissen isolated from pig meat was commonly multiresistant with 52.8% isolates MDR, displaying similar levels of resistance to *S*. Typhimurium, where 54.1% isolates were MDR.

Microbiological resistance to tigecycline was reported in 1.7% of all *Salmonella* spp. from fattening pigs and no isolates from calves under one year of age. There was a marked association of tigecycline microbiological resistance with *S*. Infantis in poultry and most microbiologically resistant strains had minimum inhibitory concentrations (MICs) just above the ECOFF at 2 or 4 mg/L. Resistance to tigecycline in *Salmonella* can be mediated by increased activity of efflux pumps, through modifications to the expression of efflux pump regulatory genes and this may explain the distribution of MICs which was obtained. Determining the susceptibility of tigecycline is not entirely straightforward as the method can be affected by oxidation of the reagents.

Main findings regarding *Campylobacter*

In humans

For 2015, 17 MSs and two non-MSs reported data on AMR in *Campylobacter* isolates from human cases of campylobacteriosis. Twelve countries provided data as measured values (quantitative data), seven more than in 2013 when this type of data collection was implemented. The reported data from the 14 countries represented 17.7% and 21.5% of the confirmed human cases with *Campylobacter jejuni* and *Campylobacter coli*, respectively, reported in the EU/EEA in 2015.

Very high to extremely high resistance levels to ciprofloxacin were reported in human *Campylobacter* isolates from all MSs except Denmark, and Norway. Eleven out of 17 reporting countries had levels of ciprofloxacin resistance in *C. coli* of 80–100% with increasing trends in 2013–2015 in two MSs. For *C. jejuni*, increasing trends of fluoroquinolone resistance was observed in five MSs. The level of acquired resistance to fluoroquinolones is so high in some MSs that this agent can no longer be considered appropriate for routine empirical treatment of human *Campylobacter* infection.

While the proportion of human *C. jejuni* isolates resistant to erythromycin was low overall (1.5%), it was markedly higher in *C. coli* (14.4%) with high to very high proportions (24.2–54.5%) of *C. coli* being resistant in 6 of 17 reporting MSs. Decreasing trends of erythromycin resistance was observed in two MSs for both *C. jejuni* and *C. coli* from humans. Clinical and microbiological co-resistance to both ciprofloxacin and erythromycin, considered critically important for treatment of campylobacteriosis, was

low in *C. jejuni* but moderate in *C. coli* with two countries reporting high to very high co-resistance levels. Of the tested *C. coli* isolates, 14% were resistant to all three antimicrobials ciprofloxacin, erythromycin and tetracycline. In five MS, this resistance combination was observed in at least a third of the tested isolates and in one MS (Portugal), in more than half of the isolates. In such cases, carbapenems have been used for treatment of severe, invasive *Campylobacter* infections.

In fattening pigs

For 2015, seven MSs and two non-MSs reported voluntary data on *Campylobacter* isolates from fattening pigs. In *C. coli* isolates from fattening pigs, overall resistance was very high for ciprofloxacin (62.1%), nalidixic acid (60.8%) and tetracycline (66.6%), whereas overall resistance to erythromycin was high (21.6%) and that to gentamicin low (3.6%). These overall levels of resistance may mask marked variation between MSs for certain antimicrobials, especially ciprofloxacin and tetracyclines (Figure 3).

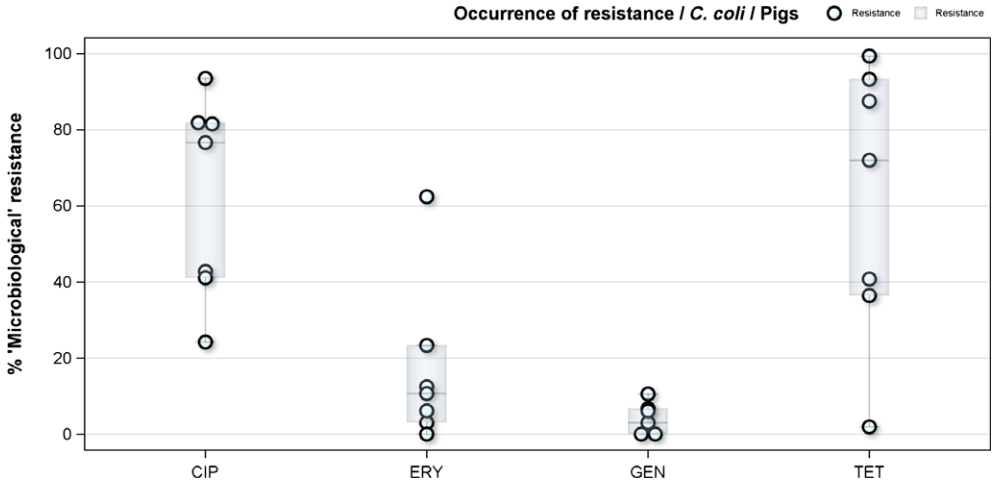


Figure 3: Distribution of the occurrence of resistance to ciprofloxacin (CIP), erythromycin (ERY), gentamicin (GEN) and tetracyclines (TET) in *C. coli* from fattening pigs in seven reporting MSs in 2015, using ECOFFs

Multidrug resistance (reduced susceptibility to at least three antimicrobial classes according to ECOFFs) was overall moderate (13.6%) in *C. coli* from fattening pigs. Co-resistance to the critically important antimicrobials ciprofloxacin and erythromycin was overall at 13.3% but at the country level, ranged from either not detected to very high levels.

Erythromycin resistance in *Campylobacter* spp.

Macrolides are important compounds for the treatment of human *Campylobacter* infections. In fattening pigs, 21.6% of *C. coli* from seven MSs, were microbiologically resistant to erythromycin. The occurrence of resistance to erythromycin in *Campylobacter* spp. varied markedly between individual MSs.

Resistance to macrolides in *Campylobacter* spp. has generally been the result of mutations in ribosomal RNA or ribosomal proteins and these mutations are thought to have incurred fitness costs, accounting for the low occurrence of erythromycin resistance in many countries (Wang et al., 2015). Ribosomal mutations can confer high-level erythromycin resistance (Gibreel and Taylor, 2006). Transferable resistance to erythromycin was first described in *Campylobacter* isolates from food-producing animals (including pigs, chickens and ducks) in China in 2014 (Qin et al., 2014; Wang et al., 2015) and frequently resulted in high level resistance to erythromycin, with MICs recorded at > 512 mg/L. Resistance is conferred by the rRNA methylase gene *erm*(B), which can be associated with either chromosomal multidrug resistance islands or transferable plasmids.

The recent emergence of transferable macrolide resistance in *Campylobacter* may provide a means whereby macrolide resistance can spread rapidly in *Campylobacter*. The situation may be compared to tetracycline resistance, which is frequently plasmid mediated in *Campylobacter*, and is frequently detected in many EU MSs at high levels.

High-level resistance to erythromycin related to the presence of the *erm*(B) gene has recently been described in a single isolate of *C. coli* from broilers in Spain (Florez-Cuadrado et al., 2016). The isolate showed high-level erythromycin resistance (MIC ≥ 1,024 mg/L erythromycin) and the *erm*(B) gene was located within a multidrug resistance island containing five antimicrobial resistance genes. The isolate was resistant to nalidixic acid, ciprofloxacin, tetracyclines and streptomycin and susceptible to gentamicin. This appears to have been the first report of *erm*(B) in *Campylobacter* in Europe.

Although transferable erythromycin resistance conferred by *erm*(B) generally results in high-level resistance to erythromycin, mutational resistance can also result in high-level resistance to erythromycin, but may equally result in lower MICs, still above the ECOFF, dependent on the particular mutations which have occurred. The distribution of erythromycin MICs can therefore be used to identify the numbers of isolates which have high MICs to erythromycin, which may be related either to high-level mutational resistance or the presence of *erm*(B). Fluctuations in the number of isolates detected with high erythromycin MICs will provide an early indication of changes in the occurrence of high-level macrolide resistance in *Campylobacter*. Genetic investigation of isolates will be necessary for definitive characterisation of the resistance mechanisms which are present.

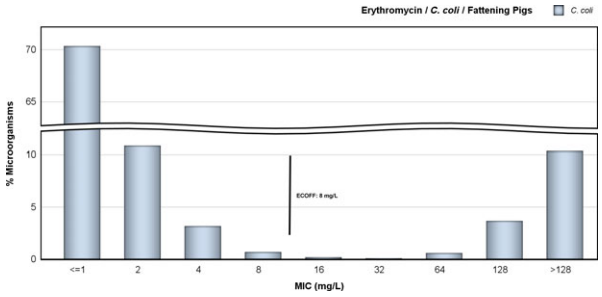


Figure 4: Distribution of MICs of erythromycin in *C. coli* from fattening pigs, 1005 isolates, 8 reporting countries, 2015

Considering the seven reporting MSs and two non-MSs which reported results for *C. coli* in fattening pigs in 2015, high-level resistance to erythromycin (MIC > 128 mg/L) was primarily detected in two reporting countries which accounted for 95/104 (91.3%) of the *C. coli* isolates displaying high-level macrolide resistance.

Main findings regarding indicator commensal *Escherichia coli*

Twenty-seven MSs and two non-MSs reported quantitative data on AMR in indicator *E. coli* isolates from fattening pigs and calves under one year of age and meat thereof in 2015.

In fattening pigs

Regarding fattening pigs, the highest overall 'microbiological' resistance levels observed at the reporting MS group level were to tetracycline (54.7%), sulfamethoxazole (44.2%), ampicillin (39.3%), and trimethoprim (35.3%). Resistance to cefotaxime was 1.4% and was similar to the resistance to ceftazidime (1.3%) in fattening pigs. There was substantial variation in the level of resistance to these

antimicrobials between reporting MSs. Interestingly, certain MSs, already implementing a national control programme of AMR in food-producing animals, registered decreasing trends in resistance, whereas other MSs reported either relatively stable or increasing resistance, in *E. coli* isolates from pigs between 2009 and 2015.

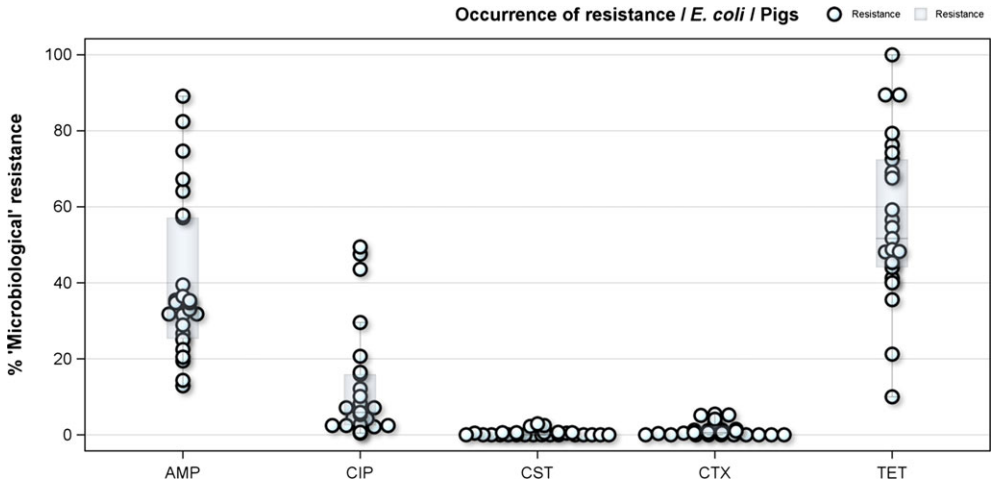


Figure 5: Distribution of the occurrence of resistance to ampicillin (AMP), ciprofloxacin (CIP), colistin (CST), cefotaxime (CTX) and tetracyclines (TET) in *E. coli* from fattening pigs in 27 MSs in 2015, using ECOFFs

MDR levels (reduced susceptibility to at least three antimicrobial classes according to ECOFFs) were generally high in indicator *E. coli* isolates from fattening pigs. Overall for all reporting countries 1,799/4,720 or 38.1% of isolates displayed MDR, although there was considerable variation between reporting countries in the proportion of isolates which were MDR. Co-resistance to ciprofloxacin and cefotaxime was detected in 0.5% (24/4,720) of *E. coli* isolates from fattening pigs, considering low levels of 'microbiological' resistance. When the resistance to ciprofloxacin and cefotaxime was interpreted using 'CBPs', only 0.3% of isolates displayed 'clinical' co-resistance.

In calves of less than one year of age

In the reporting group of MSs, resistance levels in indicator *E. coli* isolates from calves under one year of age were generally lower than among isolates from fattening pigs. The highest resistance levels observed were to tetracyclines (45.4%), sulfamethoxazole (36.6%), ampicillin (31.0%) and trimethoprim (24.7%). The occurrence of resistance was variable between MSs for most of the antimicrobials. Overall, only a few isolates (1.7%) expressed resistance to cefotaxime and 1.4% to ceftazidime.

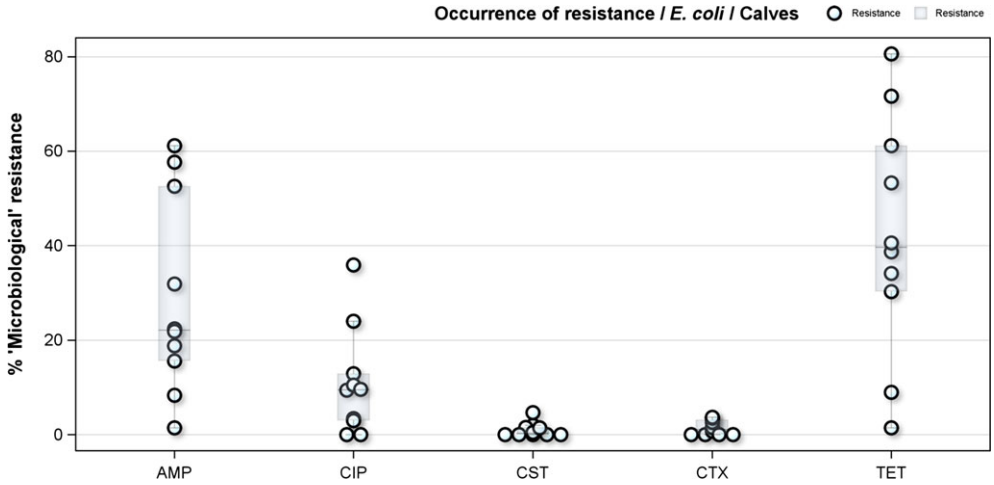


Figure 6: Distribution of the occurrence of resistance to ampicillin (AMP), ciprofloxacin (CIP), colistin (CST), cefotaxime (CTX) and tetracyclines (TET) in *E. coli* from calves of less than one year of age in 10 MSs in 2015, using ECOFFs

Co-resistance to ciprofloxacin and cefotaxime was detected in 18/2,187 (0.8%) of *E. coli* isolates from calves, interpreting resistance using ECOFFs, whereas 'clinical' co-resistance was assessed at 0.4%.

MDR levels (reduced susceptibility to at least three antimicrobial classes according to ECOFFs) were generally high in indicator *E. coli* isolates from calves under one year of age. For all reporting countries, 626/2,187 (28.6%) displayed MDR, with wide variation in the occurrence of MDR between reporting countries. The predominant MDR pattern in calves under one year of age was resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim and this was observed as a core resistance pattern in 55.6% of all MDR *E. coli* isolates from calves. This pattern was also the predominant single MDR pattern, occurring in 21.6% of MDR *E. coli* isolates from calves.

The high levels of resistance to tetracyclines, sulfamethoxazole, ampicillin and trimethoprim in *E. coli* from both fattening pigs and calves under one year of age, as well as the frequent occurrence of resistance to these compounds as a core component of MDR patterns in many reporting countries, reflects extensive usage of these antimicrobials in these countries over many years. The genes conferring resistance to these four compounds are also frequently linked together on mobile genetic elements, resulting in co-selection.

Strains of *E. coli* are not separated on phenotypic characteristics (e.g. serotype) in the current monitoring programme and a less detailed analysis is therefore possible than for *Salmonella* where isolates can be subdivided by serovar. A common pattern of 'microbiological' resistance to ampicillin, sulfamethoxazole, tetracycline and trimethoprim was observed in 20.0% of all *E. coli* isolates from fattening pigs and in 21.6% in calves under one year of age, but a diverse range of other patterns was also recorded, suggesting that a diverse range of strains was captured in the monitoring programme.

Colistin-resistant indicator *E. coli* isolates were found by several MSs originating from fattening pigs and calves under year of age; the levels for all reporting MSs were 0.4% and 0.9%, respectively. Resistance to colistin is discussed further in the section below.

Monitoring was enhanced in 2015 to allow further characterisation of third-generation cephalosporin and carbapenem resistance in indicator *E. coli*. The ESBL phenotype alone was more frequently detected than the AmpC phenotype in indicator *E. coli* from both fattening pigs and calves under one year of age, although at low levels, in less than 5% of isolates in each animal population. An AmpC together with an ESBL phenotype was detected in 0.03% of isolates from fattening pigs, but was not detected in isolates from calves under one year of age. Indicator *E. coli* can represent a reservoir of ESBL and AmpC resistance genes conferring third-generation cephalosporin resistance, which may be transferred to other organisms such as *Salmonella*. The proportions of indicator *E. coli* showing such ESBL and AmpC phenotypic resistance were higher than those observed in *Salmonella* (Table 2), but more detailed investigations, including comparison of resistance genes and plasmids, would be required to confirm the inferred phenotype and investigate whether there was any direct relationship between the resistance detected in the populations of *E. coli* and *Salmonella* included in the monitoring.

Table 2: Summary of phenotypic characterisation of third-generation cephalosporin resistance in *E. coli* from fattening pigs and calves under one year of age in 2015 (routine monitoring)

	Presumptive ESBL-producers[(a)] n (% R)	Presumptive AmpC-producers[(b)] n (% R)	ESBL + AmpC phenotype n (% R)
Fattening pigs (N = 2,956)	44 (1.5)	12 (0.4)	1 (0.03)
Calves under one year of age (N = 1,113)	25 (2.2)	2 (0.2)	1 (0.1)

N: number of the isolates tested; n: number of the isolates resistant; % R: percentage of resistant isolates; ESBL: extended-spectrum beta-lactamase.
(a) Isolates exhibiting an ESBL- and/or ESBL/AmpC-phenotype.
(b) Isolates exhibiting an AmpC- and/or ESBL/AmpC-phenotype.

A carbapenemase-producing *E. coli* detected in meat from pig

In addition, Belgium recently confirmed the detection of a presumptive carbapenemase-producing *E. coli* from meat from pig sampled at retail within the framework of a voluntary routine monitoring of indicator *E. coli* using non-selective culture media. The presence of a carbapenem-resistance gene together with an ESBL and an AmpC-encoding genes subsequently validated the presumptive profile.

Main findings regarding colistin resistance in *E. coli* and *Salmonella* spp.

Monitoring of colistin resistance has recently assumed greater importance with the discovery of transferable resistance to colistin, conferred by the genes *mcr-1* (Liu et al., 2015) and *mcr-2* (Xavier et al., 2016). The *mcr-1* and *mcr-2* genes encode phosphoethanolamine transferases, which add a phosphoethanolamine moiety to the lipid A of the lipopolysaccharide component of the bacterial cell wall, reducing the affinity for colistin. Historically, resistance to colistin was related to chromosomal alterations, which also affected lipid A in the bacterial cell wall and reduced the binding of colistin to the cell wall, but these chromosomal alterations were not transferable. 2014 was the first year in which the monitoring of colistin resistance in *E. coli* from animals was mandatory, and in that year 0.9% and 7.4% of the *E. coli* isolated from broilers and turkeys, respectively, were resistant to this antimicrobial. Colistin-resistant indicator *E. coli* isolates were found by several MSs originating from fattening pigs and calves under year of age at levels (for all reporting MSs) of 0.4% and 0.9%, respectively, similar to the figure observed in broilers in 2014.

Colistin resistance in indicator E. coli

Many countries worldwide have now reported the presence of *mcr-1* in enterobacteriaceae recovered from humans, food or animals (Skov and Monnet, 2016). Such reports demonstrated that *mcr-1* was present in *E. coli* in food-producing animals (pigs and cattle) in Belgium in 2011–2012 (Malhotra-Kumar et al., 2016) in France in veal calves in 2005 (Haenni et al., 2016) and in Germany in pigs in 2010 (Falgenhauer et al., 2016). Furthermore, the *mcr-1* gene with or without the truncated mobile genetic element IS*Apl1* in some cases occurred on a plasmid different from that reported in China, which indicated that the *mcr-1* gene has been transferred between different plasmids (Malhotra-Kumar et al., 2016). These studies also showed that plasmids carrying *mcr-1* had transferred between different bacteria, because unrelated *E. coli* strains carried *mcr-1* (Haenni et al., 2016). *E. coli* isolates reported from pigs in Germany and veal calves in France also produced extended-spectrum beta-lactamases (Falgenhauer et al., 2016; Haenni et al., 2016); although isolates from animals in Belgium did not produce ESBLs, one which was sequenced showed multidrug resistance (Malhotra-Kumar et al., 2016). Although Enterobacteriaceae from animals in Europe have not so far been reported which carry *mcr-1* and which are resistant to carbapenems, this has been reported in human clinical isolates (Poirel et al., 2016).

The colistin resistance gene *mcr-2*, described by Xavier et al., 2016; displayed 76.7% nucleotide identity to *mcr-1* and was detected in a greater proportion of colistin-resistant *E. coli* from pigs in Belgium than was *mcr-1*. The monitoring performed under the Decision 2013/652/EU is phenotypic and does not discriminate between the different mechanisms of resistance which may be present. The distribution of colistin MIC values for indicator *E. coli* from fattening pigs and calves under one year of age is shown in Figure 7. Co-resistance between colistin and cefotaxime/ceftazidime was shown by 1/4,270 (0.02%) of indicator *E. coli* isolates from fattening pigs (a single isolate from Portugal). In calves under one year of age, co-resistance to colistin and cefotaxime/ceftazidime was shown by 3/2,113 (0.1%) of indicator *E. coli* isolates (Belgium, France). A study in France demonstrated that 21% of ESBL *E. coli* from calves possessed the colistin- resistance gene *mcr-1* (Haenni et al., 2016); monitoring of indicator *E. coli* in calves under the Decision 2013/652/EU has therefore detected co-resistance to colistin and cefotaxime/ceftazidime in a very low number of isolates (3) from Belgium and France. These isolates showed extensive resistance however, including resistance to ciprofloxacin.

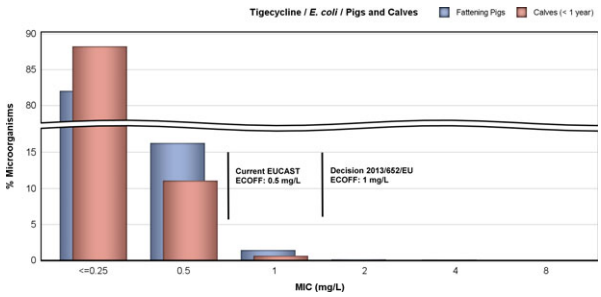


Figure 7: Colistin resistance in *E. coli* from fattening pigs and calves under one year of age

Colistin resistance in Salmonella spp.

Resistance to colistin was reported in 1.3% of 750 *Salmonella* spp. from meat from pigs, 1.3% of 80 *Salmonella* spp. from meat from bovines, 0% of 424 *Salmonella* spp. from fattening pigs and 2.2% of 45 *Salmonella* spp. from calves under one year of age.

Considering calves under one year of age, a single colistin-resistant isolate of *S.* Rissen with an MIC of 4 mg/L was reported by Spain, while France reported a single *S.* Infantis, again with a colistin MIC of 4 mg/L from bovine carcases.

In meat from fattening pigs, a range of serovars displaying colistin resistance was detected. Only one of these serovars (*S.* Dublin) belonged to serogroup D, a serogroup which shows a lower level of intrinsic susceptibility to colistin compared to other serovars. Monophasic *S*. Typhimurium was the most commonly detected serovar which exhibited colistin resistance. *S.* Rissen and monophasic *S.* Typhimurium, were the serovars in which the highest colistin MICs of 16 mg/L were observed; both isolates originated from Portugal.

There was not a consistent association between the occurrence of resistance to colistin in *Salmonella* and the occurrence in indicator *E. coli* in reporting countries.

Specific monitoring of ESBL-/AmpC-/carbapenemase-producing *E. coli*

In 2015, specific monitoring for ESBL-/AmpC-/carbapenemase-producing *E. coli* was performed on caecal contents from fattening pigs, calves under one year of age and meat derived from these animals. A screening breakpoint for cefotaxime and/or ceftazidime (> 1 mg/L) was applied to screen for ESBL and AmpC-producers as recommended by EUCAST. In 2015, the specific ESBL-/AmpC-/carbapenemase-producing monitoring was performed on a mandatory basis on meat from pigs by 23 MSs and two non-MSs, on meat from bovine animals by 24 MSs and two non-MSs, on fattening pigs by 28 MSs and two non-MSs and on calves under one year of age by 10 MSs and two non-MSs.

The specific monitoring employs culture of samples on selective media (including cefotaxime at 1 mg/L, which is the ECOFF for this antimicrobial), which is able to detect very low numbers of resistant isolates present within a sample. The occurrence and prevalence of *E. coli* showing an ESBL, AmpC and ESBL+AmpC profiles from fattening pigs, calves, meat from pigs and meat from bovine animals deriving from specific monitoring in 2015 assessed at the reporting MS-group level are presented in Table 3.

Table 3: Summary of phenotypic[(a)] characterisation of third-generation cephalosporin resistance in presumptive ESBL-/AmpC-producing *E. coli* from fattening pigs, calves, meat from pigs and meat from bovine animals deriving from specific monitoring in 2015

	Presumptive ESBL-producers[(b)]			Presumptive AmpC-producers[(c)]			ESBL + AmpC phenotype		
	n	%Occ	%Prev	n	%Occ	%Prev	n	%Occ	%Prev
Fattening pigs (N_s = 6,167; N = 2,441)[(d)]	1,869	76.6	31.9	569	23.3	9.7	87	3.6	1.5
Calves (N_s = 2,343; N = 895)[(e)]	830	92.7	36.8	108	12.1	4.8	46	5.1	2.0
Meat from pigs (N_s = 5,350; N = 319)[(f)]	252	78.9	7.0	79	24.8	2.3	14	4.4	0.4
Meat from bovines (N_s = 5,329; N = 209)[(g)]	159	76.1	5.0	57	27.3	1.8	9	4.3	0.3

N_s: number of animal/meat samples; N: number of the isolates tested; n: number of the isolates resistant; %Occ: percentage of resistant isolates; %Prev: percentage of samples harbouring a presumptive ESBL-/AmpC-producing *E. coli*.
(a): Italy submitted only genotype results.
(b): Isolates exhibiting an ESBL- and/or ESBL/AmpC-phenotype.
(c): Isolates exhibiting an AmpC- and/or ESBL/AmpC-phenotype.
(d): 27 MSs included.
(e): 9 MSs included.
(f): 22 MSs included.
(g): 23 MSs included.

In those animal populations/food matrices monitored, at the reporting MS-group level and in most but not all countries, the detection of presumptive producing *E. coli* exceeded that of AmpC-producing *E. coli*. Generally, the occurrence of *E. coli* with an ESBL phenotype varied widely between reporting countries, occurring in between 0% and 81.5% of fattening pig caecal samples examined and in between 0% and 60% of caecal samples examined from calves less than one year. Considering both meat from pigs and meat from bovine animals, the figures for all reporting countries were remarkably similar. There are several potential sources of bacteria on meat, including the animals from which the

meat was derived, other cross-contaminating products, machinery and the environment, as well as those workers who are producing and handling the meat product.

The ceftazidimase ESBL phenotype (i.e. clavulanate synergy shown only with ceftazidime) was not detected in meat from pigs or cattle and was also rarely encountered in fattening pigs and calves under one year of age. By comparison, the cefotaximase ESBL phenotype (i.e. clavulanate synergy shown only with cefotaxime) or the ESBL phenotype with clavulanate synergy to both cefotaxime and ceftazidime was predominant in isolates with an ESBL phenotype. The findings suggest that those ESBL enzymes which are predominantly ceftazidimases are currently rare in fattening pigs, calves under one year of age and in meat derived from those animals in the EU, whereas ESBLs which hydrolyse both cefotaxime and ceftazidime or which are cefotaximases are more frequent.

Among the isolates collected within the ESBL/AmpC/carbapenemase monitoring of isolates from fattening pigs, Germany also reported the presence of an *E. coli* isolate showing a carbapenemase-producer-phenotype. The presence of carbapenemase-encoding genes in this isolate was confirmed by the MS. Although there have been previous reports on the isolation of VIM-1 producing *E. coli* and *Salmonella* in food-producing animals in Germany (EFSA BIOHAZ Panel, 2013; Guerra et al., 2014), this is the first time in which carbapenemase-producing *E. coli* had been collected within the EU mandatory monitoring of livestock (Irrgang et al., 2016b). Germany has reported recurrent, sporadic detection of VIM-1 producing *E. coli* in German pig production; VIM-1 producing *E. coli* isolates from different pig farms, recovered at different times, were highly related, which was considered to suggest persistence in the pig population for at least 4 years (Irrgang et al., 2016b). The detection of such isolates in Germany through mandatory monitoring, confirm that the monitoring is capable of detecting carbapenemase-producing *E. coli*.

Overall, the specific monitoring highlighted that the occurrence of ESBL- or AmpC-producing *E. coli* on meat was much lower than that detected in the caecum of animals at slaughter. The range of occurrence of presumptive ESBL- or AmpC-producing *E. coli* in meat by different MSs also tended to be narrower than that observed in the caecum of animals at slaughter. The findings suggest that existing hygiene measures have a considerable effect in reducing the contamination of carcases with *E. coli* from the digestive tract of the animal. The relative abundance of ESBL and AmpC *E. coli* which are present in a given sample will influence the probability of selecting either type of *E. coli*. In most countries, the detection of ESBL phenotype *E. coli* exceeded AmpC phenotype *E. coli* (often considerably so). However, considering meat from pigs, AmpC phenotype *E. coli* exceeded ESBL phenotype *E. coli* in Cyprus, Finland and Norway; this was also the case in Cyprus, Estonia, Greece and Slovakia for *E. coli* from bovine meat. Combined ESBL and AmpC phenotype *E. coli* tended to occur as a low proportion of cefotaxime-resistant *E. coli*; it is possible that this proportion is below the threshold of detection in countries where the prevalence of cefotaxime resistance is low.

In fattening pigs, ESBL phenotype *E. coli* exceeded AmpC phenotype *E. coli* in all reporting countries except Denmark, Finland, Ireland, Slovakia and Sweden. Considering calves under one year of age, ESBL *E. coli* exceeded AmpC *E. coli* in all reporting countries except Denmark, Norway and Sweden. The Nordic countries are therefore over-represented amongst those countries reporting AmpC phenotype *E. coli* exceeding ESBL phenotype *E. coli* and the reason for this is unknown.

ESBL- and AmpC-producing *E. coli*

- A recent large-scale study in Sweden (Börjesson et al., 2016) found that clonal spread of cephalosporin-resistant *E. coli* from food and farm animals to man was unlikely and that there was limited dissemination of ESBL or plasmidic AmpC-genes and the plasmids carrying such genes from foods and farm animals to either healthy humans or patients.
- The occurrence of AmpC and ESBL-producing *E. coli* in the intestinal flora of animals is however undesirable and the consequences of such carriage for the human population should also be considered in terms of their role as reservoirs of resistance genes which may be transferable to organisms which are food borne zoonoses, such as *Salmonella*.
- A recent comparative exposure assessment of ESBL-producing *E. coli* through meat consumption (Evers et al., 2017) suggested that consumption of beef products (which may be consumed raw in some MSs) led to a higher exposure than chicken products (which are usually cooked), even though the prevalence of ESBL-producing *E. coli* was higher on chicken meat than on beef.
- Clearly, the epidemiology of ESBL- and AmpC-producing *E. coli* in animals, food and humans is complex; the monitoring performed makes a significant contribution to the robust data which are available.

Specific monitoring of carbapenemase-producing *E. coli* (voluntary monitoring)

Eight MSs investigated the presence of carbapenemase-producing *E. coli* in meat from pigs (1,833 samples analysed) and 10 MSs investigated in fattening pigs (2,584 samples). Eight MSs also investigated meat from bovine animals (1,818 samples), while three countries reported data on bovine animals (682 samples) and on calves under one year of age (516 samples). No carbapenemase-producing *E. coli* isolate was identified in these samples by this specific monitoring.

Main findings regarding meticillin-resistant *Staphylococcus aureus*

EFSA recommends that monitoring of food-producing animals is carried out periodically in conjunction with systematic surveillance of meticillin-resistant *Staphylococcus aureus* (MRSA) in humans, so that trends in the diffusion and evolution of zoonotically acquired MRSA in humans can be identified. Monitoring of MRSA is currently voluntary, but the findings presented in this report and summarised below underline the value of such monitoring.

A low number of MSs reported the monitoring of MRSA in food. MRSA was detected in meat from rabbits and pigs in four countries. The occurrence of MRSA in meat and products derived from animals may reflect colonisation of those animals with MRSA. MRSA is not generally regarded as being transmitted by food and the culture methods employed are often very sensitive, commonly involving multiple selective stages and consequently, are able to detect very low numbers of MRSA.

In relation to healthy food-producing animals, MRSA was detected in calves under one year of age or other types of cattle in three countries. Belgium examined dairy cows for MRSA; the proportion of animals which tested positive equalled 10.4%. There was a large degree of variation between reporting countries in the occurrence of MRSA in pigs, as 0.5–91.4% of animals/herd/slaughter batches tested positive. Some of this variation may be due to differences in sampling protocols. Molecular typing data (*spa*-typing) were reported by three countries in relation to cattle and by two countries in relation to isolates from pigs. The vast majority of *spa*-types identified were types associated with MRSA clonal complex (CC) 398, the common livestock-associated type of MRSA occurring in Europe.

Considering the three broad epidemiological classes of MRSA (livestock-associated (LA)-MRSA, hospital-associated (HA)-MRSA and community-associated (CA)-MRSA), whenever *spa*-typing data were available, then only *spa*-types associated with CC398 were reported from meat in 2015. However, *spa*-types associated with each type of MRSA – LA-MRSA, HA-MRSA and with CA-MRSA were reported from food-producing animals, although the great majority of isolates belonged to *spa*-types associated with LA-MRSA.

- In calves under one year of age, Belgium reported MRSA *spa*-type t044 a *spa*-type associated with sequence type 80 and a type observed in a widely disseminated European clone of community-associated MRSA. These isolates were negative for Panton–Valentine leucocidin (PVL); *spa*-type t044 has also been associated with ST9.
- Belgium also reported *spa*-type t037 which is associated with ST239, a dominant sequence type of HA-MRSA.
- Switzerland reported t032 from pigs, a *spa*-type associated with CC22, usually considered an HA-MRSA.
- *Spa*-type t2741, which has become dominant in fattening pigs in Finland, accounted for 7% of recent CC398 human infections in Finland.

Horizon Scanning – possible CA-MRSA in fattening pigs and calves under one year of age

- Switzerland reported MRSA *spa*-type t008 from two different calves under one year of age, out of 292 tested, both of which were positive for the PVL.
- MRSA *spa*-type t008 is associated with ST8 and possession of PVL in this *spa*-type is typical of isolates of the CA-MRSA strain 'USA300' which can cause severe infections in man. However, this combination has also been reported in strains of MRSA which were not 'USA300', from pigs in Cuba (Baez et al., 2017).
- Further typing is awaited, but the occurrence of *spa*-types associated with CA-MRSA, in calves in Belgium and Switzerland and in particular the detection of a strain with characteristics suggestive of possible 'USA300' in two different animals in Switzerland represents a significant development.
- At this stage, the findings are insufficient to confirm the presence of CA-MRSA strain 'USA300' in calves in Europe; further molecular analysis is required and is being performed in Switzerland.

  Switzerland and Belgium were the only countries to report findings for young calves and whether this reflects a wider European trend or certain particular local farm circumstances is not known at this stage.

Several MSs reported results of clinical investigations which yielded MRSA in food-producing animals, in sheep, goats and cattle. Considering companion animals, MRSA was detected in cats, dogs and horses in some MSs.

Temporal trends in the occurrence of MRSA in animals could be only assessed in Switzerland, which reported on the occurrence of MRSA in fattening pigs at slaughter – obtained by testing nasal swabs – in consecutive years from 2009 to 2015. The method used in Switzerland involved sampling one pig per herd at slaughter and may be subject to imprecision, because pigs can be intermittently colonised (Bangerter et al., 2016) and also because sampling at slaughter can be influenced by colonisation of animals in the abattoir lairage. The numbers of animals positive for MRSA slowly increased over this period, from 2.2% in 2009 to 25.7% in 2015. The majority of these MRSA isolates belonged to *spa*-type t011 or t034, typical for the clonal complex CC398, whereas much lower numbers of MRSA sequence type ST49 were also reported, although this *spa*-type was not detected in 2015. Thus the increase has been primarily the result of the diffusion within the Swiss population of fattening pigs of clones of *spa*-types t034 and t011 related to CC398.

Resistance to the important medical antimicrobials, vancomycin and linezolid, was not detected in MRSA isolates from animals or meat.

The voluntary monitoring performed reflects the priorities of MSs and although monitoring is not co-ordinated across MSs, LA-MRSA is evidently widespread geographically and present in diverse mammalian and avian host species. It is unclear whether the broad range of species in which colonisation has been detected reflects diffusion in those different species and long-term colonisation, or transient cross-colonisation between species on mixed farms, from species in which colonisation occurs readily, such as pigs.