SCIENTIFIC REPORT

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.

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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).
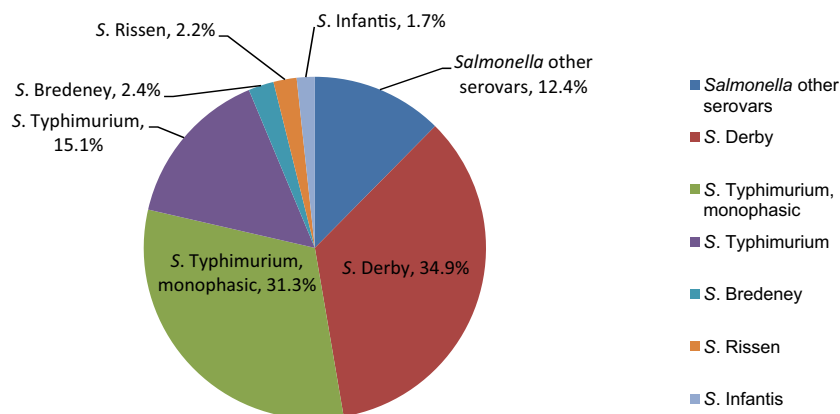
Figure 1: Breakdown of serovars in *Salmonella* isolates from fattening pigs tested for antimicrobial susceptibility in the EU, 2015
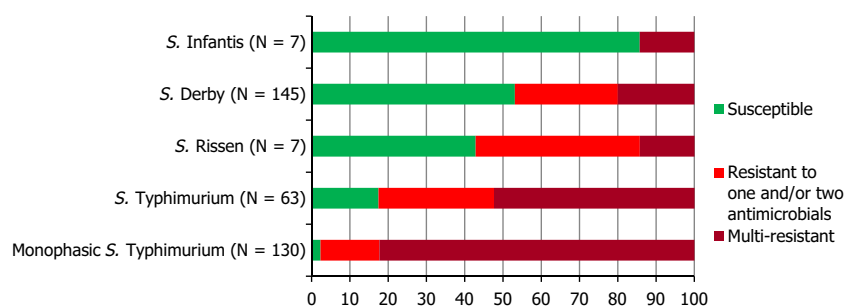
N: total number of isolates tested for susceptibility against the whole common antimicrobial.

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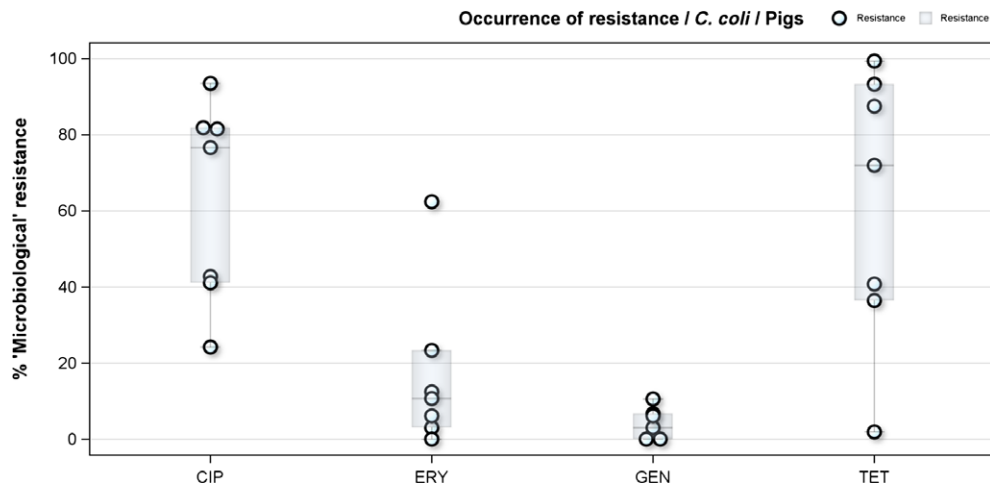
Figure 3: Distribution of the occurrence of resistance to ciprofloxacin (CIP), erythromycin (ERY), gentamicin (GEN) and tetracyclines (TET) in *C. coli* from fattening pigs in seven reporting MSs in 2015, using ECOFFs

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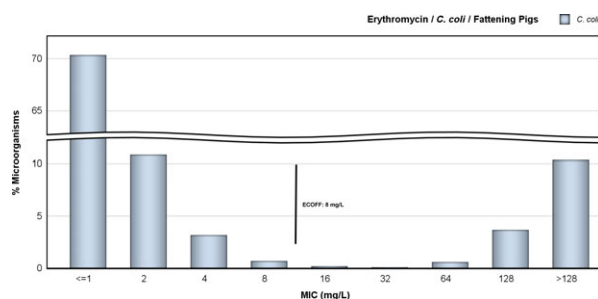
Figure 4: Distribution of MICs of erythromycin in *C. coli* from fattening pigs, 1005 isolates, 8 reporting countries, 2015

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.
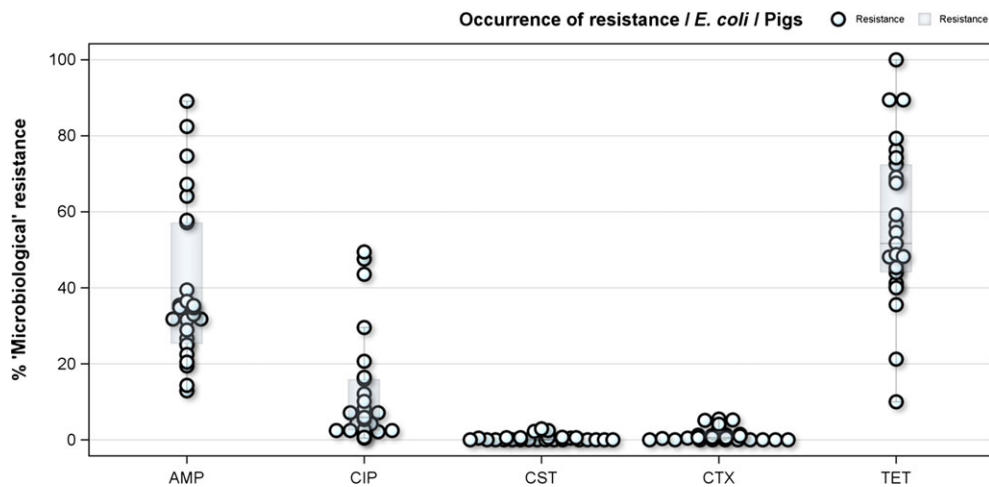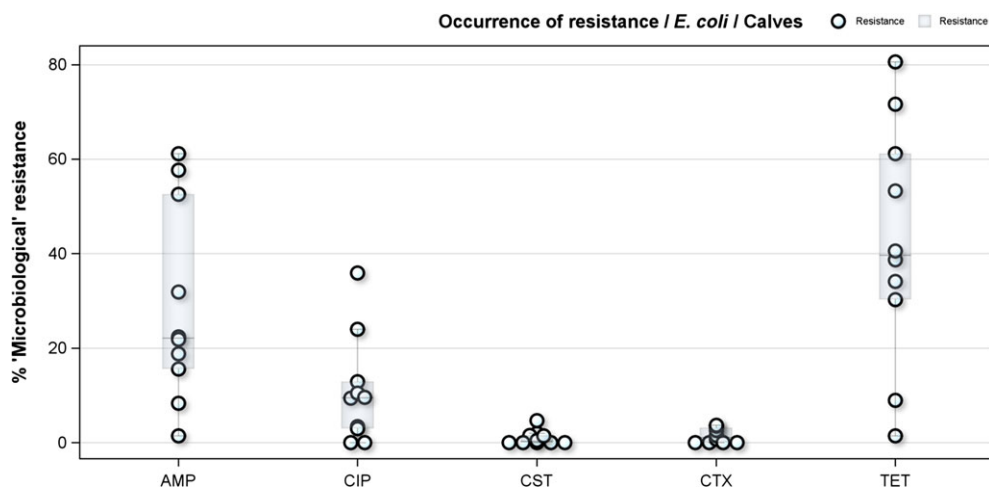

Figure 6: Distribution of the occurrence of resistance to ampicillin (AMP), ciprofloxacin (CIP), colistin (CST), cefotaxime (CTX) and tetracyclines (TET) in *E. coli* from calves of less than one year of age in 10 MSs in 2015, using ECOFFs

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 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.
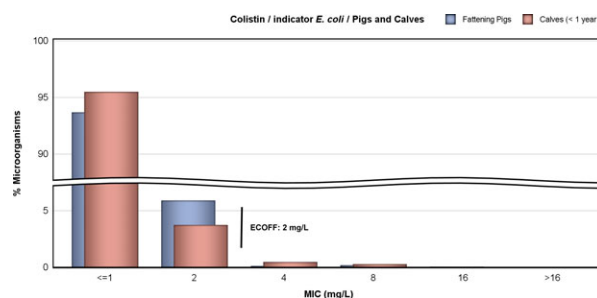

Figure 7: Colistin resistance in *E. coli* from fattening pigs and calves under one year of age

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 ESBL-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.

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Legal basis

According to Directive 2003/99/EC on the monitoring of zoonoses and zoonotic agents, Member States (MSs) are obliged to monitor and report antimicrobial resistance (AMR) in *Salmonella* and *Campylobacter* isolates obtained from healthy food-producing animals and from food. Commission Implementing Decision 2013/652/EU of 12 November 2013[1] sets up priorities for the monitoring of AMR from a public health perspective, establishes a list of combinations of bacterial species, food-producing animal populations and foodstuffs and lays down detailed requirements on the harmonised monitoring and reporting of AMR.

The data collection on human diseases from MSs is conducted in accordance with Decision 1082/2013/EU[2] on serious cross-border threats to health, which in October 2013 replaced Decision 2119/98/EC on setting up a network for the epidemiological surveillance and control of communicable diseases in the European Union (EU). The case definitions to be followed when reporting data on infectious diseases, including AMR, to the European Centre for Disease Prevention and Control (ECDC) are described in Decision 2012/506/EU.[3] ECDC has provided data on zoonotic infections in humans, as well as their analyses, for the Community Summary Reports since 2005. Since 2007, data on human cases have been reported from The European Surveillance System (TESSy), maintained by ECDC.

About EFSA

The European Food Safety Authority (EFSA), located in Parma, Italy, and established and funded by the EU as an independent agency in 2002, provides objective scientific advice, in close collaboration with national authorities and in open consultation with its stakeholders, with a direct or indirect impact on food and feed safety, including animal health and welfare and plant protection. EFSA is also consulted on nutrition in relation to EU legislation. EFSA's risk assessments provide risk managers (the European Commission (EC), the European Parliament and the Council) with a sound scientific basis for defining policy-driven legislative or regulatory measures required to ensure a high level of consumer protection with regard to food and feed safety. EFSA communicates to the public in an open and transparent way on all matters within its remit. Collection and analysis of scientific data, identification of emerging risks and scientific support to the EC, particularly in the case of a food crisis, are also part of EFSA's mandate, as laid down in founding Regulation (EC) No 178/2002[4] of 28 January 2002.

About ECDC

The European Centre for Disease Prevention and Control (ECDC), an EU agency based in Stockholm, Sweden, was established in 2005. The objective of ECDC is to strengthen Europe's defences against infectious diseases. According to Article 3 of founding Regulation (EC) No 851/2004[5] of 21 April 2004, ECDC's mission is to identify, assess and communicate current and emerging threats to human health posed by infectious diseases. In order to achieve this goal, ECDC works in partnership with national public health bodies across Europe to strengthen and develop EU-wide disease surveillance and early warning systems. By working with experts throughout Europe, ECDC pools Europe's knowledge in health to develop authoritative scientific opinions about the risks posed by current and emerging infectious diseases.

Terms of Reference

The EU system for the monitoring and collection of information on zoonoses is based on the Zoonoses Directive 2003/99/EC, which obliges EU MSs to collect relevant and, where applicable, comparable data on zoonoses, zoonotic agents, AMR and food-borne outbreaks. In addition, MSs are required to assess trends and sources of these agents, as well as outbreaks in their territory, submitting an annual report each year by the end of May to the EC covering the data collected. EFSA

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[1] Commission Implementing Decision 2013/652/EU of 12 November 2013 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria. OJ L 303, 14.11.2013, p. 26–39.

[2] Decision No 1082/2013/EU of the European Parliament and of the Council of 22 October 2013 on serious cross-border threats to health and repealing Decision No 2119/98/EC. OJ L 293, 5.11.2013, p. 1–15.

[3] Commission Decision 2012/506/EU amending Decision 2002/253/EC laying down case definitions for reporting communicable diseases to the Community network under Decision No 2119/98/EC of the European Parliament and of the Council. OJ L 262, 27.9.2012, p. 1–57.

[4] Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the EFSA and laying down procedures in matters of food safety. OJ L 31, 1.2.2002, p. 1–24.

[5] Regulation (EC) No 851/2004 of the European Parliament and of the Council of 21 April 2004 establishing a European centre for disease prevention and control. OJ L 142, 30.4.2004, p. 1–11.

is assigned the tasks of examining these data and publishing the EU annual Summary Reports. In accordance with Article 9 of the Zoonoses Directive 2003/99/EC, EFSA shall examine the submitted national reports of the EU MSs and publish by the end of November a summary report on the trends and sources of zoonoses, zoonotic agents and AMR in the EU.

1. Introduction

The antimicrobial agents used in food-producing animals in Europe are frequently the same, or belong to the same classes, as those used in human medicine. Antimicrobial resistance (AMR) is the main undesirable side effect of antimicrobial use in both humans and animals, and results from the continuous positive selection of resistant bacterial clones, whether these are pathogenic, commensal or even environmental bacteria. This will modify the population structure of microbial communities, leading to accelerated evolutionary trends with unpredictable consequences for human and animal health. Both the route of administration and the administered quantities of antimicrobials may differ between humans and food-producing animals; moreover, there are important variations between and within food-producing animal populations, as well as between countries.

Bacterial resistance to antimicrobials occurring in food-producing animals can spread to people not only via food-borne routes, but also by routes such as water or other environmental contamination, as well as through direct animal contact. *Campylobacter*, *Salmonella* and some strains of *Escherichia coli* are examples of zoonotic bacteria which can infect people by the food-borne route. Infections with bacteria which are resistant to antimicrobials may result in treatment failures or necessitate the use of second-line antimicrobials for therapy. The commensal bacterial flora can also form a reservoir of resistance genes, which may be transferred between bacterial species, including organisms capable of causing disease in both humans and animals (EFSA, 2008).

The monitoring of AMR in zoonotic and commensal bacteria in food-producing animals and food thereof is a prerequisite for understanding the development and diffusion of resistance, providing relevant risk assessment data, and evaluating targeted interventions. Resistance monitoring entails specific and continuous data collection, analysis and reporting and enables to follow temporal trends in the occurrence and distribution of resistance to antimicrobials. Resistance monitoring should also allow for the identification of emerging or specific patterns of resistance.

1.1. Monitoring and reporting of antimicrobial resistance at the EU level

Based on Article 33 in Regulation (EC) 178/2002, EFSA is responsible for examining data on AMR collected from the Member States (MSs) in accordance with Directive 2003/99/EC and for preparing the European Union (EU) Summary Report from the results. This EU Summary Report 2015 includes data related to the occurrence of AMR both in isolates from animals and foodstuffs and in isolates from human cases. The report is a joint collaboration between the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) with the assistance of EFSA's contractor – the Animal and Plant Health Agency (APHA) in the United Kingdom. MSs, other reporting countries, the European Commission (EC) and the relevant EU Reference Laboratory (EURL-AR) were consulted, while preparing the report. The efforts made by MSs, the reporting non-MSs and the EC in the reporting of data on AMR and in the preparation of this report are gratefully acknowledged.

1.2. Further harmonised monitoring of antimicrobial resistance

The main issues when comparing AMR data originating from different countries are the use of different laboratory methods and different interpretive criteria of resistance. These issues have been addressed by the development of ECDC's protocol for harmonised monitoring and reporting of resistance in humans and recent legislation on harmonised monitoring in food-producing animals and food thereof.

1.2.1. New legislation on antimicrobial resistance monitoring in animals and food

Commission Decision 2013/652/EU of 12 November 2013[6] establishes a list of combinations of bacterial species, food-producing animal populations and food products and sets up priorities for the

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[6] Commission Implementing Decision 2013/652/EU of 12 November 2013 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria. OJ L 303, 14.11.2013, p. 26–39.

monitoring of AMR from a public health perspective. Monitoring of AMR in *E. coli* became mandatory, as it is for *Salmonella* and *Campylobacter jejuni* in the major food-producing animal populations – broilers, laying hens, fattening turkeys, fattening pigs, calves – and their derived meat. The specific monitoring of extended-spectrum beta-lactamase (ESBL)-, AmpC- and carbapenemase-producing *Salmonella* and indicator commensal *E. coli* is also foreseen. The collection and reporting of data are to be performed at the isolate level, in order to enable more in-depth analyses to be conducted, in particular on the occurrence of MDR. Representative sampling should be performed according to general provisions of the legislation and to detailed technical specifications issued by EFSA. Monitoring of AMR in food-producing animals should be performed at the level of domestically produced animal populations, corresponding to different production types with the aim of collecting data that, in the future, could be combined with those on exposure to antimicrobials. Provisions have been taken where possible to exploit samples that would be collected under other existing control programmes. Commission Implementing Decision 2013/652/EU entered into force in 2014, as did Commission Implementing Decision 2013/653/EU of 12 November 2013 concerning financial aid towards a coordinated control plan for AMR monitoring in zoonotic agents in MSs in 2014.

Microdilution methods for testing should be used and results should be interpreted by the application of EUCAST epidemiological cut-off (ECOFF) values[7] for the interpretation of 'microbiological' resistance. The harmonised panel of antimicrobials used for *Salmonella*, *Campylobacter*, *E. coli* and *Enterococcus* spp. is broadened with the inclusion of substances that either are important for human health or can provide clearer insight into the resistance mechanisms involved. The concentration ranges to be used ensure that both the ECOFF and the CBP are included so that comparability of results with human data is made possible. Within the animal and food monitoring programmes, the new legislation has specified those types of animals which should be monitored in particular years. Ensuring that all MSs test the same species in a given year has simplified the presentation and increased the comparability of the results, because each annual report will now focus primarily on the target species for a given year.

A particular feature of the revised monitoring protocol for *Salmonella* and *E. coli* is the use of a supplementary panel of antimicrobials for testing isolates which show resistance to third-generation cephalosporins or carbapenems in the first panel. The reporting of isolate-based data, which was introduced several years ago, has facilitated the introduction of this change, which allows in depth phenotypic characterisation of certain mechanisms of resistance, for example, third-generation cephalosporin resistance and carbapenem resistance can be further characterised. It seems likely that this principle can be further developed and refined in time.

External quality assurance is provided by the EURL-AR, which distribute panels of well-characterised organisms to all MSs for susceptibility testing. MSs must test and obtain the correct results in such tests to ensure proficiency. The EURL-AR also provides a source of reference for MSs in cases where there are issues or problems with the susceptibility test methodology and runs, in collaboration with EFSA and the MSs, a reference testing exercise (AST-retesting and whole genome sequencing of selected isolates).

1.2.2. Developments in the harmonised monitoring of antimicrobial resistance in humans

Together with its Food- and Waterborne Diseases and Zoonoses (FWD) network, ECDC developed an EU protocol for harmonised monitoring of AMR in human *Salmonella* and *Campylobacter* isolates (ECDC, 2014, 2016). This document is intended for the National Public Health Reference Laboratories to guide the susceptibility testing required for EU surveillance and reporting to ECDC. Consultation was also sought from EFSA, EUCAST and the EU reference laboratory for antimicrobial resistance to facilitate comparison of data between countries and with results from the AMR monitoring performed in isolates from animals and from food products. The protocol is effective from 2014 and supports the implementation of the Commission Action Plan on AMR. One of the recommendations is that, for the purpose of the joint report with EFSA, human data should also be interpreted based on ECOFFs. As

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[7] The epidemiological cut-off (ECOFF) values separate the naive, susceptible wild-type bacterial populations from isolates that have developed reduced susceptibility to a given antimicrobial agent (Kahlmeter et al., 2003). The ECOFFs may differ from breakpoints used for clinical purposes, which are defined against a background of clinically relevant data, including therapeutic indication, clinical response data, dosing schedules, pharmacokinetics and pharmacodynamics. The use of harmonised methods and ECOFFs ensures the comparability of data over time at the country level and also facilitated the comparison of resistance between MSs.

this requires quantitative data, ECDC introduced reporting of quantitative antimicrobial susceptibility testing (AST) results in the 2013 data collection and encourages countries to use it. As the EU protocol is not a legal document but a recommendation and joint agreement, it is for each National Public Health Reference Laboratory to decide whether to adapt their practices to the protocol. Most laboratories adopted the priority panel of antimicrobials suggested in the protocol in 2015, whereas the optional antimicrobials were tested by fewer laboratories. The protocol also proposes a testing algorithm for screening and confirmation of extended-spectrum beta-lactamase (ESBL)-producing *Salmonella* spp., including detection of AmpC. However, not all countries have implemented this algorithm, or they modified it and hence cannot report the results to The European Surveillance System (TESSy) at ECDC in the current set-up (instead, data were collected via mail). This issue will be addressed in 2017.

Since the majority of laboratories use disk diffusion for AST, ECDC collaborates with EUCAST to establish inhibition zone diameter ECOFFs for *C. jejuni*, *C. coli* and *Salmonella* spp., where missing (Matuschek et al., 2015).

External quality assurance to support laboratories in implementing the recommended test methods and antimicrobials and obtaining high-quality AST results is provided by Statens Serum Institute in Denmark through a contract with ECDC.

1.3. The 2015 EU summary report on AMR

The majority of the data reported to EFSA by MSs comprises data collected in accordance with Commission implementing Decision 2013/652/EU. The antimicrobial susceptibility data reported to EFSA for 2015 for *Campylobacter*, *Salmonella*, indicator *E. coli* isolates from animals and food were analysed and all quantitative data were interpreted using ECOFFs. This report also includes results of phenotypic monitoring of resistance to third-generation cephalosporins caused by ESBLs and AmpC beta-lactamases in *Salmonella* and indicator *E. coli*, as well as the investigation at the EU level of the occurrence of complete susceptibility and MDR in data reported at the isolate level. A list of the antimicrobials included in this evaluation of MDR can be found in Section 2, 'Materials and methods'.

The report also includes resistance in *Salmonella* and *Campylobacter* isolates from human cases of salmonellosis and campylobacteriosis, respectively. These data were reported by MSs to TESSy either as quantitative or categorical/qualitative data. The quantitative data were interpreted using EUCAST ECOFFs, where available. The qualitative data had been interpreted using CBPs to guide medical treatment of the patient. The breakpoints for 'clinical' resistance are, in many cases, less sensitive than the ECOFF for a specific bacterium–drug combination resulting in higher levels of 'microbiological' resistance than 'clinical' resistance. By combining the categories of 'clinically' resistant and intermediate resistant into a non-susceptible category, however, close correspondence with the ECOFF was achieved.

CBPs enable clinicians to choose the appropriate treatment based on information relevant to the individual patient. ECOFFs recognise that epidemiologists need to be aware of small changes in bacterial susceptibility, which may indicate emerging resistance and allow for appropriate control measures to be considered. ECOFFs, CBPs and related concepts regarding antimicrobial resistance/susceptibility are presented in detail hereafter.

2. Materials and methods

2.1. Antimicrobial susceptibility data from humans available in 2015

About 60% of the reporting countries submitted isolate-based measured values (quantitative AST data) to ECDC for 2015, which is a substantial increase from 30% of the countries reporting measured values for 2013 when isolate-based reporting was introduced. The remaining countries submitted interpreted categorical (qualitative) AST data. As the data collected by EFSA are also quantitative, moving towards quantitative data from human isolates improves comparability between the two sectors, as the same interpretive criteria can be applied to the two data sets.

As in the two previous reports, the categories of 'clinically' intermediate and 'clinically' resistant in the interpreted data were combined in a 'non-susceptible' group. Alignment of the susceptible category with the 'wild type' category based on ECOFFs and of the non-susceptible category with the ECOFF-based 'non-wild type' category provides better comparability and more straightforward interpretation of the data for most antimicrobial agents included (Figures 9 and 40).

2.1.1. *Salmonella* data of human origin

Twenty-two MSs, Iceland and Norway provided data for 2015 on human *Salmonella* isolates. Fourteen countries (Austria, Cyprus, Denmark, Estonia, Finland, France, Greece, Ireland, Italy, Luxembourg, the Netherlands, Norway, Portugal and Romania) reported isolate-based AST results as measured values (inhibition zone diameters or MICs) which was two countries more than for 2014. Ten countries reported case-based AST results interpreted as susceptible (S), intermediate (I) or resistant (R) according to the CBPs applied (Table 4).

In 2013, the national public health laboratories within the FWD network agreed on a panel of priority antimicrobials and optional antimicrobials to test for and report to ECDC (ECDC, 2014). Two antimicrobials – ceftazidime and meropenem – were new in the priority panel compared to earlier recommendations. Whereas only a few laboratories had started to test for susceptibility to these substances in 2013, all but two MSs reported results on meropenem for 2015 and all but three for ceftazidime.

Due to the problems in detecting low-level fluoroquinolone resistance in *Salmonella* spp. using disk diffusion, nalidixic acid was for long used as a marker for fluoroquinolone resistance. After the discovery that plasmid-mediated fluoroquinolone resistance is often not detected using nalidixic acid, EUCAST studied alternative disks and concluded that pefloxacin was an excellent surrogate marker (except for isolates having the *aac(6′)-Ib-cr* gene as the only resistance determinant) (Skov et al., 2015). Since 2014, EUCAST recommend this agent for screening of low-level fluoroquinolone resistance in *Salmonella* with disk diffusion (EUCAST, 2014) and since June 2016, this is also reflected in the EU protocol. Nine of 15 MSs using disk diffusion had replaced the ciprofloxacin testing with pefloxacin in 2015. For three MSs, the information was missing.

Some of the optional antimicrobials – azithromycin, colistin and tigecycline – are included in the report, where available, to enable comparison with the data reported from food and animals. Most countries also reported the combination drug co-trimoxazole (sulfamethoxazole and trimethoprim) in addition to or instead of testing the substances separately, partly because this combination is used for clinical treatment and partly because no EUCAST interpretive criterion exists for sulfamethoxazole for *Salmonella*.

Information on the methods and guidelines used for testing and interpretation in 2015 were provided by the public health reference laboratories. Eight MSs, Iceland and Norway used only disk diffusion methods (DDs) for their AST, seven MSs used dilution methods (DLs) and another seven MSs used a combination of the two, mostly disk diffusion and gradient strip, depending on the situation and the antimicrobial (Table 4). With the exception of Germany, the data from all countries were interpreted applying criteria from EUCAST in 2015, where available. For two countries, either no update on the criteria had been provided in the last years or the data came from primary laboratories using different methods and criteria. For countries reporting quantitative measured values, all isolates had been tested at a central laboratory.

As resistance levels differ substantially between *Salmonella* serovars, results are presented separately for selected serovars of importance, particularly those found in pigs and cattle due to the focus of the 2015 report. The serovars presented in the report are *S.* Typhimurium, monophasic *S.* Typhimurium and *S.* Derby while data on additional serovars among the ten most common in human cases in 2015 are available in appendices (*S.* Enteritidis, *S.* Infantis, *S.* Kentucky, *S.* Newport, *S.* Paratyphi B var. L+ tartrate+ (var. Java), *S.* Stanley and *S.* Virchow). The proportion of resistant isolates is only shown when at least 10 isolates were tested in that MS.

In order to better assess the impact from food consumed within each reporting country on the AMR levels found in human *Salmonella* isolates, the analysis focused on domestically acquired cases. However, as several countries had not provided any information on travel (or non-travel) of their cases, cases with unknown travel status were also included in addition to domestically acquired cases. The proportions of travel-associated, domestic and unknown cases among the tested *Salmonella* isolates are presented in Table SALMTRAVHUM.

Temporal trend graphs were presented by country for *S.* Typhimurium and monophasic *S.* Typhimurium showing the resistance to ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime, ampicillin and tetracycline from 2013 to 2015 (the years following the agreement on harmonised testing and reporting by public health reference laboratories), by plotting the level of resistance for each year. The statistical significance of temporal trends was assessed with logistic regression in Stata 14.2 for countries providing data for all 3 years. A p-value of < 0.05 was considered to be significant.

The proportions of human isolates resistant to (fluoro)quinolones (ciprofloxacin, pefloxacin or nalidixic acid) or to cefotaxime were also presented in maps to provide an overview of the spatial distribution of resistance. Data were only shown for countries reporting at least 10 isolates.

Multidrug resistance (MDR) of human *Salmonella* spp. to nine antimicrobial classes was analysed, harmonised between ECDC and EFSA for better comparison between the two sectors. Multidrug resistance of an isolate was defined as resistance or non-susceptibility to at least three different antimicrobial classes (Magiorakos et al., 2012). The antimicrobials included were ampicillin, cefotaxime/ceftazidime, chloramphenicol, ciprofloxacin/pefloxacin/nalidixic acid, gentamicin, meropenem, sulfonamides/sulfame-thoxazole, tetracyclines and trimethoprim/sulfamethoxazole (co-trimoxazole). Resistance to nalidixic acid, ciprofloxacin and pefloxacin were addressed together, as they belong to the same class of antimicrobials: quinolones. Isolates that were resistant or non-susceptible to any of these antimicrobials were classified as resistant or non-susceptible to the class of quinolones. The same method was applied to the two-third-generation cephalosporins cefotaxime and ceftazidime. Trimethoprim and co-trimoxazole were also addressed together since a few countries had only tested for susceptibility to the combination. This approach was considered appropriate because among the eight countries that provided data on both trimethoprim alone and the combination co-trimoxazole, the proportion of resistant or non-susceptibles corresponded closely between the two. Co-resistance to ciprofloxacin and cefotaxime was also analysed as these two antimicrobials are considered the most important for treatment of severe salmonellosis (ECDC et al., 2009). Both 'microbiological' co-resistance (using EUCAST ECOFFs) and 'clinical' co-resistance (using EUCAST CBPs) were determined.

EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2015

Table 4: Antimicrobials reported, methods used, type of data reported and interpretive criteria applied by MSs for human *Salmonella* AST data in 2015

Country	Ampicillin	Azithromycin	Cefotaxime	Ceftazidime	Chloramphenicol	Ciprofloxacin/pefloxacin	Colistin	Gentamicin	Meropenem	Nalidixic acid	Sulfonamides	Tetracyclines	Tigecycline	Trimethoprim	Trimethoprim-sulfa	Method used	Quantitative (Q) or categorical (SIR)	Interpretive criteria
Austria	●		●	●	●	●(a)		●	●	●	●	●	●	●		DD	Q	Interpreted by ECDC. EUCAST ECOFFs 2015 for all except CLSI CBP 2015 for SUL
Cyprus	●	●	●	●			●	●	●			●	●			DL	Q	Interpreted by ECDC, as for Austria, except for CTX and MEM where EUCAST CBP were used
Denmark	●	●	●	●	●	●	●	●	●	●	●	●	●	●		DL	Q	Interpreted by ECDC, as for Austria. EFSA criteria for AZM MIC
Estonia	●		●	●	●	●	●	●	●	●	●	●		●		DL	Q	Interpreted by ECDC, as for Austria
Finland	●		●	●	●	●(a)	●	●	●	●		●		●		DD	Q	Interpreted by ECDC, as for Austria
France	●	●	●	●	●	●(a)	●	●	●	●	●	●	●	●	●	DD/DLG	Q	Interpreted by ECDC, as for Austria, except for MEM where EUCAST CBP were used
Germany	●		●	●	●	●		●	●	●		●			●	DL	SIR	German DIN standard CBP. Only R included for GEN & TET to align with ECOFF
Greece	●		●	●	●	●		●	●	●	●	●		●		DD	Q	Interpreted by ECDC, as for Austria
Hungary	●		●	●	●	●(a)		●	●	●	●	●		●	●	DD	SIR	EUCAST CBP 2015 except CLSI CBP 2015 for NAL, SUL and TET
Iceland	●		●	●		●(a)			●						●	DD	SIR	EUCAST CBP 2015
Ireland	●	●	●	●	●	●		●	●	●	●	●	●	●		DL	Q	Interpreted by ECDC, as for Austria. EFSA criteria for AZM MIC
Italy	●		●	●	●	●(a)		●	●	●	●	●		●	●	DD	Q	Interpreted by ECDC, as for Austria
Latvia	●	●	●	●	●	●		●	●	●	●	●		●	●	DD	SIR	No information on guideline. Earlier used CLSI
Lithuania	●		●	●	●	●(a)		●	●	●	●	●		●	●	DL/DD	SIR	EUCAST CBP 2015
Luxembourg	●		●	●	●	●(a)		●	●	●	●	●		●	●	DD/DLG	Q	Interpreted by ECDC, as for Austria
Malta	●					●	●	●(b)							●	DL	SIR	No update provided. Earlier Biomerieux Vitek II system; follows EUCAST CBP 2014
Netherlands	●	●	●	●	●	●	●	●	●	●	●	●	●	●		DL	Q	Interpreted by ECDC, as for Austria. EFSA criteria for AZM MIC
Norway	●	●	●	●	●	●		●	●	●		●			●	DD	Q	Interpreted by ECDC, as for Austria

Country	Ampicillin	Azithromycin	Cefotaxime	Ceftazidime	Chloramphenicol	Ciprofloxacin/ pefloxacin	Colistin	Gentamicin	Meropenem	Nalidixic acid	Sulfonamides	Tetracyclines	Tigecycline	Trimethoprim	Trimethoprim - sulfa	Method used	Quantitative (Q) or categorical (SIR)	Interpretive criteria
Portugal	●		●	●	●	●(a)		●	●	●	●	●		●		DD	Q	Interpreted by ECDC, as for Austria
Romania	●		●	●	●	●		●	●	●	●	●		●	●	DD/DLG	Q	Interpreted by ECDC, as for Austria
Slovakia	●		●	●	●	●		●(b)	●			●			●	DD/DL	SIR	No update provided. In 2013, EUCAST CBP 2013 except CLSI CBP 2013 for NAL, SUL and TET
Slovenia	●		●	●	●	●(a)		●	●		●	●		●	●	DD/DLG	SIR	EUCAST CBP 2015 except CLSI CBP 2015 for SMX and TET
Spain	●		●	●	●	●		●	●	●	●	●		●		DD	SIR	EUCAST CBP 2015 except CLSI CBP 2013 for NAL, SUL and TET
United Kingdom	●		●	●	●	●		●	●	●	●	●		●	●	DD/DL/DLG	SIR	Varies depending on clinical microbiology laboratory

MSs: Member States; AST: antimicrobial susceptibility testing; DD: disk diffusion; DL: dilution; DLG: dilution with gradient strip; Q: quantitative data; SIR: susceptible, intermediate, resistant (categorical data);
ECDC: European Centre for Disease Prevention and Control; EUCAST: European Committee on Antimicrobial Susceptibility Testing; ECOFF: epidemiological cut-off; CLSI: Clinical and Laboratory Standards Institute;
CBP: clinical breakpoint; AZM: azithromycin; CTX: cefotaxime; GEN: gentamicin; MEM: meropenem; NAL: nalidixic acid; SUL: sulfonamides; TET: tetracycline.
(a): Pefloxacin.
(b): All gentamicin results for *Salmonella* automatically reported as resistant and therefore excluded.
●: Antimicrobials tested.

2.1.2. *Campylobacter* data of human origin

Seventeen MSs, Iceland and Norway provided data on human *Campylobacter* isolates for 2015. Twelve countries (Austria, Cyprus, Denmark, Estonia, Finland, Italy, Luxembourg, Norway, Portugal, Romania, Slovenia and Spain) reported quantitative isolate-based AST results as measured values of either inhibition zone diameters or MICs (Table 5). Seven countries reported case-based or isolate-based AST results interpreted as susceptible (S), intermediate (I) or resistant (R) according to the CBPs applied.

The antimicrobials included in the 2015 report followed the panel of antimicrobials from the EU protocol for harmonised monitoring of AMR in human *Salmonella* and *Campylobacter* isolates (ECDC, 2014). The priority panel for *Campylobacter* includes ciprofloxacin, erythromycin and tetracyclines. Gentamicin and co-amoxiclav (amoxicillin and clavulanic acid) were included from the list of optional antimicrobials. From June 2016, gentamicin is in the priority panel since ECOFFs are now available and is recommended for screening of invasive isolates (ECDC, 2016).

Information on the methods and guidelines used for testing and interpretation in 2015 were provided by the public health reference laboratories. Eight MSs used only disk diffusion methods for their AST, four MSs and Norway used dilution methods and five MSs and Iceland used a combination of the two, mostly disk diffusion and gradient strip, depending on the situation and the antimicrobial (Table 5). All countries providing data from the national public health reference laboratory were using EUCAST guidelines and interpretive criteria in their routine monitoring. Criteria from the French Society for Microbiology (CA-SFM) were also used when EUCAST was lacking interpretive criteria. Three countries received the data from primary laboratories and could therefore not tell which criteria that had been used to interpret the data. With the exception of Finland, all data provided as quantitative measured values were from antimicrobial susceptibility testing performed at a central laboratory.

Table 5: Antimicrobials reported, method used, type of data reported and interpretive criteria applied by MSs for human *Campylobacter* AST data in 2015

Country	Ciprofloxacin	Co-amoxiclav	Erythromycin	Gentamicin	Tetracyclines	Method used	Quantitative (Q) or categorical (SIR)	Interpretive criteria
Austria	●		●	●	●	DL	Q	Interpreted by ECDC. EUCAST ECOFF (CIP, ERY, GEN, TET), CA-SFM CBP 2015 (AMC)
Cyprus	●		●		●	DD	Q	Interpreted by ECDC, as for Austria
Denmark	●		●	●	●	DL	Q	Interpreted by ECDC, as for Austria
Estonia	●		●		●	DD	Q	Interpreted by ECDC, as for Austria
Finland	●		●		●	DD/DLG	Q	Interpreted by ECDC, as for Austria
France	●	●	●	●	●	DD	SIR	EUCAST CBP 2013 (CIP, ERY, TET), CA-SFM CBP 2015 (AMC, GEN)
Iceland	●		●			DD/DLG	SIR	EUCAST CBP 2015
Italy	●		●		●	DD	Q	Interpreted by ECDC, as for Austria
Lithuania	●		●		●	DD	SIR	EUCAST CBP 2015
Luxembourg	●	●	●		●	DD/DLG	Q	Interpreted by ECDC, as for Austria
Malta	●		●			DLG/DD/DL	SIR	EUCAST CB 2014
Netherlands	●		●		●	DD/DL	SIR	Survey in 12 clinical labs in NL in 2009 (Ned Tijdschr Med Microbiol 2009;17:nr1)
Norway	●		●	●	●	DL	Q	Interpreted by ECDC, as for Austria
Portugal	●		●	●	●	DD	Q	Interpreted by ECDC, as for Austria
Romania	●	●	●	●	●	DD	Q	Interpreted by ECDC, as for Austria
Slovakia	●	●	●	●	●	DL	SIR	In 2013, CLSI CB
Slovenia	●		●		●	DD	Q	Interpreted by ECDC, as for Austria
Spain	●	●	●	●	●	DLG	Q	Interpreted by ECDC, as for Austria

Country	Ciprofloxacin	Co-amoxiclav	Erythromycin	Gentamicin	Tetracyclines	Method used	Quantitative (Q) or categorical (SIR)	Interpretive criteria
United Kingdom	●		●		●	DD/DL/DLG	SIR	Varies depending on clinical microbiology laboratory

MSs: Member States; AST: antimicrobial susceptibility testing; DD: disk diffusion; DL: dilution; DLG: dilution with gradient strip; Q: quantitative data; SIR: susceptible, intermediate, resistant (categorical data); ECDC: European Centre for Disease Prevention and Control; EUCAST: European Committee on Antimicrobial Susceptibility Testing; CA-SFM: French Society for Microbiology; ECOFF: epidemiological cut-off; CBP: clinical breakpoint; CIP: ciprofloxacin; ERY: erythromycin; GEN: gentamicin; TET: tetracycline; AMC: amoxicillin/clavulanate.
●: Antimicrobials tested.

Resistance levels differ quite substantially between the two most important *Campylobacter* species, *C. jejuni* and *C. coli*, and data are therefore presented by species. The proportion of resistant isolates is only shown when at least 10 isolates were reported from a MS.

In order to better assess the impact from food consumed within each reporting country on the antimicrobial resistance levels found in human *Campylobacter* isolates, the analysis focused on domestically acquired cases. However, as several countries had not provided any information on travel (or non-travel) of their cases, cases with unknown travel status were included in the analysis. The proportions of travel-associated, domestic and unknown cases among the tested *Campylobacter* isolates are presented in Table CAMPTRAVHUM.

Temporal trend graphs were presented by country showing the resistance in *C. jejuni* and *C. coli* to ciprofloxacin/pefloxacin/nalidixic acid, erythromycin and tetracycline from 2013 to 2015 (the years following the agreement on harmonised testing and reporting by public health reference laboratories), by plotting the level of resistance for each year. The statistical significance of temporal trends was assessed with logistic regression in Stata 14.2 for countries providing data for all 3 years in the period. A p-value of < 0.05 was considered to be significant.

The proportions of human isolates resistant to ciprofloxacin or to erythromycin were also presented in maps to provide an overview of the spatial distribution of resistance. Data were only shown for countries reporting at least 10 isolates.

Multidrug resistance of a *C. jejuni* or *C. coli* isolate was defined as resistance or non-susceptibility to at least three different antimicrobial classes (Magiorakos et al., 2012). The antimicrobials in the MDR analysis were harmonised between EFSA and ECDC and included ciprofloxacin, erythromycin, gentamicin and tetracyclines. Co-resistance to ciprofloxacin and erythromycin was also analysed, as these two antimicrobials are considered the most important for treatment of severe campylobacteriosis (ECDC et al., 2009). Both 'microbiological' co-resistance (using EUCAST ECOFFs) and 'clinical' co-resistance (using EUCAST CBPs) were determined.

2.2. Antimicrobial susceptibility data from animals and food in 2015

2.2.1. Data reported under Directive 2003/99/EC and Decision 2013/652/EU

For 2015, MSs reported mandatory data collected from AMR routine monitoring for *Salmonella* spp. and commensal *E. coli*, as well as from the *E. coli* specific ESBL-/AmpC-/Carbapenemase-producing monitoring, according to Decision 2013/652/EU.

For the AMR routine monitoring of *Salmonella* isolates, 17 MSs and one non-MS reported data on AMR in meat from pigs and 7 MSs reported data on meat from bovine animals, six MSs reported data on fattening pigs and three in calves under one year of age. For the AMR routine monitoring of commensal *E. coli* isolates, 27 MSs and two non-MSs reported data from fattening pigs and 10 MSs and two non-MSs reported AMR data from calves under one year of age. Data from AMR isolates for *Salmonella* and *E. coli* from different poultry populations were reported on a voluntary basis.

For the specific monitoring of *E. coli* ESBL-/AmpC-/carbapenemase-producers, 22 MSs and two non-MSs reported AMR data from fresh pig meat and 21 MSs and two non-MSs reported AMR data from fresh bovine meat at retail. AMR data on the specific monitoring of *E. coli* ESBL-/AmpC-/ carbapenemase-producers was reported from fattening pigs by 25 MSs and two non-MSs and from calves under one year of age by 10 MSs and two non-MSs.

Isolates were sampled through harmonised national schemes. Microbroth dilution testing methods were used for susceptibility testing, and quantitative[8] isolate-based data were reported to EFSA and considered for the purpose of this report. Resistance was interpreted using EUCAST ECOFF values (see following text box for further information). The antimicrobials incorporated in this summary analysis were selected based on their public health relevance and as representatives of different antimicrobial classes.

Data on *C. coli* in fattening pigs and data on meticillin-resistant *Staphylococcus aureus* (MRSA) and on specific monitoring of carbapenemase-producing microorganisms were reported on a voluntary basis.

2.2.1.1. Harmonised representative sampling and monitoring

Representative sampling should be performed according to general provisions of the legislation and to detailed technical specifications issued by EFSA (EFSA, 2014).

Salmonella

In 2015, representative *Salmonella* isolates for monitoring AMR were collected by MSs from carcases of fattening pigs sampled for testing and verification of compliance, in accordance with point 2.1.4 of Chapter 2 of Annex I to Regulation (EC) No 2073/2005; as well as carcases of bovines under one year of age where the production of meat of those bovines in the MSs is more than 10,000 tonnes slaughtered per year sampled for testing and verification of compliance, in accordance with point 2.1.3 of Chapter 2 of Annex I to Regulation (EC) No 2073/2005. MSs sampled carcases of fattening pigs/carcases of bovines under one year of age of healthy slaughter at the slaughterhouse. A two-stage stratified sampling design, with slaughterhouses as primary sampling units and carcases as secondary units, with proportional allocation of the number of samples to the annual throughput of the slaughterhouse, was applied in the reporting countries.

Not more than one isolate per *Salmonella* serovar from the same epidemiological unit (herd/holding) per year should be included in the AMR monitoring. In most MSs, the isolates tested for antimicrobial susceptibility constituted a representative subsample of the total *Salmonella* isolates available at the National Reference Laboratory (NRL) and/or other laboratories involved, obtained in a way that ensured geographical representativeness and even distribution over the year. Conversely, in the case of low prevalence, all the *Salmonella* isolates available should be tested for susceptibility.

Caecal samples gathered at slaughter from fattening pigs and calves under one year of age and faeces gathered at farm from fattening pigs were collected on a voluntary basis. Only one representative caecal sample (single or pooled) per epidemiological unit (batch of carcases deriving from the same herd), was gathered to account for clustering.

Routine monitoring of indicator E. coli

MSs collected indicator *E. coli* isolates as part of their national monitoring programme of AMR according to the provisions of the Decision 2013/652/EU, based on random sampling of caecal samples gathered at slaughter from fattening pigs and calves under one year of age where the production of meat of those bovines in the MSs is more than 10,000 tonnes slaughtered per year. Only one representative caecal sample (single or pooled) per epidemiological unit (batch of carcases deriving from the same herd), was gathered to account for clustering. Isolates were recovered from caecal contents samples (single or pooled), in accordance with EFSA's recommendations (EFSA, 2014). MSs shall test 170 isolates for antimicrobial susceptibility testing for each of animal population listed above. However, in MSs with a production of less than 100,000 tonnes of pig meat slaughtered per year they shall test 85 isolates instead of 170 isolates. The sample collection was approximately evenly distributed over the year 2015.

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

Caecal samples gathered at slaughter from fattening pigs and bovines under one year of age where the production of meat of those bovines in the MSs is more than 10,000 tonnes slaughtered per year and samples of fresh pig meat and bovine meat gathered at retail were collected. Only one representative caecal sample (single or pooled) per epidemiological unit (batch of carcases deriving from the same herd), was gathered to account for clustering. Isolates were recovered from caecal contents samples (single or pooled), in accordance with EFSA's recommendations (EFSA, 2014). MSs shall analyse 300 samples of each of the animal population and food category, listed in above. However, in MSs with a production of less than 100,000 tonnes of pig meat slaughtered per year and

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[8] 'Quantitative data' derived from dilution methods consisted of the number of isolates having a specific MIC value (measured in mg/L) relative to the total number of isolates tested, for each antimicrobial agent and specific food/animal category.

less than 50,000 tonnes bovine meat slaughtered per year, the MS shall analyse 150 samples instead of 300 samples for each corresponding specific combination. The sample collection was approximately evenly distributed over the year 2015.

Epidemiological cut-off values (ECOFFs) and clinical breakpoints (CBPs)

A microorganism is defined as 'clinically' resistant when the degree of resistance shown is associated with a high likelihood of therapeutic failure. The microorganism is categorised as resistant by applying the appropriate CBP in a defined phenotypic test system, and this breakpoint may alter with legitimate changes in circumstances (for example alterations in dosing regimen, drug formulation, patient factors). A microorganism is defined as wild type for a bacterial species when no acquired or mutational resistance mechanisms are present to the antimicrobial in question. A microorganism is categorised as wild type for a given bacterial species presenting a lower MIC to the antimicrobial in question than the appropriate ECOFF in a defined phenotypic test system. This cut-off value will not be altered by changing circumstances (such as alterations in frequency of antimicrobial administration). Wild-type microorganisms may or may not respond clinically to antimicrobial treatment. A microorganism is defined as non-wild type for a given bacterial species by the presence of an acquired or mutational resistance mechanism to the antimicrobial in question. A microorganism is categorised as non-wild type for a given bacterial species by applying the appropriate ECOFF value in a defined phenotypic test system; non-wild-type organisms are considered to show 'microbiological' resistance (as opposed to 'clinical' resistance). CBPs and ECOFFs may be the same, although it is often the case that the ECOFF is lower than the CBP. EUCAST has defined CBPs and ECOFFs.

Clinical breakpoints (clinical resistance)

The clinician, or veterinarian, choosing an antimicrobial agent to treat humans or animals with a bacterial infection requires information that the antimicrobial selected is effective against the bacterial pathogen. Such information will be used, together with clinical details such as the site of infection, ability of the antimicrobial to reach the site of infection, formulations available and dosage regimes, when determining an appropriate therapeutic course of action. The *in vitro* susceptibility of the bacterial pathogen can be determined and CBPs used to ascertain whether the organism is likely to respond to treatment. CBPs will take into account the distribution of the drug in the tissues of the body following administration and assume that a clinical response will be obtained if the drug is given as recommended and there are no other adverse factors which affect the outcome. Conversely, if the CBP indicates resistance, then it is likely that treatment will be unsuccessful. Frequency of dosing is one factor that can affect the antimicrobial concentration achieved at the site of infection. Therefore, different dosing regimens can lead to the development of different CBPs, as occurs in some countries for certain antimicrobials where different therapeutic regimes are in place. Although the rationale for the selection of different CBPs may be clear, their use makes the interpretation of results from different countries in reports of this type problematic, as the results are not directly comparable between those different countries.

Epidemiological cut-off values (microbiological resistance)

For a given bacterial species, the pattern of the MIC distribution (i.e. the frequency of occurrence of each given MIC plotted against the MIC value) can enable the separation of the wild-type population of microorganisms from those populations which show a degree of acquired resistance. The wild-type susceptible population is assumed to have no acquired or mutational resistance and commonly shows a normal distribution. When bacteria acquire resistance by a clearly defined and efficacious mechanism, such as the acquisition of a plasmid bearing a gene which produces an enzyme capable of destroying the antimicrobial, then the MIC commonly shows two major subpopulations, one a fully susceptible normal distribution of isolates and the other a fully resistant population which has acquired the resistance mechanism. Resistance may be achieved by a series of small steps, such as changes in the permeability of the bacterial cell wall to the antimicrobial or other mechanisms which confer a degree of resistance. In this case, there may be populations of organisms which occur lying between the fully susceptible population and more resistant populations. The epidemiological cut-off (ECOFF) value indicates the MIC or zone diameter above which the pathogen has some detectable reduction in susceptibility. ECOFFs are derived by testing an adequate number of isolates to ensure that the wild-type population can be confidently identified for a given antimicrobial. The clinical breakpoint, which is set to determine the therapeutic effectiveness of the antimicrobial, may fail to detect emergent resistance. Conversely, the ECOFF detects any deviation in susceptibility from the wild-type population, although it may not be appropriate for determining the likelihood of success or failure for clinical treatment.

Campylobacter coli

Caecal samples gathered at slaughter from fattening pigs were collected on a voluntary basis. Only one representative caecal sample (single or pooled) per epidemiological unit (batch of carcases deriving from the same herd), was gathered to account for clustering. Isolates were recovered from caecal contents samples (single or pooled), in accordance with EFSA's recommendations (EFSA, 2014). The sample collection was approximately evenly distributed over the year 2015.

MRSA

Isolates may have been collected by different monitoring approaches, either by active monitoring of animals and foods or, in some cases, by passive monitoring based on diagnostic submission of samples from clinical cases of disease in animals, or from foods sampled as part of investigatory work.

2.2.1.2. Harmonised antimicrobial susceptibility testing

Routine monitoring antimicrobial susceptibility

MSs tested antimicrobials and interpreted the results using the epidemiological cut-off values and concentration ranges shown in Tables 6 and 7 to determine the susceptibility of *Salmonella* spp., *C. coli* and indicator commensal *E. coli*. All *E. coli* isolates, randomly selected isolates of *Salmonella* spp. and *E. coli* that, after testing with the first panel of antimicrobials in accordance with Table 6 were found to be resistant to cefotaxime, ceftazidime or meropenem, were further tested with a second panel of antimicrobial substances as shown in Table 8. This panel notably includes cefoxitin, cefepime and clavulanate in combination with cefotaxime and ceftazidime for the detection of presumptive ESBL- and AmpC-producers, as well as imipenem, meropenem and ertapenem to phenotypically identify presumptive carbapenemase-producers.

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

For the specific monitoring of ESBL-/AmpC-/carbapenemase-producing *E. coli*, the isolation method started with a non-selective pre-enrichment step, followed by inoculation on McConkey agar containing a third-generation cephalosporin in a selective concentration (cefotaxime 1 mg/L), in accordance with the most recent version of the detailed protocol for standardisation of the EURL-AR.[9] Using this protocol, also carbapenemase-producing isolates can also be recovered.

If available, one presumptive ESBL-/AmpC-/carbapenemase-producing *E. coli* isolate obtained from each positive caecal sample and meat sample was tested for its antimicrobial susceptibility to the first panel of antimicrobials (Table 6) to confirm the microbiological resistance to cefotaxime (expected as the antimicrobial is present in the isolation medium at a concentration higher than the ECOFF), and identify possible resistance to ceftazidime and/or ceftzidime and/or meropenem. In a second step, the isolate should be tested using the second panel of antimicrobials (Table 8) to infer the presumptive ESBL-/AmpC-/carbapenemase-producing phenotype according to the beta-lactam resistance phenotype obtained (Figure 8).

Specific monitoring of carbapenemase-producing microorganism

This monitoring programme was performed and reported on a voluntary basis. For the specific monitoring of carbapenemase-producing microorganisms, isolation required the use of non-selective pre-enrichment and subsequent selective plating on carbapenem-containing media, in accordance with the most recent version of the detailed protocol of the EURL-AR.[9] The microbial species was identified using an appropriate method.

If available, one presumptive carbapenemase-producing isolate (primarily *E. coli,* but also *Salmonella*) obtained from each positive caecal sample and meat sample was tested for its antimicrobial susceptibility to the first panel of antimicrobials (Table 6) to confirm the microbiological resistance to meropenem, and identify possible resistance to cefotaxime and/or ceftzidime. In a second step, the isolate should be tested using the second panel of second panel of antimicrobials (Table 8) to infer the presumptive carbapenemase-producer phenotype according to the beta-lactam resistance phenotype obtained (Figure 8).

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[9] Available online: www.crl-ar.eu

The EUCAST epidemiological cut-off values applied for the antimicrobial susceptibility testing (Tables 3–5) are the ones available during the drafting of the Decision 2013/652/EU (2013). For some antimicrobials these values have been updated by EUCAST (www.eucast.org, last accessed 28.11.16). Currently, for *Salmonella*, there is no ECOFF available for colistin, and for tigecycline the ECOFF of 1 mg/L, is based on the one for *S.* Typhimurium, *S.* Typhi and *S.* Paratyphi, whereas for *S.* Enteritidis is 2 mg/L. For *E. coli*, the current tigecycline ECOFF is 0.5 mg/L. To allow comparison with the data collected in the previous years, the ECOFFs laid down in the Legislation are considered.

Table 6: Panel of antimicrobial substances included in AMR monitoring, EUCAST ECOFFs and concentration ranges tested in *Salmonella* spp. and indicator commensal *E. coli* (first panel) as laid down in Decision 2013/652/EU

Antimicrobial	*Salmonella* EUCAST ECOFF[a]	*E. coli* EUCAST ECOFF[a]	Concentration range, mg/L (no of wells)
Ampicillin	> 8	> 8	1–64 (7)
Cefotaxime	> 0.5	> 0.25	0.25–4 (5)
Ceftazidime	> 2	> 0.5	0.5–8 (5)
Meropenem	> 0.125	> 0.125	0.03–16 (10)
Nalidixic acid	> 16	> 16	4–128 (6)
Ciprofloxacin	> 0.064	> 0.064	0.015–8 (10)
Tetracycline	> 8	> 8	2–64 (6)
Colistin	> 2	> 2	1–16 (5)
Gentamicin	> 2	> 2	0.5–32 (7)
Trimethoprim	> 2	> 2	0.25–32 (8)
Sulfamethoxazole	NA[b]	> 64	8–1,024 (8)
Chloramphenicol	> 16	> 16	8–128 (5)
Azithromycin	NA[c]	NA[c]	2–64 (6)
Tigecycline	> 1	> 1	0.25–8 (6)

AMR: antimicrobial resistance; EUCAST: European Committee on Antimicrobial Susceptibility Testing; ECOFFs: epidemiological cut-off values; NA: not available.
(a): EUCAST epidemiological cut-off values as laid down in Decision 2013/652/EU.
(b): > 256 mg/L was used.
(c): > 16 mg/L was used.

Table 7: Panel of antimicrobial substances included in AMR monitoring, EUCAST ECOFFs and concentration ranges tested in *C. coli*

Antimicrobial	*C. coli* EUCAST ECOFF[a]	Concentration range, mg/L (no of wells)
Erythromycin	> 8	1–128 (8)
Ciprofloxacin	> 0.5	0.12–16 (8)
Tetracycline	> 2	0.5–64 (8)
Gentamicin	> 2	0.12–16 (8)
Nalidixic acid	> 16	1–64 (7)
Streptomycin[b]	> 4	0.25–16 (7)

AMR: antimicrobial resistance; EUCAST: European Committee on Antimicrobial Susceptibility Testing; ECOFFs: epidemiological cut-off values; NA: not available.
(a): EUCAST epidemiological cut-off values.
(b): On a voluntary basis.

Table 8: Panel of antimicrobial substances, EUCAST ECOFFs and concentration ranges used for testing only *Salmonella* spp. and indicator commensal *E. coli* isolates resistant to cefotaxime, ceftazidime or meropenem (second panel)

Antimicrobial	*Salmonella* EUCAST ECOFF[a]	*E. coli* EUCAST ECOFF[a]	Concentration range, mg/L (no of wells)
Cefoxitin	> 8	> 8	0.5–64 (8)
Cefepime	NA[b]	> 0.125	0.06–32 (10)
Cefotaxime + clavulanic acid	NA	NA	0.06–64 (11)
Ceftazidime + clavulanic acid	NA	NA	0.125–128 (11)
Meropenem	> 0.125	> 0.125	0.03–16 (10)
Temocillin	NA[c]	NA[c]	0.5–64 (8)
Imipenem	> 1	> 0.5	0.12–16 (8)
Ertapenem	> 0.06	> 0.06	0.015–2 (8)
Cefotaxime	> 0.5	> 0.25	0.25–64 (9)
Ceftazidime	> 2	> 0.5	0.25–128 (10)

EUCAST: European Committee on Antimicrobial Susceptibility Testing; ECOFFs: epidemiological cut-off values; NA: not available.
(a): EUCAST epidemiological cut-off values as laid down in the Decision 2013/652/EU. For some antimicrobials these values have been updated (see below).
(b): For cefepime, the cut-off value used in the analysis for *Salmonella* was > 0.125 mg/L.
(c): For temocillin, the cut-off value used in the analysis was > 32 mg/L.

2.2.2. Data validation

2.2.2.1. Validation against business rules

The reported data were first checked for usability against a series of 'business rules' which were automatically applied in the EFSA data collection system once a file was transmitted. This automatic data validation process refers to the first validation of incoming data. Quality checks are related to a specific business only. The positive result of the automatic validation process places the file in a valid state and makes it available for further steps of validation performed by EFSA.

2.2.2.2. Scientific data validation

The scientific validation of the data collected by the MSs/non-MSs and submitted to EFSA consisted on the revision of data and comparison between data reported for the same antimicrobials when tested by different panels. Special attention was given to new antimicrobials included for the first time in the panels (i.e. carbapenems, azithromycin, tigecycline, colistin, cefepime) and to possible discrepancies between results for antimicrobials present in both panels (i.e. cefotaxime, ceftazidime, meropenem).

Reference testing:

To ensure the quality of data submitted, a reference testing exercise was run by the EURL-AR in close collaboration with the MSs. The exercise consisted in retesting the AST of the isolates received using both Panel 1 and Panel 2 of antimicrobials, as well as whole genome sequencing (WGS) analyses of the isolates (WGS analyses still on-going by the time of drafting the present report). Based on the data submitted to EFSA, a selection of 200 isolates was done. The selection of these isolates was based on different criteria:

- The EURL-AR had reported technical issues when testing azithromycin, tigecycline and colistin during the EURL workshop hold in Lyngby (Denmark) 2016 (www.eurl-ar.eu). Resistant isolates from countries with outstanding prevalence for these antimicrobials were asked to provide selected isolates to the EURL-AR. Most of the *E. coli* isolates chosen were selected among the ones reported for the specific ESBL/AmpC/carbapenemase monitoring and had been classified as ESBL/AmpC producer.
- There was a discrepancy between MIC values reported for the antimicrobials present in both panels (impacting the categorisation of the isolate as resistant or susceptible.
- If according to the criteria applied, the presence of carbapenemase-producers was suspected.
- Isolates representing the categorisations presumptive ESBLs, AmpC and ESBL-AmpC-producers.
- Isolates with odd phenotypes.

The MSs/non-MSs sent the selected isolates to the EURL-AR, where were retested. EFSA, EURL-AR and MSs liaised together to address possible discrepancies found.

2.2.3. Analyses of antimicrobial resistance data

Data are reported in separate sections dedicated to each microorganism. Clinical investigation data were not accounted for in this report.

2.2.3.1. Overview tables of the resistance data reported

Data generated from the antimicrobial susceptibility testing and reported as quantitative at the isolate level by MSs have been described in the overview tables published on the EFSA website.

2.2.3.2. Minimum inhibitory concentration distributions

For each combination of microorganism, antimicrobial and food category/animal population were tested, MIC distributions were tabulated in frequency tables, giving the number of isolates tested that have a given MIC at each test dilution (mg/L) of the antimicrobial. Isolate-based dilution results allowed MIC distributions reported:

- for *Salmonella* for ampicillin, azithromycin, cefepime, cefotaxime, cefotaxime and clavulanic acid, ceftazidime, ceftazidime and clavulanic acid, cefoxitin, chloramphenicol, ciprofloxacin, colistin, ertapenem, gentamicin, imipenem, meropenem, nalidixic acid, sulfamethoxazole, temocillin, tetracycline, tigecycline and trimethoprim.
- for *Campylobacter* for ciprofloxacin, erythromycin, gentamicin, nalidixic acid, streptomycin and tetracycline.
- for indicator *E. coli* for ampicillin, azithromycin, cefepime, cefotaxime, cefotaxime and clavulanic acid, ceftazidime, ceftazidime and clavulanic acid, cefoxitin, chloramphenicol, ciprofloxacin, colistin, ertapenem, gentamicin, imipenem, meropenem, nalidixic acid, sulfamethoxazole, temocillin, tetracycline, tigecycline and trimethoprim.
- for MRSA for cefoxitin, chloramphenicol, ciprofloxacin, clindamycin, erythromycin, fusidic acid, gentamicin, kanamycin, linezolid, mupirocin, penicillin, quinupristin/dalfopristin, rifampicin, streptomycin, sulfamethoxazole, tetracycline, tiamulin, trimethoprim and vancomycin.

2.2.3.3. Epidemiological cut-off values and the occurrence of resistance

ECOFFs, as listed in Decision 2013/652/EC, have been used in this report to interpret the isolate-based reported MIC data and determine non-wild-type organisms also termed 'microbiologically' resistant organisms (i.e. displaying a decreased susceptibility), and to ensure that results from different MSs are comparable. Hereafter in this report, 'microbiologically' antimicrobial-resistant organisms are referred to as 'resistant' for brevity. This report also incorporates re-evaluation of the historical data accounting for the revised EU legislation, which included the revised ECOFFs.

The occurrence of resistance[10] to a number of antimicrobials was determined for *Salmonella*, *Campylobacter*, indicator *E. coli* isolates from fattening pigs, calves under one year of age, and meat from pigs and bovine animals, and are tabulated at the production-type level in this report. The occurrence of resistance (i.e. resistance levels) in reporting MS groups was calculated as totals (the total number of resistant isolates out of the total number of tested isolates across reporting MSs) and not the weighted means.

2.2.3.4. Resistance in *Salmonella* serovars of public health importance

In this report, AMR in tested *Salmonella* isolates were aggregated to give a value for *Salmonella* spp. for each country and food/animal category. In addition, the most prevalent *Salmonella* serovars were also reported separately for particular food/animal category. Additional tables have been included in this report to describe the occurrence of AMR among selected *Salmonella* serovars of public health importance or of high prevalence in animals (monophasic *S.* Typhimurium, *S.* Typhimurium, *S.* Derby and *S.* Rissen). In order to present a complete overview of the animal populations and food categories in which specific *Salmonella* serovars of public health importance have been recovered, all the data reported (derived even from fewer than four reporting countries and less than 10 isolates tested) have been included.

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[10] Giving the percentage of isolates 'microbiologically' resistant out of those tested.

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Data description

Throughout the report, *level or occurrence of AMR* means the percentage of resistant isolates as a proportion of the isolates tested of that microorganism. *MSs reporting group* means the MSs that provided data and were included in the relevant table of antimicrobial resistance for that bacterium–food or animal category–antimicrobial combination. Terms used to describe the levels or occurrence of antimicrobial resistance are 'rare: < 0.1%', 'very low: 0.1–1.0%', 'low: > 1–10.0%', 'moderate: > 10.0–20.0%', 'high: > 20.0–50.0%', 'very high: > 50.0–70.0%', 'extremely high: > 70.0%'. Although these terms are applied to all antimicrobials, the significance of a given level of resistance depends on the particular antimicrobial and its importance in human and veterinary medicine.

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2.2.3.5. Temporal trends in resistance

Where the minimum criteria[11] for data inclusion in this report were met, temporal trend graphs were generated showing the resistance to different antimicrobials from 2009 to 2015, by plotting the level of resistance for each year of sampling. Graphs were created for those countries for which resistance data were available for four or more years in the 2009–2015 period for at least one of the two antimicrobials. MS-specific resistance levels trend graphs use a unique scale and countries are shown in alphabetical order. For ampicillin, cefotaxime, ciprofloxacin, nalidixic acid and tetracyclines (*Salmonella* and indicator *E. coli*), ciprofloxacin, erythromycin, nalidixic acid, streptomycin and tetracycline (*Campylobacter*), resistance trends over time were visually explored by trellis graphs, using the lattice package in the R software (R version 2.14.2 (29/2/2012)).

In order to assess the statistical significance of temporal trends, the proportions of resistance were modelled against time in a logistic regression. This analysis was carried out using the PROC LOGISTIC of SAS 9.2 for each country where there were 5 years or more of available data to use in the model. The PROC LOGISTIC function uses a logit transform to model the proportion of prevalence against year, and provides estimates for both intercepts and slope. Models where the likelihood ratio test suggested it to be meaningful and resulting in a p-value associated with slope of < 0.05 were considered to be significant.

2.2.3.6. Spatial analysis of resistance through maps

MS-specific AMR levels for selected bacterium–food category/animal population combinations were plotted in maps for 2015, using ArcGIS 9.3. In the maps, resistance levels are presented with colours reflecting the continuous scale of resistance to the antimicrobial of interest among reporting MSs; thus, there might be some apparent discrepancies between the colours and resistance levels between maps.

2.2.4. Analysis of multidrug resistance and co-resistance data

As a consequence of the availability of AMR data at the isolate level in the MSs, the analysis of MDR and co-resistance data becomes an important exercise in the light of the public health relevance of the emergence of multiresistant bacteria. The intention is to focus mainly on multi/co-resistance patterns involving critically important antimicrobials (Collignon et al., 2016; WHO, 2016) according to the bacterial species, such as cephalosporins, fluoroquinolones and macrolides, and to summarise important information in the EU Summary Report. The occurrence of the isolates of a serotype/resistance pattern of interest is studied at the MS level and at the reporting MS group/EU level, as the overall picture for all MSs might show a more definite pattern of emergence and spread. In addition, the analysis of data may reveal the existence of new or emerging patterns of MDR, particularly in *Salmonella* serotypes.

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[11] More than 10 isolates tested by a MS and more than four MSs reporting results for that antimicrobial, microorganism, food or animal category.

> **Definitions**
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> For the purpose of this analysis, **a multiresistant isolate** is one defined as resistant to at least three different antimicrobial substances, belonging to any three antimicrobial families listed in the harmonised set of antimicrobials included in the Decision 2013/652/EU. Tables 6 and 7 list those recommended antimicrobials. Resistance to nalidixic acid and resistance to ciprofloxacin, as well as the resistance to cefotaxime and to ceftazidime are, respectively, addressed together.
>
> In contrast, **a fully susceptible isolate** is one defined as non-resistant to all of the antimicrobial substances included in the harmonised set of substances for *Salmonella*, *Campylobacter* and indicator *E. coli*.
>
> The term **co-resistance** has been defined as two or more resistance genes which are genetically linked, i.e. located adjacent or close to each other on a mobile genetic element (Chapman, 2003). For brevity, the term is used slightly more loosely in this report and indicates two or more phenotypic resistances to different classes of antimicrobials, exhibited by the same bacterial isolate.

2.2.4.1. MDR patterns

The frequency and percentage of isolates exhibiting various MDR patterns considering the antimicrobials tested were determined for *Salmonella* (*Salmonella* spp., *S*. Enteritidis, *S*. Typhimurium and monophasic *S*. Typhimurium), *Campylobacter* species and indicator *E. coli* for each country and each animal population/food category. Isolates for which no susceptibility data were provided for some of the antimicrobial substances were disregarded.

2.2.4.2. Summary indicators' and 'diversity' of MDR

The objective is first to give an overview of the situation on MDR through summary indicators: (1) the proportion of fully susceptible isolates; (2) the proportion of multiresistant isolates. To illustrate the relative proportions of multiresistant isolates and the diversity of the resistance to multiple antimicrobials, graphical illustration was chosen. The percentage of isolates susceptible and resistant to one, two, three, etc., antimicrobials are shown using a composite bar graph displaying stacked bars, but only for certain combinations of bacterium–animal population or food category–MSs of particular interest.

2.2.4.3. The co-resistance patterns of interest

In *Salmonella* and *E. coli* isolates, co-resistance to cefotaxime (CTX) and ciprofloxacin (CIP) was estimated, as these two antimicrobials are of particular interest in human medicine. Co-resistance was addressed using both ECOFFs (CTX > 0.25 mg/L and CIP > 0.064 mg/L) and CBPs (CTX > 2 mg/L and CIP > 1 mg/L) for *E. coli*. In *C. jejuni* and *C. coli* isolates, co-resistance to ciprofloxacin and erythromycin (ERY) was estimated, as these two antimicrobials are of particular interest in human medicine in the treatment of severe campylobacteriosis. The interpretive ECOFFs used to address co-resistance to ciprofloxacin and erythromycin were, for *C. jejuni*, CIP > 0.5 mg/L and ERY > 4 mg/L and, for *C. coli*, CIP > 0.5 mg/L and ERY > 8 mg/L. These values may be considered as very similar to CBPs.

2.2.5. Identification of presumptive ESBL-, AmpC- and/or carbapenemase-producers

The categorisation of isolates resistant to third-generation cephalosporins and/or carbapenems in presumptive ESBL-, AmpC- or carbapenemase-producers was carried out based on the EUCAST guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance (EUCAST, 2013). In these expert guidelines, and based on other EUCAST and CLSI guidelines to detect ESBL/AmpC producers, a screening breakpoint of > 1 mg/L is recommended for cefotaxime and ceftazidime. This screening breakpoint is higher than the ECOFFs applied for antimicrobial susceptibility of both antimicrobials for *E. coli*, and to cefotaxime for *Salmonella*. For this report, a first condition for classifying isolates as putative ESBL/AmpC-producers related to their MIC for either cefotaxime or ceftazidime, was to apply this screening breakpoint of MICs greater 1 mg/L. Only isolates which presented MIC values accomplishing with this requisite (as expected for most of the ESBL/AmpC-producers) were further considered.

In total, for the 3rd generation cephalosporin- and/or carbapenem-resistant isolates, five main categorisations are made: (1) ESBL-phenotype, (2) AmpC-phenotype, (3) ESBL/AmpC-phenotype, (4) CP-phenotype and (5) other phenotypes (Figure 8).

1) To detect the production of ESBLs, a synergy test for cefotaxime and ceftazidime, in combination with clavulanic acid was performed. An eightfold reduction in the MIC for the cephalosporin combined with clavulanic acid compared with that obtained for the cephalosporin alone was interpreted as a positive synergy test. In all other cases, the synergy test was considered negative. For the present report, isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime and a synergy test positive for any of these antimicrobials, together with susceptibility to cefoxitin ($\leq$ 8 mg/L) and meropenem (MEM $\leq$ 0.12 mg/L see CP-phenotype) were classified as ESBL-phenotype (Figure 8).

2) Regarding the AmpC phenotype, the combination MIC > 8 mg/L (ECOFF) for cefoxitin together with MICs > 1 mg/L for cefotaxime and/or ceftazidime was used as phenotypic criteria to investigate the presence of AmpC production in *E. coli*. It should be also underlined that there are a few AmpC-enzymes that do not confer resistance to cefoxitin (i.e. ACC-1), and that there are other mechanisms (porin loss, presence of carbapenemases, a few ESBLs like cefotaximase (CTX-M)-5) that could generate similar MIC values for the different antimicrobials (EFSA, 2012a; EUCAST, 2013). Phenotypic AmpC confirmation tests (i.e. cloxacillin synergy) were not required for the present monitoring. For the present report, isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime and cefoxitin MIC > 8 mg/L, together with negative synergy test for both cefotaxime and ceftazidime/clavulanic acid, together with susceptibility to meropenem (MEM $\leq$ 0.12 mg/L) were classified in the AmpC phenotype category. No distinction between acquired AmpC and natural AmpC was done (Figure 8).

3) For the present report, isolates with MICs > 1 mg/L for cefotaxime and/or ceftazidime, positive synergy tests for any of these antimicrobials/clavulanic acid and cefoxitin MIC > 8 mg/L, together with susceptibility to meropenem (MEM $\leq$ 0.12 mg/L) were classified under the ESBL/AmpC-phenotype category (Figure 8).

For the occurrence and prevalence tables shown in Section 3.5, presumptive ESBL-producers were considered as those exhibiting an ESBL- and/or ESBL-/AmpC-phenotype, and presumptive AmpC-producers, those with an AmpC and AmpC-/ESBL-phenotype.

In some isolates, several mechanisms can be present at the same time, making it very difficult to differentiate the phenotypes. Also the high-level expression of AmpC β-lactamases can mask the presence of ESBLs. AmpC can also be present in isolates with positive ESBL tests (clavulanic acid synergy). In this case, the cefepime/clavulanic acid synergy test should be used to overturn/confirm the presence of ESBLs in these isolates (EUCAST, 2013), but unfortunately, the combination cefepime/clavulanic acid was not included among the substances tested for the monitoring. The inclusion of resistance to cefepime with a MIC value $\geq$ 4 mg/L, as an additional criteria proposed elsewhere (EFSA, 2012a), could be useful to ascertain the presence of an ESBL-producer.

4) For the classification of isolates into the putative carbapenem producers (CPs), a meropenem screening cut-off of > 0.12 mg/L (which coincides with the harmonised ECOFF) was chosen. It is known that other mechanisms (i.e. hyperproduction or combination of ESBLs and/or AmpC and porin loss) can also affect to the MIC values generated for the different carbapenems, especially for ertapenem. The confirmation of the carbapenemase production recommended by the EUCAST guidelines cannot be inferred from the carbapenem susceptibility testing data reported, but needs further phenotypic or molecular testing. Those MS which reported data suggesting the presence of putative CPs were recommended to validate the results by performing further confirmatory testing, and the EURL-AR offered to apply whole genome sequencing of the isolates. For the present report, isolates with MIC > 0.12 mg/L for meropenem would be considered as putative CP and were classified under the CP-phenotype. The presence of other resistance mechanisms (ESBLs, AmpC, etc.) within the isolates placed in this group cannot be ruled out.

5) In this group, phenotypes not included in the categorisations defined above were included: isolates with a MIC > 0.12 for ertapenem and/or MIC > 1 mg/L for imipenem (EUCAST screening cut-offs, one dilution step higher than the currently defined ECOFFs) but no resistance to meropenem (MIC < 12 mg/L) were classified under the category 'other phenotype'. Finally, isolates with MICs ≤ 1 mg/L for cefotaxime and ceftazidime would be considered as not ESBL- and/or AmpC-producers. This implied that some isolates considered microbiologically resistant (MICs over the ECOFFS) would not be further classified, as probably other mechanisms or technical issues in the MIC testing (i.e. MIC value close to the ECOFF) would be responsible for the MIC values obtained. For the present report, cefotaxime- and ceftazidime-resistant isolates with MICs ≤ 1 mg/L for both antimicrobials were considered as putative non ESBL-/AmpC-producers and were classified under the category 'other phenotype'.

We are aware that without a further molecular characterisation of the isolates, it will not be possible to know exactly which resistance mechanisms are present. For epidemiological purposes and based on the EUCAST guidelines, the classification of 'putative' producers for the different mechanism conferring resistance to third-generation cephalosporins and/or carbapenems was considered. Molecular characterisation of these mechanisms is recommended.

1. ESBL-Phenotype
- FOT or TAZ > 1 mg/L AND
- MERO ≤ 0.12 mg/L AND
- FOX ≤ 8 mg/L AND
- SYN FOT/CLV and/or TAZ/CLV

2. AmpC-Phenotype
- FOT or TAZ > 1 mg/L AND
- MERO ≤ 0.12 mg/L AND
- FOX > 8 mg/L AND
- No SYN FOT/CLV nor TAZ/CLV
- (Not excluded presence of ESBLs)

3. ESBL + AmpC-Phenotype
- FOT or TAZ > 1 mg/L AND
- MERO ≤ 0.12 mg/L AND
- FOX >8 mg/L AND
- SYN FOT/CLV and/or TAZ/CLV

4. Carbapenemase-Phenotype
- MERO > 0.12 mg/L
- Needs confirmation
- (Not excluded presence of ESBLs or AmpC)

Susceptible
FOT-TAZ-FOX-MEM ≤ ECOFF

5. Other phenotypes
1) If FOT or TAZ > 1 mg/ml AND
- MEM ≤ 0.12 mg/L AND
- FOX ≤ 8 mg/L AND
- NO SYN FOT/CLV nor TAZ/CLV
- Not excluded CPs (consult EURL)

2) If FOT and/or TAZ ≤ 1 mg/L AND > ECOFF AND
- MERO ≤ 0.12 mg/L
- FOX ≤ 8 mg/L

3) If FOT and TAZ ≤ 1 mg/L
- MERO ≤ 0.12 mg/L
- FOX > 8 mg/L
*cAmpCs could be included here

4) If MERO ≤ 0.12 mg/L BUT
- ETP > ECOFF AND/OR
- IMI > ECOFF
- Not excluded CPs, needs confirmation (consult EURL)

5) Any other combinations not described in previous boxes (consult EURL)

Presumptive ESBL-producers include isolates exhibiting Phenotype 1 or 3.
Presumptive AmpC-producers include isolates exhibiting Phenotype 2 or 3.

Figure 8: Phenotypes inferred based on the resistance to the beta-lactams included in Panel 2

2.2.6. Data on meticillin-resistant *Staphylococcus aureus* (MRSA)

In 2015, Belgium reported data on susceptibility testing of MRSA isolates cattle (calves under one year of age, dairy cows and meat production animals), Finland meat from pigs and Switzerland reported data from cattle (calves under one year of age), meat from pigs and fattening pigs. Details of the antimicrobials selected by Belgium and Switzerland are provided in Section 3.5. For further information on reported MIC distributions and the number of resistant isolates, refer to the submitted and validated MS data published on the EFSA website.

Data relating to MRSA prevalence were reported by seven MSs and two non-MSs (Norway and Switzerland). The methods for collecting and testing samples for MRSA are not harmonised between MSs and, as a result, MSs may use differing procedures. Owing to the variety of methods employed by MSs, these are explained in detail within Section 3.5 to enable readers to better follow the procedures carried out by individual countries.

3. Assessment

3.1. Antimicrobial resistance in *Salmonella*

Human infections with *Salmonella*

The majority of *Salmonella* infections result in mild, self-limiting, gastrointestinal illness and usually do not require antimicrobial treatment. In some patients, the infection may be more serious as the bacteria may spread from the intestines to the blood stream and then to other body sites, which can be life-threatening. Acute *Salmonella* infections may sometimes also result in long-term sequelae affecting the joints (reactive arthritis). In cases of severe enteric disease or invasive infection, effective antimicrobials are essential for treatment. Fluoroquinolones are widely recommended for treating adults and third-generation cephalosporins are recommended for treating children. Infection with *Salmonella* strains resistant to these antimicrobials may be associated with treatment failure, which in turn can lead to poor outcomes for patients. Therefore, recommended treatment should take account of up-to-date information on local patterns of resistance.

For 2015, 22 MSs, Iceland and Norway provided data on AMR in human *Salmonella* isolates. Fourteen countries (Austria, Cyprus, Denmark, Estonia, Finland, France, Greece, Ireland, Italy, Luxembourg, the Netherlands, Norway, Portugal and Romania) reported isolate-based AST results as measured values (inhibition zone diameters or MICs), two countries more than for 2014. Ten countries reported case-based AST results interpreted as susceptible (S), intermediate (I) or resistant (R) according to the CBPs applied (Table SALMOVERVIEW). Seventeen MSs reported quantitative MIC data on the AMR of *Salmonella* isolates recovered from pig carcases, six reported data from pigs, and six MSs reported data on isolates from the carcases of calves under one year of age in 2015, while two reported data on calves under one year of age (Table SALMOVERVIEW).

3.1.1. Antimicrobial resistance in *Salmonella* isolates from humans

When referring to '*Salmonella* spp.', this includes results for all non-typhoidal *Salmonella* serovars from human cases with AST results reported. The resistance levels for *Salmonella* spp. are greatly influenced by the serovars included, with some serovars exhibiting greater resistance to certain antimicrobials or expressing multidrug resistance to a higher degree than other serovars. Results are therefore presented separately for selected serovars prevalent in pigs and cattle (*S.* Typhimurium, monophasic *S.* Typhimurium and *S.* Derby) due to the legislative monitoring of isolates in these animal species in 2015. Data on additional serovars among the ten most common in human cases in 2015 are available in appendices (*S.* Enteritidis, *S.* Infantis, *S.* Kentucky, *S.* Newport, *S.* Paratyphi B var. L+ tartrate+ (var. Java), *S.* Stanley and *S.* Virchow). Findings of ESBL- and AmpC-producing *Salmonella* in isolates from humans is available in Section 3.5 'Third-generation resistance to cephalosporins and carbapenems in *Escherichia coli* and *Salmonella*'.

In total, 15,070 *Salmonella* isolates of 281 different serovars and serogroups were tested for resistance to one or more antimicrobials and reported by 22 MSs, Iceland and Norway. This represents 15.8% of all 95,597 confirmed human salmonellosis cases reported in the EU/EEA in 2015. The number of antimicrobials tested per isolate varied by country, from one country testing two antimicrobials to 19 countries testing all ten antimicrobial substances in the priority panel for 2015, but with four of these countries testing the combination drug trimethoprim–sulfamethoxazole (co-trimoxazole) instead of the substances separately. Since the implementation of the agreed panel in 2014 (ECDC, 2014), the number of countries reporting ceftazidime and meropenem has increased from only a few in 2013 to all countries except a few in 2015. Five to six countries also tested the antimicrobials azithromycin, colistin and/or tigecycline which were optional in 2015, but, are included in the priority panel since June 2016 (ECDC, 2016). Colistin could only be tested by the few laboratories using dilution methods since its chemical properties render it unsuitable for routine disc diffusion methods.

To better assess the impact of food consumed within each reporting country on the AMR levels found in human *Salmonella* isolates, the analysis focused on domestically acquired cases. Travel information was however missing for a high proportion of cases in some countries (see further Table SALMTRAVHUM).

Methods and interpretive criteria used for antimicrobial susceptibility testing of *Salmonella* isolates from humans

The method of testing for antimicrobial susceptibility and the selection of the isolates to be tested varied between countries. The methods and interpretive criteria used for antimicrobial susceptibility testing of *Salmonella* are presented in Table 4.

Quantitative data were interpreted by ECDC based on the EUCAST ECOFF values, where available, in the same way as for the animal and food data. Where ECOFFs do not exist, EUCAST or Clinical and Laboratory Standards Institute (CLSI) CBPs were applied. For the qualitative SIR[12] data, intermediate and resistant results were combined into a non-susceptible category.

For 11 antimicrobials, for which results were reported both as quantitative and interpreted data, the commonly used interpretive criteria were aligned (Figure 9). For this purpose, susceptible isolates were aligned with wild-type isolates based on ECOFFS and non-susceptible isolates (intermediate and resistant) were aligned with non-wild-type isolates. When analysed in this way, there is generally close concordance ($\pm$ 1 dilution) across categories, also for ciprofloxacin after the CBPs for *Salmonella* was lowered in 2014. A notable exception is the EUCAST CBPs for meropenem, which is substantially higher ($+$ 4 dilutions) than the ECOFF.
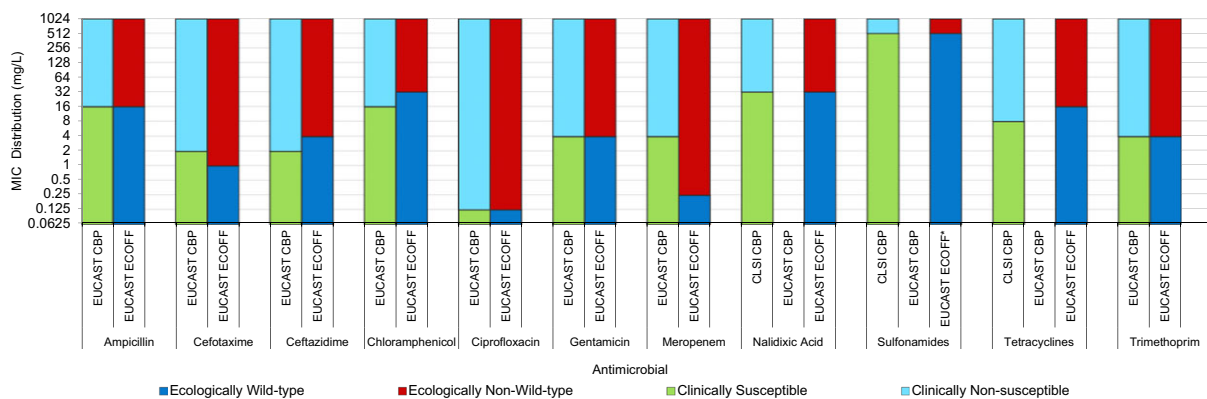
Figure 9: Comparison of CBPs for non-susceptibility (intermediate and resistant categories combined) and ECOFFs used to interpret MIC data reported for *Salmonella* spp. from humans, animals or food

3.1.1.1. Antimicrobial resistance in *Salmonella* spp. in humans

Interpretation of monitoring results must take into account the wide variation in the sampling and testing strategies for *Salmonella* between MSs. While the number of reported isolates may in part be related to true differences in the incidence of salmonellosis, it is also likely to be greatly influenced by practices in the country related to the capture of isolates and/or data from primary clinical laboratories. In France, for example, AST is performed on all isolates of specific serovars of interest, whereas, for the most common serovars, a representative sample is tested. In Slovakia, non-invasive isolates are tested against only a few antimicrobials, whereas invasive isolates are tested against a larger panel. The serovar distribution within the *Salmonella* spp. varies by country depending on their frequency among human cases and/or specific sampling strategies for further typing and AST at the national public health reference laboratories. For this reason, comparisons between countries should be avoided at the level of *Salmonella* spp.

Resistance levels in Salmonella *spp. isolates from humans*

The highest proportions of resistance in human *Salmonella* spp. isolates in 2015 were reported for sulfonamides/sulfamethoxazole (32.4%), tetracyclines (28.1%) and ampicillin (27.8%) (Table 9).

Resistance to ciprofloxacin was reported in 13.3% of isolates and resistance to cefotaxime or ceftazidime in 0.9%. These antimicrobials represent the clinically most important antimicrobial classes (fluoroquinolones and 3rd generation cephalosporins) for treatment of salmonellosis. Ciprofloxacin

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[12] SIR stands for susceptible, intermediate, resistant.

resistance increased compared to 2014 (when it was 8.8%). A relatively high resistance to cefotaxime and ceftazidime was observed in Italy (5.6%, all in *S.* Infantis). No isolates were reported resistant to meropenem in 2015, although it should be noted that meropenem results were interpreted with clinical breakpoints in half of the reporting countries and the clinical breakpoint for intermediate resistance differs from the ECOFF by four dilutions. Resistance to colistin was detected in 11.4% of isolates although the country average among the five MSs reporting this antimicrobial was 4.0%. The highest proportion of colistin resistance was reported by the Netherlands (16.9%) which could be due to that a large proportion of the Dutch isolates were *S.* Enteritidis. *S.* Enteritidis has been reported to have inherent resistance to colistin (Agersø et al., 2012). The relatively high proportion of resistance to tigecycline in Cyprus may be an effect of the low number of isolates tested for this antimicrobial (n = 15) as only one isolate was found resistant, an ESBL-producing isolate of *S.* Saintpaul (see more on ESBL in human *Salmonella* in Section 3.5).

Multidrug resistance in Salmonella *spp. isolates from humans*

Fourteen MSs tested at least ten isolates for the nine antimicrobial classes included in the MDR analysis. On average 49.4% of *Salmonella* spp. isolates were susceptible to all nine antimicrobial classes (13 MSs, N = 6,762, Table COMSALMHUM). Few isolates exhibited 'microbiological' (0.4%) or 'clinical' (0.3%) co-resistance to both ciprofloxacin and cefotaxime. Of the 18 isolates exhibiting clinical co-resistance, five were *S.* Infantis, two *S.* Enteritidis, two *S.* Kentucky, two *S.* Stanley and the remaining seven-one each of *S.* Chester, *S.* Haifa, *S.* Heidelberg, monophasic *S.* Typhimurium 1,4, [5],12:i:-, *S.* Thompson, *S.* Typhimurium and *S.* Virchow. Multidrug resistance was high at EU level (29.3%). The highest proportion was reported from France (64.9%), but this is not representative for all *Salmonella* isolates in France as the extended panel, with ceftazidime, cefotaxime and all beta-lactams, is only tested for isolates resistant to ampicillin. Twenty-eight isolates (0.4% of the 6,830 tested in the 14 MSs for resistance to nine drug classes) were resistant to seven or eight antimicrobial classes, including 14 isolates of monophasic *S.* Typhimurium, five of *S.* Infantis, four *S.* Typhimurium, two *S.* Chester and one each of *S.* Kentucky, *S.* Stanley and *S.* Thompson. No isolates were reported resistant to all nine classes.

Table 9: Antimicrobial resistance in *Salmonella* spp. (all non-typhoidal serovars) from humans per country in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin[b]		Colistin	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	1,556	13.5	–	–	1,556	0.4	1,556	0.4	1,556	2.4	1,556	22.4	–	–
Cyprus	94	30.9	–	–	37	2.7[a]	83	1.2	–	–	–	–	17	0
Denmark	275	33.1	275	1.1	275	1.5	275	1.1	275	5.8	275	4.0	275	2.9
Estonia	72	22.2	–	–	73	0	73	0	73	2.7	73	8.2	16	0
Finland	313	13.4	–	–	313	1.6	–	–	313	2.9	313	9.3	–	–
France	1,052	32.6	1,052	0.7	560	1.8	560	1.8	1,047	11.2	1,052	21.8	139	0
Germany[a]	1,818	28.7	–	–	1,818	1	1,818	0.9	1,816	5.2	1,817	1.6	–	–
Greece	509	6.3	–	–	509	0	500	0	510	1.6	509	0.4	–	–
Hungary[a]	813	37.4	–	–	813	0.7	802	3.2	777	9.4	791	36.7	–	–
Ireland	199	33.7	199	1.5	199	0	199	0	199	7.0	199	15.6	–	–
Italy	71	54.9	–	–	71	5.6	71	5.6	71	11.3	71	11.3	–	–
Latvia[a]	24	12.5	–	–	2	NA	–	–	–	–	7	NA	–	–
Lithuania[a]	938	28.9	–	–	793	0.1	437	0.2	438	1.4	672	14.1	–	–
Luxembourg	106	35.8	–	–	106	0.9	106	0.9	106	3.8	106	17.9	–	–
Malta[a]	126	68.3	–	–	–	–	–	–	–	–	126	61.1	–	–
Netherlands	787	27.4	787	0.3	787	1.1	787	0.5	787	5.1	787	13.2	787	16.9
Portugal	140	51.4	–	–	140	0	140	0	140	8.6	140	10.0	–	–
Romania	169	25.4	–	–	169	0.6	169	0.6	169	3.6	169	10.1	–	–
Slovakia[a]	775	6.6	–	–	249	3.2	12	0	–	–	385	1.3	–	–
Slovenia[a]	390	15.6	–	–	390	0.8	390	0.8	390	4.9	390	21.8	–	–
Spain[a]	1,999	45.1	–	–	1,999	0.8	1,999	0.6	1,996	7.3	1,998	9.7	–	–
United Kingdom[a]	615	21.3	–	–	581	2.4	1	NA	568	6.3	563	1.8	–	–
Total (22 MSs)	**12,842**	**27.8**	**2,313**	**0.6**	**11,419**	**0.9**	**9,978**	**0.9**	**11,232**	**5.8**	**12,015**	**13.3**	**1,240**	**11.4**
Iceland[a]	16	18.8	–	–	–	–	–	–	3	NA	16	12.5	–	–
Norway	350	15.7	120	0.8	350	1.1	350	1.4	120	7.5	350	4.0	–	–

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole[c]		Tetracycline		Tigecycline		Trimethoprim		Co-trimoxazole	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	1,556	1.1	1,556	22.1	1,556	15.7	1,556	16.0	1,556	0.3	1,556	2.2	–	–
Cyprus	54	16.7	–	–	–	–	37	18.9	15	6.7	–	–	–	–
Denmark	275	0.7	275	4.0	275	42.5	275	30.9	275	1.5	275	10.2	–	–
Estonia	73	1.4	22	9.1	73	20.5	73	20.5	–	–	72	5.6	–	–
Finland	313	1.6	313	8.9	–	–	313	13.7	–	–	313	2.6	–	–
France	1,051	7.5	1,051	19.5	1,052	40.7	1,052	41.8	1,046	0.6	1,052	15.2	515	24.9
Germany[a]	1,817	1.4	1,817	10.2	–	–	1,817	26.3	–	–	–	–	1,816	7.6
Greece	507	0.4	509	3.7	504	16.1	510	9.6	–	–	504	5.8	–	–
Hungary[a]	777	0.9	–	–	–	–	69	58.0	–	–	777	3.3	813	7
Ireland	199	3.5	199	13.6	199	33.2	199	34.2	199	0	199	8.0	–	–
Italy	71	0	71	9.9	71	49.3	71	50.7	–	–	71	12.7	71	9.9
Latvia[a]	2	NA	–	–	–	–	–	–	–	–	–	–	24	4.2
Lithuania[a]	359	0.6	350	25.7	–	–	351	17.1	–	–	352	3.4	916	2.4
Luxembourg	106	0.9	–	–	106	53.8	105	47.6	–	–	106	8.5	106	8.5
Malta[a]	–	–	–	–	–	–	–	–	–	–	–	–	126	58.7
Netherlands	787	1.1	787	10.7	787	29.1	787	29.9	787	1.1	787	8.8	–	–
Portugal	140	0.7	140	7.9	140	45.7	140	50.7	–	–	140	5.0	–	–
Romania	169	1.2	169	11.2	169	20.1	169	14.8	–	–	169	6.5	169	3.6
Slovakia[a]	–	–	–	–	–	–	423	7.3	–	–	–	–	295	1.4
Slovenia[a]	390	1.0	–	–	389	26.7	390	16.2	–	–	390	2.8	390	2.8
Spain[a]	1,999	3.8	1,998	19.5	1,997	47.6	1,998	43.9	–	–	1,998	6.3	2	NA
United Kingdom[a]	553	1.4	573	16.4	550	22.7	551	24.0	–	–	611	6.5	58	6.9
Total (22 MSs)	11,220	2.4	9,819	15.4	7,885	32.4	10,887	28.1	3,878	0.6	9,373	6.4	5,301	8.7
Iceland[a]	–	–	–	–	–	–	–	–	–	–	–	–	16	0
Norway	350	2.0	120	7.5	–	–	120	38.3	–	–	–	–	350	4.0

All *Salmonella* isolates tested were susceptible to meropenem.

N: number of isolates tested; % Res: percentage of microbiologically resistant isolates (either interpreted as non-wild type by ECOFFs or clinically non-susceptible by combining resistant and intermediate categories); –: no data reported; NA: not applicable – if less than 10 isolates were tested, the percentage of resistance was not calculated; MS: Member State.

(a): Data interpreted with clinical breakpoints.

(b): In several countries, ciprofloxacin has been replaced by pefloxacin for screening for fluoroquinolone resistance with disk diffusion, as recommended by EUCAST.

(c): Combined data on the class of sulfonamides and the substance sulfamethoxazole within this group.

Table 10: Antimicrobial resistance in *Salmonella* Typhimurium from humans per country in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin[b]		Colistin	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	203	44.3	–	–	203	1	203	1	203	10.8	203	5.4	–	–
Cyprus	25	76.0	–	–	6	NA	21	0	–	–	–	–	6	NA
Denmark	64	32.8	64	0.0	64	3.1	64	3.1	64	12.5	64	3.1	64	1.6
Estonia	12	25.0	–	–	12	0	12	0	12	8.3	12	0	3	NA
Finland	80	10.0	–	–	80	0.0	–	–	80	1.3	80	5.0	–	–
France	141	73.0	141	0	141	0	141	0.0	140	57.1	141	9.2	2	NA
Germany[a]	509	71.1	–	–	509	1.2	509	1.0	509	9.0	509	0.2	–	–
Greece	63	19.0	–	–	63	0	62	0	63	3.2	63	0	–	–
Hungary[a]	256	43.8	–	–	256	0.8	256	2.7	256	23.4	254	11.0	–	–
Ireland	46	41.3	46	2.2	46	0	46	0	46	21.7	46	4.3	–	–
Italy	11	81.8	–	–	11	0	11	0	11	54.5	11	9.1	–	–
Latvia[a]	8	NA	–	–	–	–	–	–	–	–	4	NA	–	–
Lithuania[a]	122	71.3	–	–	79	1.3	57	0	57	5.3	98	4.1	–	–
Luxembourg	17	23.5	–	–	17	5.9	17	0	17	17.6	17	11.8	–	–
Malta[a]	18	77.8	–	–	–	–	–	–	–	–	18	33.3	–	–
Netherlands	184	44.6	184	0	184	2.7	184	0	184	9.8	184	7.1	184	1.6
Portugal	23	87.0	–	–	23	0	23	0	23	39.1	23	34.8	–	–
Romania	43	65.1	–	–	43	0	43	0	43	2.3	43	0	–	–
Slovakia[a]	50	42.0	–	–	21	0	–	–	–	–	25	0	–	–
Slovenia[a]	48	60.4	–	–	48	0	48	0	48	39.6	48	41.7	–	–
Spain[a]	226	73.5	–	–	226	0.9	226	0	225	29.8	226	12.4	–	–
United Kingdom[a]	113	54.9	–	–	109	3.7	–	–	107	18.7	106	0	–	–
Total (22 MSs)	**2,262**	**56.3**	**435**	**0.2**	**2,136**	**1.1**	**1,923**	**0.8**	**2,088**	**18.0**	**2,178**	**6.6**	**259**	**1.5**
Iceland[a]	4	NA	–	–	–	–	–	–	–	–	4	NA	–	–
Norway	76	10.5	18	0	76	0	76	0	18	22.2	76	2.6	–	–

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole[c]		Tetracycline		Tigecycline		Trimethoprim		Co-trimoxazole	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	203	1.0	203	5.4	203	42.9	203	43.3	203	0	203	2.0	–	–
Cyprus	14	35.7	–	–	–	–	6	NA	5	NA	–	–	–	–
Denmark	64	0	64	3.1	64	35.9	64	20.3	64	4.7	64	10.9	–	–
Estonia	12	8.3	5	NA	12	41.7	12	25.0	–	–	12	8.3	–	–
Finland	80	0	80	5.0	–	–	80	5.0	–	–	80	2.5	–	–
France	141	5.7	140	8.6	141	74.5	141	76.6	141	1.4	141	40.4	130	53.1
Germany[a]	509	0.6	508	3.1	–	–	508	63.4	–	–	–	–	508	11.0
Greece	63	0	63	0	63	38.1	63	36.5	–	–	63	7.9	–	–
Hungary[a]	256	1.6	–	–	–	–	19	52.6	–	–	256	3.5	256	6.3
Ireland	46	2.2	46	2.2	46	43.5	46	43.5	46	0	46	8.7	–	–
Italy	11	0	11	0	11	27.3	11	18.2	–	–	11	9.1	11	9.1
Latvia[a]	–	–	–	–	–	–	–	–	–	–	–	–	8	NA
Lithuania[a]	45	4.4	44	9.1	–	–	44	75.0	–	–	45	8.9	112	7.1
Luxembourg	17	0	–	–	17	58.8	17	58.8	–	–	17	0	17	5.9
Malta[a]	–	–	–	–	–	–	–	–	–	–	–	–	18	27.8
Netherlands	184	1.1	184	6.0	184	36.4	184	33.2	184	2.2	184	14.1	–	–
Portugal	23	4.3	23	34.8	23	65.2	23	73.9	–	–	23	4.3	–	–
Romania	43	0	43	0	43	39.5	43	34.9	–	–	43	7.0	43	2.3
Slovakia[a]	–	–	–	–	–	–	29	31.0	–	–	–	–	21	9.5
Slovenia[a]	48	0	–	–	47	63.8	48	56.3	–	–	48	6.3	48	6.3
Spain[a]	226	0.9	226	21.2	226	67.3	226	59.3	–	–	226	10.6	–	–
United Kingdom[a]	104	1.0	108	7.4	103	60.2	103	65.0	–	–	129	9.3	25	4.0
Total (22 MSs)	**2,094**	**1.6**	**1,746**	**7.2**	**1,187**	**52.4**	**1,870**	**51.9**	**643**	**1.4**	**1,591**	**10.2**	**1,197**	**13.7**
Iceland[a]	–	–	–	–	–	–	–	–	–	–	–	–	4	NA
Norway	76	1.3	18	11.1	–	–	18	50.0	–	–	–	–	76	1.3

All *Salmonella* isolates tested were susceptible to meropenem.

N: number of isolates tested; % Res: percentage of microbiologically resistant isolates (either interpreted as non-wild type by ECOFFs or clinically non-susceptible by combining resistant and intermediate categories); –: no data reported; NA: not applicable – if less than 10 isolates were tested, the percentage of resistance was not calculated; MS: Member State.

(a): Data interpreted with clinical breakpoints.

(b): In several countries, ciprofloxacin has been replaced by pefloxacin for screening for fluoroquinolone resistance with disk diffusion, as recommended by EUCAST.

(c): Combined data on the class of sulfonamides and the substance sulfamethoxazole within this group.

3.1.1.2. Antimicrobial resistance in *Salmonella* Typhimurium in humans

Resistance levels in S. Typhimurium isolates from humans

As in previous years, *S.* Typhimurium was the second most common *Salmonella* serovar identified in 2015 with 10,997 cases reported in the EU/EEA (excluding monophasic *S.* Typhimurium 1,4,[5],12:i:). The highest proportion of resistance in *S.* Typhimurium was observed for ampicillin (56.3%), sulfonamides (52.4%) and tetracyclines (51.9%) (22 MSs, Table 10). The proportions of resistance to these antimicrobials were high to extremely high in all reporting MSs, except in Finland where low resistance to both ampicillin and tetracyclines was observed, and Greece where moderate resistance to ampicillin was observed. Norway also reported moderate resistance to ampicillin. The proportions of isolates resistant to either of to the two clinically most critical antimicrobials were on average 6.6% for ciprofloxacin and 1.1% for cefotaxime. The highest proportion of isolates resistant to ciprofloxacin was reported from Slovenia (41.7%), Portugal (34.8%) and Malta (33.3%) whereas the highest proportion of cefotaxime resistance was reported from Luxembourg (5.9%). It should be noted, however, that the numbers of isolates tested in these instances were low (n = 17–48).

Temporal trends in resistance among S. *Typhimurium isolates from human cases*

Temporal trend analysis was performed for the 3 years 2013–2015 following the agreement on harmonised data collection (ECDC, 2014). Fifteen MSs and Norway provided resistance data for all 3 years and a minimum of ten isolates tested (Figure 10). Resistance to (fluoro)quinolones was assessed as resistance to either ciprofloxacin, pefloxacin or nalidixic acid due to recent breakpoint changes and methodological issues (see further in Materials and methods). Statistically significant increases in (fluoro)quinolone resistance were observed in Hungary and Slovenia. Resistance to ampicillin and tetracycline increased significantly in Austria, France and Slovenia and tetracycline also in Norway. Both ampicillin and tetracycline decreased significantly in Finland, Germany and Hungary, while significant decreases in ampicillin were observed in Luxembourg and Norway and in tetracycline in the Netherlands and Spain. No significantly increasing or decreasing trends were observed for cefotaxime resistance.
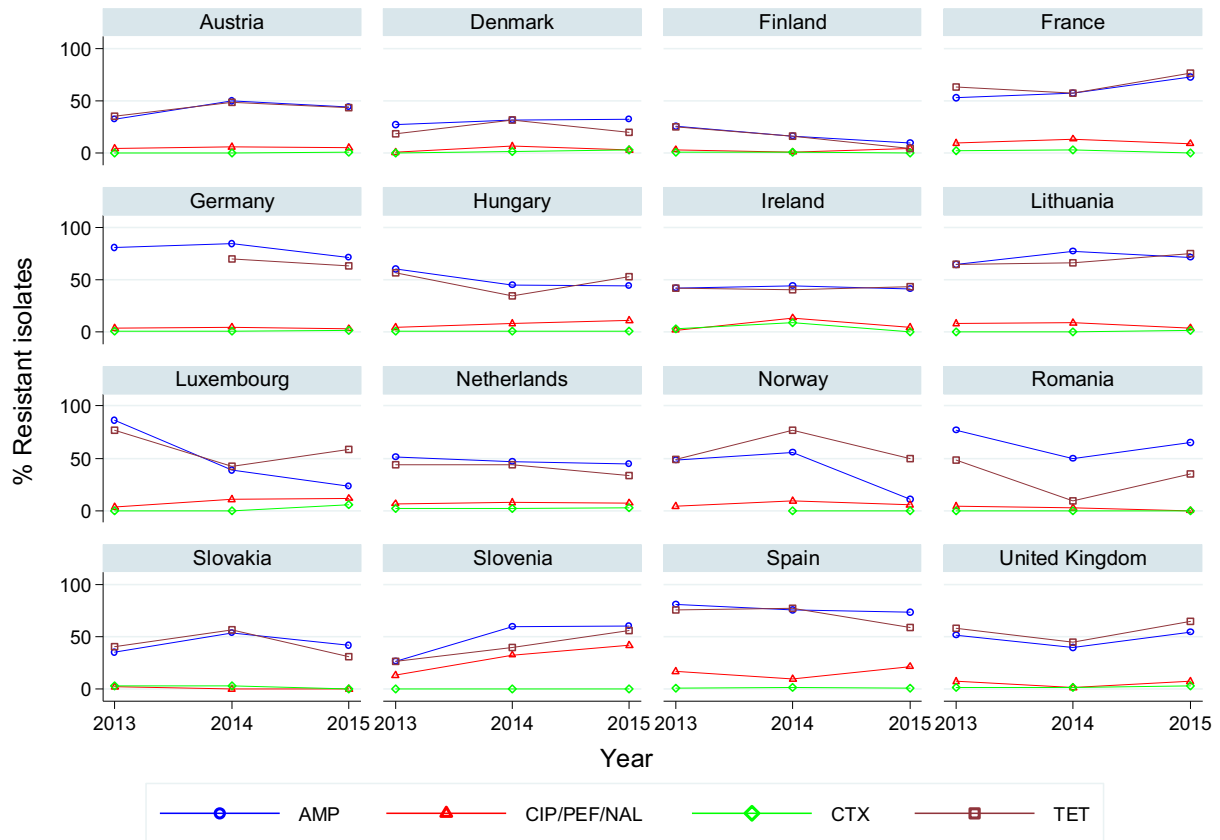
Figure 10: Trends in resistance to ampicillin, ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime and tetracycline in *Salmonella* Typhimurium from humans in 16 reporting countries, 2013–2015

Statistically significant increasing trends over 3 years, as tested by logistic regression (p ≤ 0.05), were observed for ciprofloxacin in Hungary and Slovenia (↑), for ampicillin in Austria, France and Slovenia (↑) and for tetracyclines in Austria, France, Norway and Slovenia (↑). Statistically significant decreasing trends over 3 years were observed for ampicillin in Finland, Germany, Hungary, Luxembourg and Norway (↓) and for tetracyclines in Finland, Germany, Hungary, the Netherlands and Spain (↓). Only countries testing at least 10 isolates per year were included in the analysis.

Spatial distribution of resistance among S. *Typhimurium isolates from human cases*

Proportions of (fluoro)quinolone resistance in *S.* Typhimurium isolates from human cases (Figure 11) were the highest in some countries in southern Europe and Slovenia. Cefotaxime resistance levels were generally low but slightly higher in north-western Europe (Figure 12).
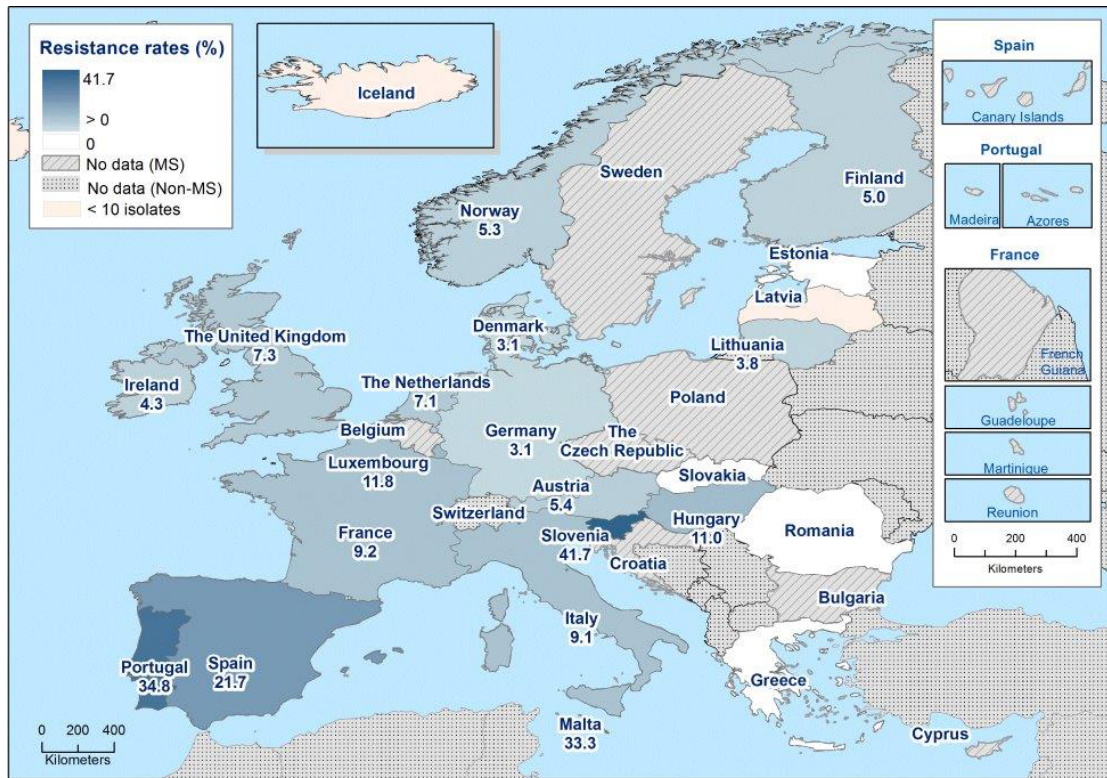
Figure 11: Spatial distribution of (fluoro)quinolone resistance among *S.* Typhimurium from human cases in reporting countries in 2015
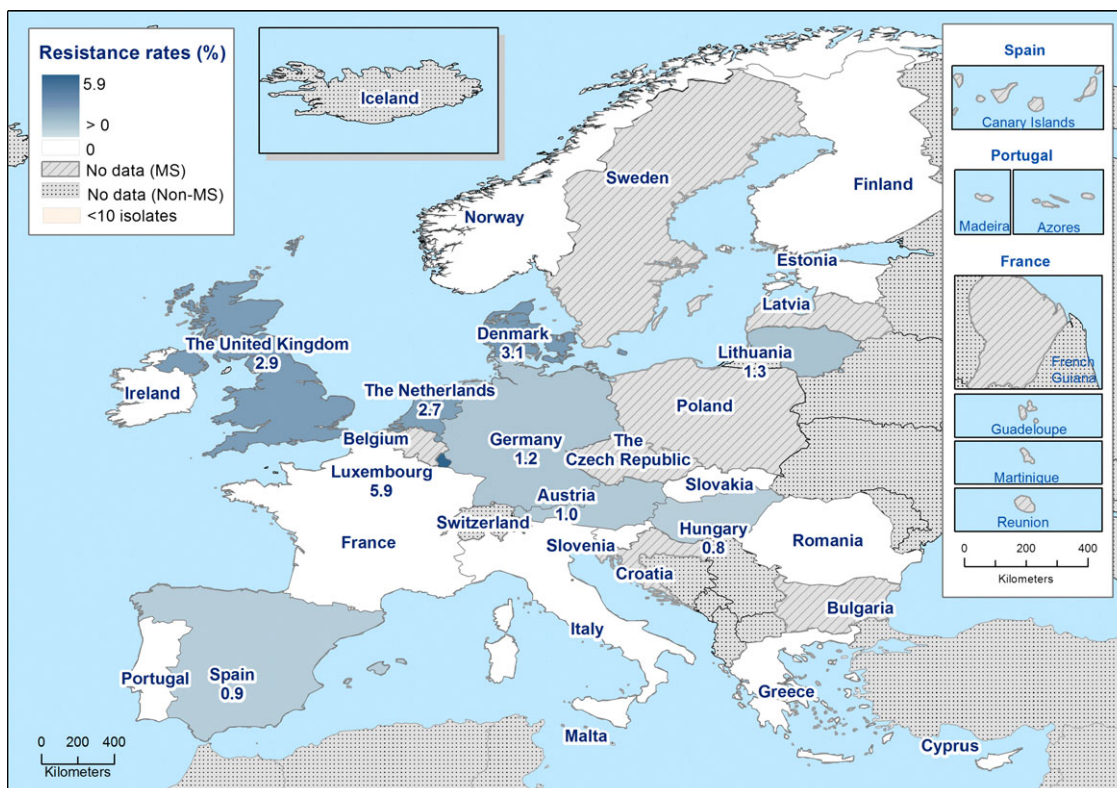
Figure 12: Spatial distribution of cefotaxime resistance among *S.* Typhimurium from human cases in reporting countries in 2015

Multidrug resistance in S. *Typhimurium isolates from humans*

In humans, 44.4% (12 MSs, N = 1,063) of the *S.* Typhimurium isolates were multiresistant (Table COMTYPHIHUM, Figure 13). This is an increase compared to 2014 when 32.5% of isolates from 8 MSs were multiresistant. The largest increase from 2014 to 2015, with 20%, was observed in France and Romania. Extremely high MDR was reported in *S.* Typhimurium in Portugal (73.9%) and France (72.1%) in 2015 and very high MDR in Spain (60.8%) and Slovenia (55.3%). *S.* Typhimurium isolates resistant to six, seven or eight antimicrobial classes were identified in six of 12 reporting MSs.

'Microbiological' and 'clinical' co-resistance to ciprofloxacin and cefotaxime were reported in 0.6% and 0.1% of isolates, with the highest proportion of 'microbiological' co-resistance in Luxembourg (5.9%, N = 17) (Table COMTYPHIHUM).
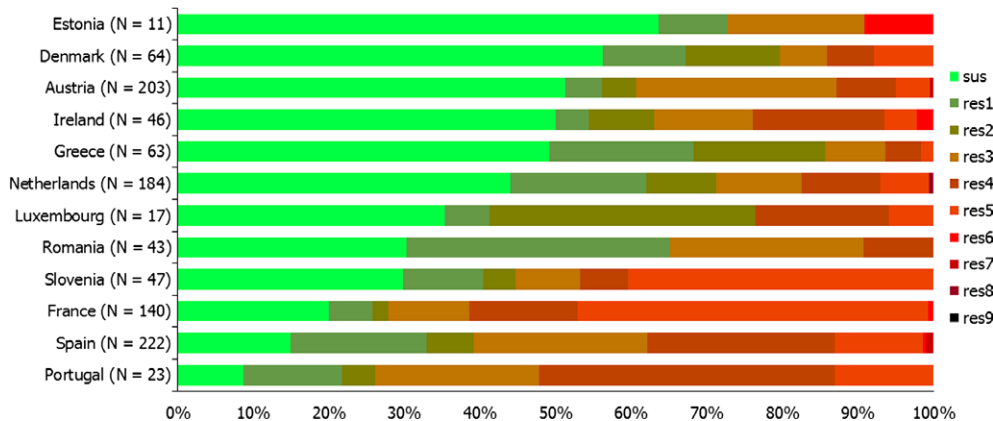
N: total number of isolates tested for susceptibility against the whole common antimicrobial set for *Salmonella*; sus: susceptible to all antimicrobial classes of the common set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the common set for *Salmonella*.

Figure 13: Frequency distribution of *Salmonella* Typhimurium isolates from humans completely susceptible or resistant to one to nine antimicrobial classes in 2015

3.1.1.3. Antimicrobial resistance in monophasic *Salmonella* Typhimurium in humans

Resistance in monophasic S. *Typhimurium 1,4,[5],12:i:- isolates from humans*

For the purpose of this report, monophasic *S.* Typhimurium 1,4,[5],12:i:- is treated as a separate serovar, and as such, it is currently the third most common serovar in Europe. For 2015, 5,770 cases were reported by the EU/EEA countries. Extremely high levels of resistance were observed for tetracyclines (89.8%), ampicillin (87.3%) and sulfonamides (87.3%) (11 MSs, Table 11). The resistance pattern, ASuT,[13] is a well-known characteristic of monophasic *S.* Typhimurium 1,4,[5],12:i:- and was observed at similar levels in all reporting MSs with the exception of Estonia which reported lower levels of resistance to sulfonamides. The proportion of isolates resistant to either of the two clinically most important antimicrobials was 3.3% for ciprofloxacin and 0.9% for cefotaxime, with the highest levels of ciprofloxacin resistance observed in Estonia (10.0% but few isolates tested, n = 10) and of cefotaxime resistance in the Netherlands (2.2%).

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[13] This pattern of MDR (resistance to ampicillin, sulfonamide and tetracycline) typically also includes resistance to streptomycin; however, as described in the Materials and methods section, data on this antimicrobial are no longer included in this report.

Table 11: Antimicrobial resistance in monophasic *Salmonella* Typhimurium 1,4,[5],12:i:- from humans per country in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin[b]		Colistin	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	42	95.2	–	–	42	0	42	0	42	2.4	42	4.8	–	–
Denmark	65	96.9	65	0	65	1.5	65	1.5	65	10.8	65	0	65	3.1
Estonia	10	90.0	–	–	10	0	10	0	10	10.0	10	10.0	3	NA
France	117	88.0	117	0	117	0.9	117	0.9	114	0.9	117	2.6	2	NA
Hungary[a]	203	85.7	–	–	203	0.5	203	3.9	203	4.4	203	3.4	–	–
Ireland	32	93.8	32	0	32	0	32	0	32	6.3	32	3.1	–	–
Italy	24	95.8	–	–	24	0	24	0	24	0	24	0	–	–
Luxembourg	32	90.6	–	–	32	0	32	0	32	0	32	3.1	–	–
Netherlands	137	78.1	137	0.7	137	2.2	137	2.2	137	7.3	137	7.3	137	2.2
Portugal	52	84.6	–	–	52	0	52	0	52	1.9	52	1.9	–	–
Spain[a]	723	87.4	–	–	723	1	723	0.6	722	6.2	722	2.9	–	–
Total (11 MSs)	**1,437**	**87.3**	**351**	**0.3**	**1,437**	**0.9**	**1,437**	**1.2**	**1,433**	**5.4**	**1,436**	**3.3**	**207**	**2.4**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole[c]		Tetracycline		Tigecycline		Trimethoprim		Co-trimoxazole	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	42	2.4	42	4.8	42	92.9	42	92.9	42	0	42	0	–	–
Denmark	65	1.5	65	0	65	95.4	65	89.2	65	0	65	18.5	–	–
Estonia	10	0	–	–	10	60.0	10	90.0	–	–	10	10.0	–	–
France	117	1.7	117	2.6	117	88.9	117	94.0	117	0	117	5.1	117	6
Hungary[a]	203	1.0	–	–	–	–	15	93.3	–	–	203	5.9	203	14.8
Ireland	32	9.4	32	3.1	32	93.8	32	96.9	32	0	32	9.4	–	–
Italy	24	0	24	0.0	24	95.8	24	100.0	–	–	24	4.2	24	0
Luxembourg	32	0	–	–	32	93.8	31	87.1	–	–	32	3.1	32	3.1
Netherlands	137	2.2	137	7.3	137	81.8	137	89.1	137	0.7	137	8.0	–	–
Portugal	52	0	52	0	52	80.8	52	90.4	–	–	52	3.8	–	–
Spain[a]	723	6.9	723	8.7	722	87.0	722	88.5	–	–	722	5.5	–	–
Total (11 MSs)	1,437	4.3	1,192	6.6	1,233	87.3	1,247	89.8	393	0.3	1,436	6.2	376	10.1

All Salmonella isolates tested were susceptible to meropenem.

N: number of isolates tested; % Res: percentage of microbiologically resistant isolates (either interpreted as non-wild type by ECOFFs or clinically non-susceptible by combining resistant and intermediate categories); –: no data reported; NA: not applicable – if less than 10 isolates were tested, the percentage of resistance was not calculated; MS: Member State.

(a): Data interpreted with clinical breakpoints.

(b): In several countries, ciprofloxacin has been replaced by pefloxacin for screening for fluoroquinolone resistance with disk diffusion, as recommended by EUCAST.

(c): Combined data on the class of sulfonamides and the substance sulfamethoxazole within this group.

Temporal trends in resistance among monophasic S. *Typhimurium 1,4,[5],12:i:- from human cases*

Nine MSs provided resistance data for all 3 years in the period 2013–2015 and a minimum of ten isolates tested (Figure 14). A significant increase was observed in ampicillin resistance in Denmark while significant decreases in resistance were observed in Spain for ampicillin, cefotaxime and tetracycline. No significantly increasing or decreasing trends were observed for (fluoro)quinolone resistance.
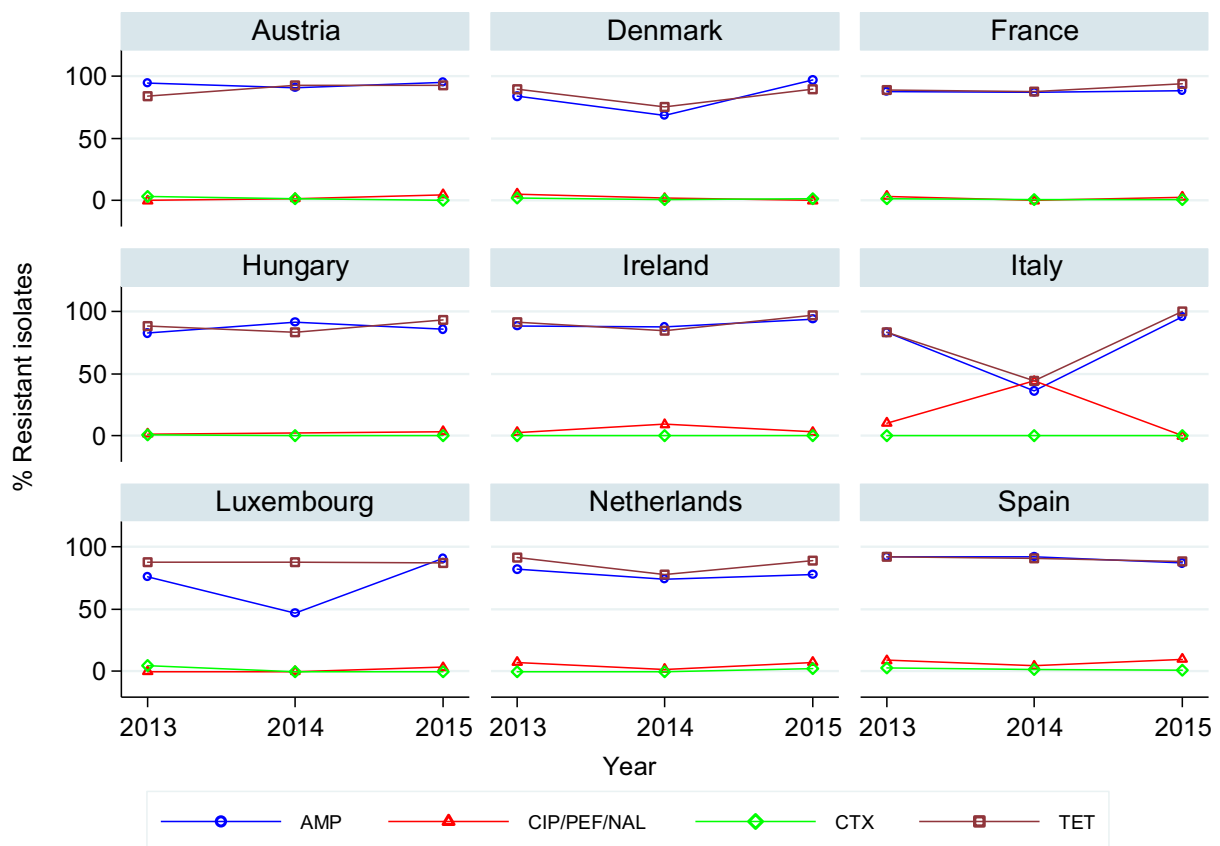
A statistically significant increasing trend over 3 years, as tested by logistic regression (p ≤ 0.05), was observed for ampicillin in Denmark (↑). Statistically significant decreasing trends over 3 years were observed for ampicillin, cefotaxime and tetracycline in Spain (↓). Only countries testing at least 10 isolates per year were included in the analysis.

Figure 14: Trends in resistance to ampicillin, ciprofloxacin/pefloxacin/nalidixic acid, cefotaxime and tetracycline in monophasic *Salmonella* Typhimurium 1,4,[5],12:i:- from humans in reporting countries, 2013–2015

Spatial distribution of resistance among monophasic S. *Typhimurium 1,4,[5],12:i:- isolates from human cases*

No clear geographical patterns were observed in (fluoro)quinolone resistance levels in monophasic *S.* Typhimurium isolates from human cases (Figure 15) where the highest proportions of resistance were reported by Estonia and Spain. Cefotaxime resistance levels were generally low (Figure 16).

Figure 15: Spatial distribution of (fluoro)quinolone resistance among monophasic *S.* Typhimurium 1,4,[5],12:i:- from human cases in reporting countries in 2015
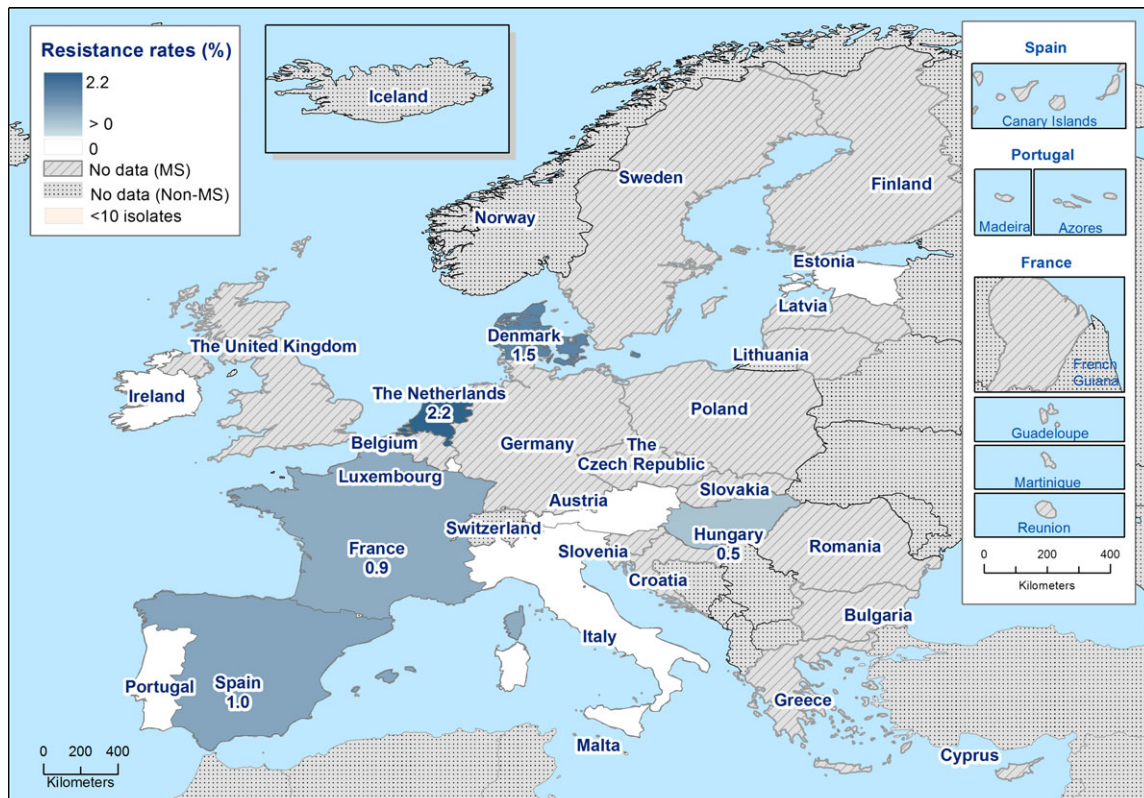
Figure 16: Spatial distribution of cefotaxime resistance among monophasic *S.* Typhimurium 1,4,[5],12:i:- from human cases in reporting countries in 2015

Multidrug resistance in monophasic S. *Typhimurium 1,4,[5],12:i:- isolates from humans*

In humans, 81.1% (10 MSs, N = 1,219) of the monophasic *S.* Typhimurium isolates were multiresistant (Figure 17). This is an increase compared to 2014 when 69.4% of isolates from 7 MSs were multiresistant. The largest increases in MDR from 2014 to 2015 were observed in Italy (62% increase although few isolates tested, n = 15), Luxembourg (31% increase) and Denmark (23% increase). Extremely high MDR was observed in monophasic *S.* Typhimurium from all reporting MSs. Isolates resistant to six, seven or eight antimicrobial classes were identified in six of 11 reporting MSs, and one isolate resistant to eight of nine classes (only susceptible to meropenem) was reported by the Netherlands.

'Microbiological' and 'clinical' co-resistance to ciprofloxacin and cefotaxime were only reported in two isolates (one from the Netherlands and one from Spain), and one isolates from the Netherlands, respectively, resulting in 0.2% and 0.1% co-resistance among the eleven reporting MSs (Table COMMONTYPHIHUM).
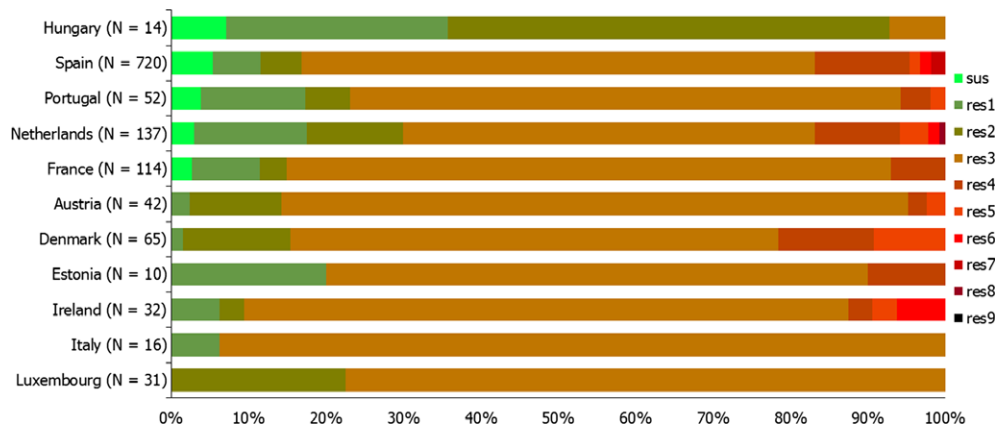
N: total number of isolates tested for susceptibility against the whole common antimicrobial set for *Salmonella*; sus: susceptible to all antimicrobial classes of the common set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the common set for *Salmonella*.

Figure 17: Frequency distribution of monophasic *Salmonella* Typhimurium 1,4,[5],12:i:- isolates from humans completely susceptible or resistant to one to nine antimicrobial classes in 2015

3.1.1.4. Antimicrobial resistance in *Salmonella* Derby in humans

Resistance levels in S. *Derby isolates from humans*

S. Derby was the seventh most common serovar in 2015 with 648 cases reported by the EU/EEA countries. Resistance to sulfonamides and tetracycline was relatively common in *S.* Derby (42.4% and 36.3%, respectively) while ampicillin resistance was low (5.8%) (Table 12). The proportion of isolates resistant to either of the two clinically most important antimicrobials was on average 4.1% for ciprofloxacin and 0.9% for cefotaxime.

Multidrug resistance in monophasic S. *Derby isolates from humans*

Multidrug resistance was high (23.8%) in the two MSs that reported data on at least 10 isolates (N = 21, Table COMDERBYHUM, Figure 18). No isolates were co-resistant to ciprofloxacin and cefotaxime.
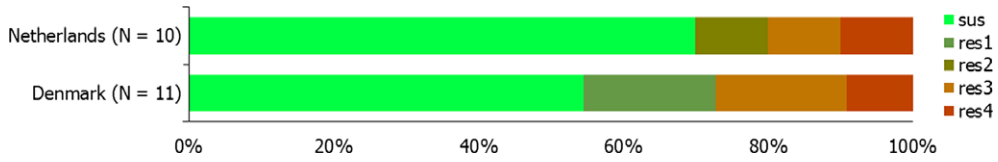
N: total number of isolates tested for susceptibility against the whole common antimicrobial set for *Salmonella*; sus: susceptible to all antimicrobial classes of the common set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the common set for *Salmonella*.

Figure 18: Frequency distribution of monophasic *Salmonella* Derby isolates from humans completely susceptible or resistant to one to nine antimicrobial classes in 2015

Table 12: Antimicrobial resistance in *Salmonella* Derby from humans per country in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin[b]		Colistin	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	8	NA	–	–	8	NA	8	NA	8	NA	8	NA	–	–
Denmark	11	18.2	11	0	11	0	11	0	11	0	11	0	11	0
Estonia	1	NA	–	–	1	NA	1	NA	1	NA	1	NA	–	–
France	60	0	60	0	–	–	–	–	60	0	60	1.7	–	–
Germany[a]	27	11.1	–	–	27	3.7	27	3.7	27	7.4	27	3.7	–	–
Greece	2	NA	–	–	2	NA	2	NA	2	NA	2	NA	–	–
Hungary[a]	1	NA	–	–	1	NA	1	NA	1	NA	1	NA	–	–
Ireland	1	NA	1	NA	1	NA	1	NA	1	NA	1	NA	–	–
Italy	4	NA	–	–	4	NA	4	NA	4	NA	4	NA	–	–
Lithuania[a]	14	0	–	–	13	0	14	0	14	7.1	14	7.1	–	–
Luxembourg	3	NA	–	–	3	NA	3	NA	3	NA	3	NA	–	–
Netherlands	10	10.0	10	0	10	0	10	0	10	10	10	10	10	0
Portugal	1	NA	–	–	1	NA	1	NA	1	NA	1	NA	–	–
Romania	1	NA	–	–	1	NA	1	NA	1	NA	1	NA	–	–
Slovakia[a]	4	NA	–	–	1	NA	–	–	–	–	3	NA	–	–
Slovenia[a]	1	NA	–	–	1	NA	1	NA	1	NA	1	NA	–	–
Spain[a]	17	0	–	–	17	0	17	0	17	0	17	5.9	–	–
United Kingdom[a]	5	NA	–	–	5	NA	–	–	5	NA	5	NA	–	–
Total (18 MSs)	**171**	**5.8**	**82**	**0**	**107**	**0.9**	**102**	**1**	**167**	**3.6**	**170**	**4.1**	**21**	**0**
Norway	1	NA	1	NA	1	NA	1	NA	1	NA	1	NA	–	–

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Country	Gentamicin		Nalidixic acid		Sulfamethoxazole[c]		Tetracycline		Tigecycline		Trimethoprim		Co-trimoxazole	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	8	NA	8	NA	8	NA	8	NA	8	NA	8	NA	–	–
Denmark	11	0	11	0	11	36.4	11	27.3	11	0	11	27.3	–	–
Estonia	1	NA	–	–	1	NA	1	NA	–	–	1	NA	–	–
France	60	0	60	1.7	60	55.0	60	55.0	60	0	60	5	–	–
Germany[a]	26	0	27	11.1	–	–	27	3.7	–	–	–	–	27	7.4
Greece	2	NA	2	NA	2	NA	2	NA	–	–	2	NA	–	–
Hungary[a]	1	NA	–	–	–	–	–	–	–	–	1	NA	1	NA
Ireland	1	NA	1	NA	1	NA	1	NA	1	NA	1	NA	–	–
Italy	4	NA	4	NA	4	NA	4	NA	–	–	4	NA	4	NA
Lithuania[a]	14	0	14	7.1	–	–	14	14.3	–	–	14	14.3	14	14.3
Luxembourg	3	NA	–	–	3	NA	3	NA	–	–	3	NA	3	NA
Netherlands	10	0	10	0	10	30.0	10	30.0	10	10.0	10	0	–	–
Portugal	1	NA	1	NA	1	NA	1	NA	–	–	1	NA	–	–
Romania	1	NA	1	NA	1	NA	1	NA	–	–	1	NA	1	NA
Slovakia[a]	–	–	–	–	–	–	2	NA	–	–	–	–	3	NA
Slovenia[a]	1	NA	–	–	1	NA	1	NA	–	–	1	NA	1	NA
Spain[a]	17	0	17	0	17	35.3	17	47.1	–	–	17	0	–	–
United Kingdom[a]	5	NA	5	NA	5	NA	5	NA	–	–	5	NA	–	–
Total (18 MSs)	**166**	**0**	**161**	**3.7**	**125**	**42.4**	**168**	**36.3**	**90**	**1.1**	**140**	**7.9**	**54**	**11.1**
Norway	1	NA	1	NA	–	–	1	NA	–	–	–	–	1	NA

All *Salmonella* isolates tested were susceptible to meropenem.

N: number of isolates tested; % Res: percentage of microbiologically resistant isolates (either interpreted as non-wild type by ECOFFs or clinically non-susceptible by combining resistant and intermediate categories); –: no data reported; NA: not applicable – if less than 10 isolates were tested, the percentage of resistance was not calculated; MS: Member State.

(a): Data interpreted with clinical breakpoints.

(b): In several countries, ciprofloxacin has been replaced by pefloxacin for screening for fluoroquinolone resistance with disk diffusion, as recommended by EUCAST.

(c): Combined data on the class of sulfonamides and the substance sulfamethoxazole within this group.

3.1.2. Antimicrobial resistance in *Salmonella* isolates from animals and food

Based on the legislative requirements, the active monitoring of AMR in *Salmonella* isolates from carcases of fattening pigs and carcases of bovines under one year of age was mandatory in 2015. *Salmonella* isolates from fattening pigs and of bovines under one year of age were obtained from carcase samples collected from slaughterhouses, as part of *Salmonella* testing and verification of compliance, in accordance with Regulation (EC) No 2073/2005.

Salmonella spp. includes results for all *Salmonella* serovars reported for different animal populations and food. As the potential for acquiring AMR markedly varies between serovars, the relative contribution of different serovars may significantly influence the general level of resistance presented for *Salmonella* spp. Trends in the dissemination of specific clones or resistance traits should ideally be considered individually for the different serovars and results are presented for selected serovars of importance.

3.1.2.1. Antimicrobial resistance in *Salmonella* in carcases of fattening pigs

Resistance levels in Salmonella *spp. isolates from carcases of fattening pigs*

In 2015, 17 MSs reported data on isolates of *Salmonella* spp. from carcases of fattening pigs according to the provisions of Decision 2013/652/EU (Table 13). The reported levels of resistance to ampicillin, sulfamethoxazole and tetracycline ranged from moderate to extremely high (13.0–100%) in *Salmonella* spp. from carcases of fattening pigs in most of the reporting MSs, whereas no resistance to ampicillin was recorded in Latvia (N = 2). Resistance to trimethoprim was generally low to moderate in most reporting MSs (4.3–20.0%), although high levels were also observed in four reporting countries, extremely high level in one MS and three MSs did not register any resistance. Overall resistance to gentamicin (1.5%) remained at low level, although high level (50%) (N = 4) of resistance was registered in one MS. The levels of resistance to chloramphenicol ranged from low (4.3%) to high (25%) and it was moderate considering all reporting MSs. Resistance was not detected or low levels of resistance to tigecycline were reported by most MSs (0–3.9%), however one MS reported high levels of resistance (20.8%). 'Microbiological' resistance to cefotaxime and ceftazidime was reported by five MSs at very low or low levels. Resistance to azithromycin was recorded at high level in two MSs, at low levels in four MSs and not detected in all the others reporting countries. Meropenem resistance was not recorded in any of the reporting countries.

Temporal trends in resistance among Salmonella *spp. meat from pigs*

Ten MSs provided resistance data on 5 years or more to be included in the statistical analysis. Over the 7 years of data, levels of resistance to ciprofloxacin, nalidixic acid and cefotaxime remained mostly constant for most of the reporting MSs. Within each MS, similar levels of resistance to ciprofloxacin and nalidixic acid were observed from 2009 to 2015. Although slight but statistically significant decreasing occurred for both ciprofloxacin and nalidixic acid in one MS, and only for nalidixic acid in one MS. Resistance to cefotaxime is generally very low; however, a statistically significant increasing trend was observed in two MSs, whereas the trend in one MS was decreasing (Figure 19). Tetracycline resistance exceeded ampicillin resistance in many MSs and although tetracycline resistance showed some fluctuations, ampicillin resistance tended to show parallel fluctuations, maintaining the interval between tetracycline and ampicillin resistance.

As antimicrobial resistance is associated with particular serovars or clones within serovars, fluctuations in the occurrence of resistance in *Salmonella* spp. isolates within a country may be the result of changes in the proportions of different *Salmonella* serovars which contribute to the total numbers of *Salmonella* spp. isolates.
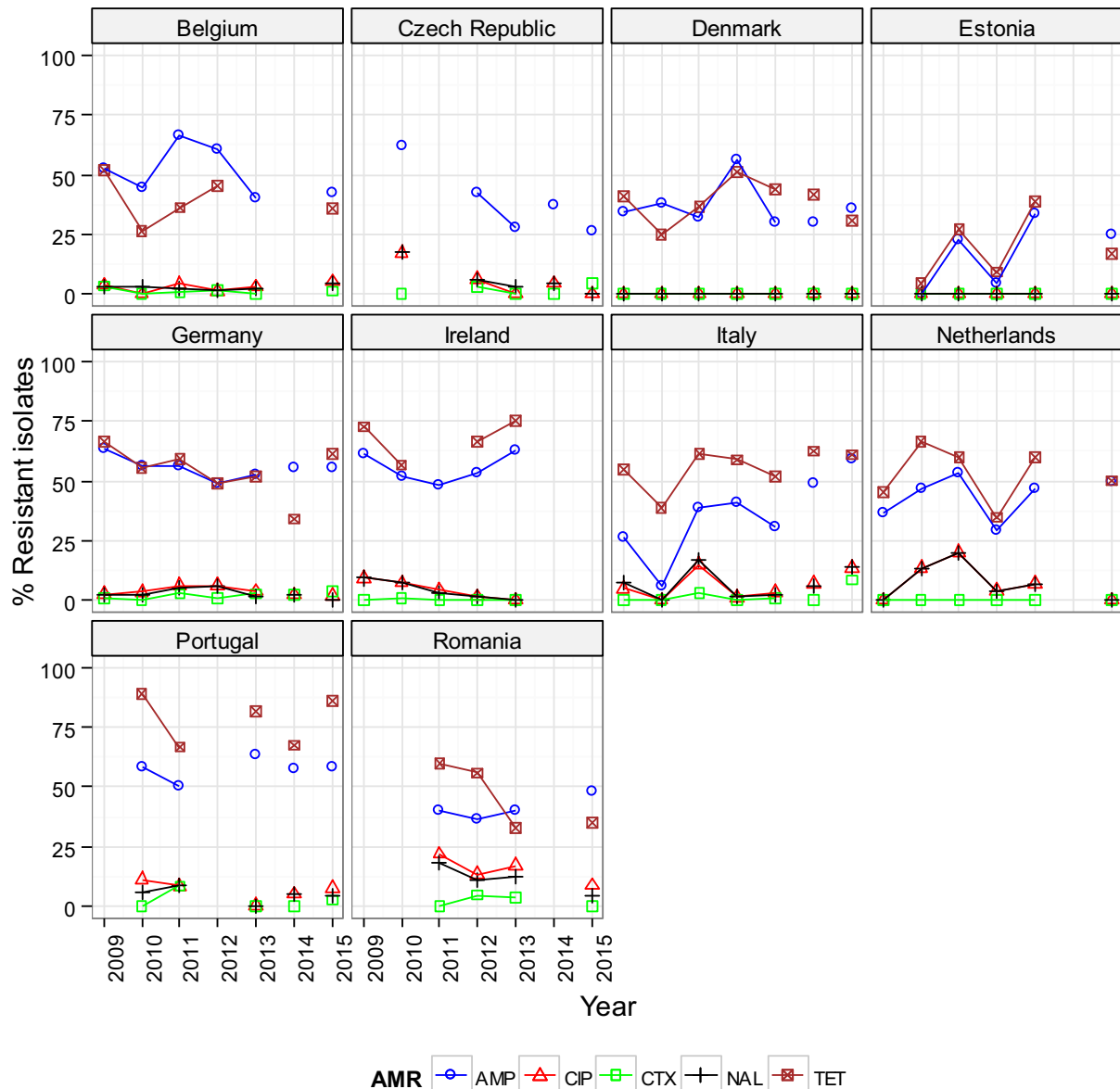
Figure 19: Trends in ampicillin, cefotaxime, ciprofloxacin nalidixic acid and tetracycline resistance in tested *Salmonella* spp. isolates from meat from pigs in reporting MSs, 2009–2015, quantitative data

Multidrug resistance in Salmonella *spp. isolates from carcases of fattening pigs*

Eighteen reporting countries reported data for individual isolates, which were addressed in the MDR analysis (N = 757). From 17.4% to 100% of the *Salmonella* spp. isolates were multiresistant, whereas the proportion of fully susceptible isolates varied from 0% to 80.0% (Figure 20). 'Microbiological' co-resistance to ciprofloxacin and cefotaxime was not observed in any isolate (Table COMSALMPIGMEAT).
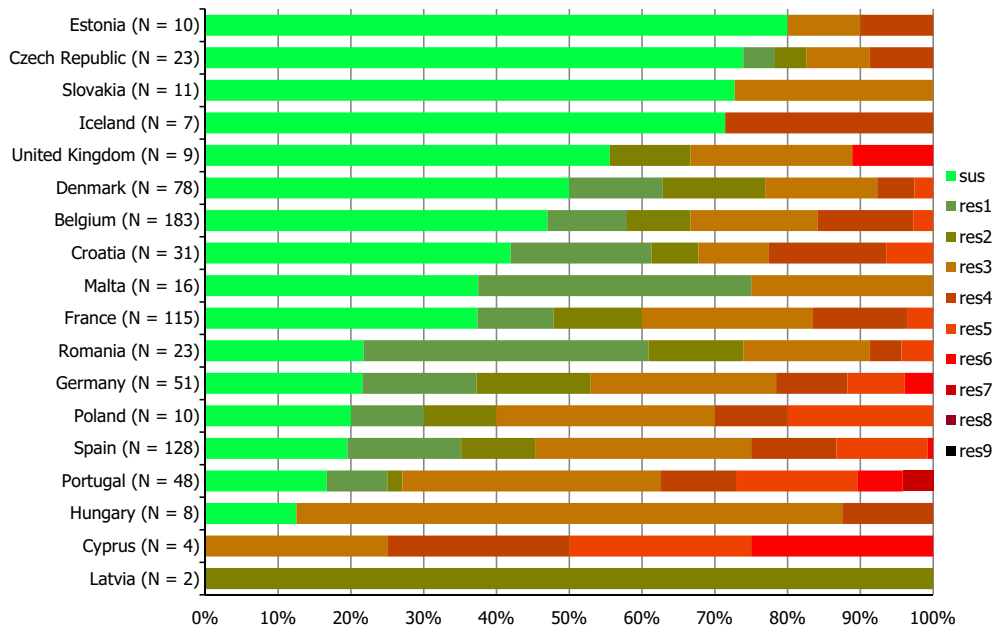
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set of antimicrobials for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 20: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in *Salmonella* spp. from carcases of fattening pigs in reporting countries in 2015

Resistance levels in certain Salmonella *serovars from carcases of fattening pigs*

Among the isolates for which serovar information was provided (N = 729), the most common serovars detected in carcases of fattening pigs (Table SERPIGMEATD) were *S.* Derby (15 MSs, 25.9%), monophasic *S.* Typhimurium, including the antigenic formulas, (14 MSs, 25.7%), *S.* Typhimurium (11 MSs, 18.5%), *S.* Rissen (7 MSs, 7.3%) and *S.* Infantis (9 MSs, 4.3%). Resistance and MDR levels in *S.* Derby were much lower than those recorded in *S.* Typhimurium, monophasic *S.* Typhimurium and *Salmonella* spp.

In **S. Derby** isolates from carcases of fattening pigs (15 MSs, N = 189), resistance to azithromycin, colistin, gentamicin, meropenem, nalidixic acid and tigecycline was not detected; overall resistance to ampicillin and trimethoprim was observed at low levels, whereas ceftazidime and cefotaxime resistance was detected by only one MS. Resistance to sulfamethoxazole and tetracycline ranged from not detected to extremely high (0–100%), with high overall resistance (17.5% and 19.6%, respectively). Resistance to ciprofloxacin was recorded by only two MS (Table 15). It has been shown that 73.0% of *S.* Derby isolates were susceptible to all 11 antimicrobials included in the MDR analysis (50–100%) (Figure 21, Table COMDERBYPIGMEAT).

Overall extremely high resistance to ampicillin, sulfamethoxazole and tetracycline was observed in **monophasic *Salmonella* Typhimurium** isolates from carcases of fattening pigs (N = 187, 13 MSs) (Table 14). In contrast to *S.* Derby, a very high proportion of isolates (73.4%) were multiresistant (41.7–100%) (Figure 22, Table COMMOTYPHIPIGMEAT).
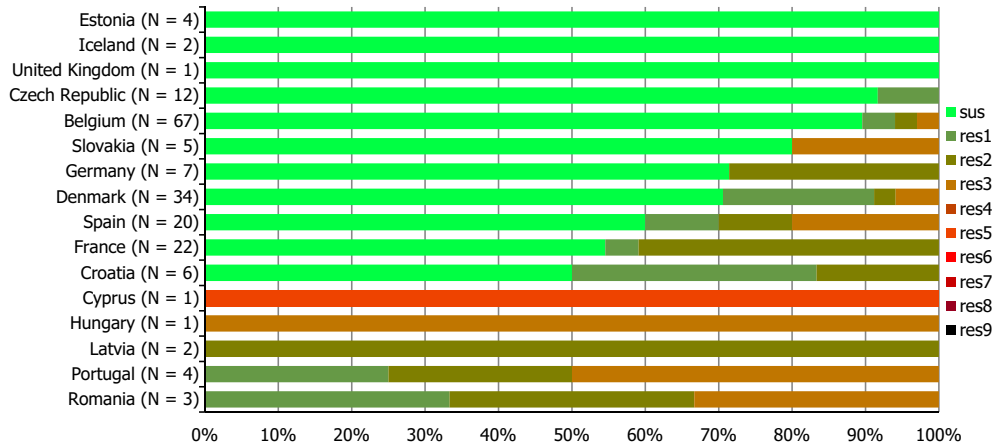
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella* sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 21: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in *Salmonella* Derby from carcases of fattening pigs in reporting countries in 2015
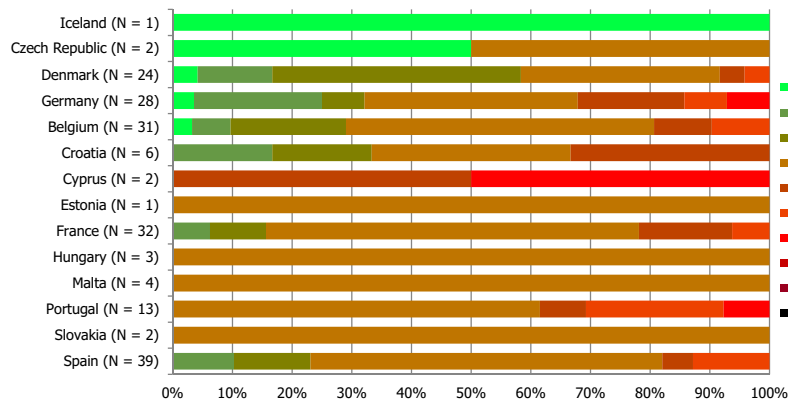
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 22: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in monophasic *Salmonella* Typhimurium from carcases of fattening pigs in MSs in 2015

Overall very high resistance to ampicillin, sulfamethoxazole and tetracycline was observed in *S.* **Typhimurium** isolates from carcases of fattening pigs (N = 135, 11 MSs) (Table 14). Colistin and meropenem resistance was not detected by any MSs. Azithromycin was detected only by Denmark and tigecycline resistance was detected only by Spain. Both cefotaxime and ceftazidime resistance were reported by Belgium, whereas Spain reported only cefotaxime resistance. It is of note that 54.8% of the *S.* Typhimurium isolates originated from Belgium and France, but generally the levels of resistance are comparable to most other reporting MSs. In contrast to *S.* Derby, a high proportion of isolates (54.1%) were multiresistant (28.6–95.5%) (Figure 23, Table COMTYPHIPIGMEAT).
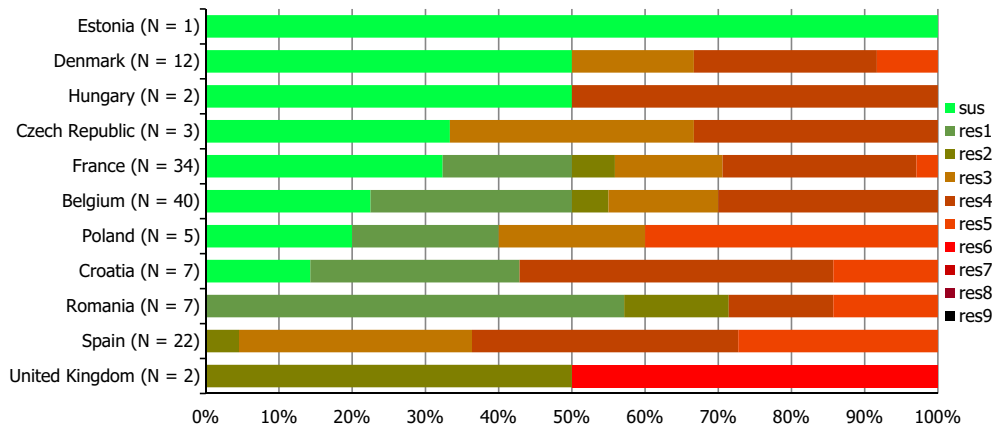
N: total number of isolates tested for susceptibility against the whole harmonised sef of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 23: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in *Salmonella* Typhimurium from carcases of fattening pigs in MSs in 2015

In **S. Rissen** isolates from carcases of fattening pigs (7 MSs, N = 53), resistance to ceftazidime, cefotaxime, ciprofloxacin, gentamicin, meropenem, nalidixic acid and tigecycline was not detected; overall resistance to ampicillin, sulfamethoxazole and trimethoprim was observed at high levels, whereas resistance to colistin was detected by only one MS. Resistance to tetracycline ranged from not detected to extremely high (0–94.1%), with high overall resistance (83.0%). Resistance to azithromycin was recorded by two MSs at very high (65.0%) and moderate (11.8%) levels (Table 15). Similar with *S.* Typhimurium, more than half (52.8%) of *S.* Rissen isolates were multiresistant (0–80%) (Figure 24, Table COMRISSENPIGMEAT).
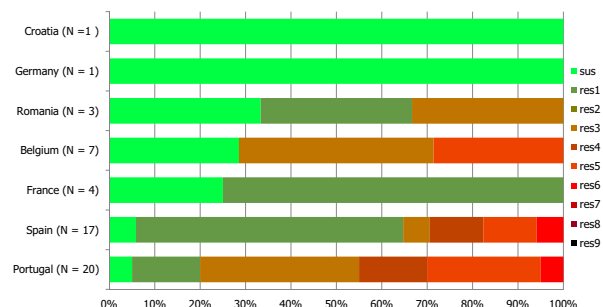
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 24: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in *Salmonella* Rissen from carcases of fattening pigs in MSs in 2015

In **S. Infantis** isolates from carcases of fattening pigs (9 MSs, N = 31), resistance to azithromycin, gentamicin, meropenem and tigecycline was not detected; overall resistance to ciprofloxacin, nalidixic acid, sulfamethoxazole and trimethoprim was observed at high levels, whereas resistance to ampicillin and tetracycline was detected at moderate levels (Table INFANTISPIGMEATD). It is of note that 66.7% of *S.* Infantis isolates were susceptible to all 11 antimicrobials included in the MDR analysis (0.0–100%) (Figure 25, Table COMINFANTISPIGMEAT).
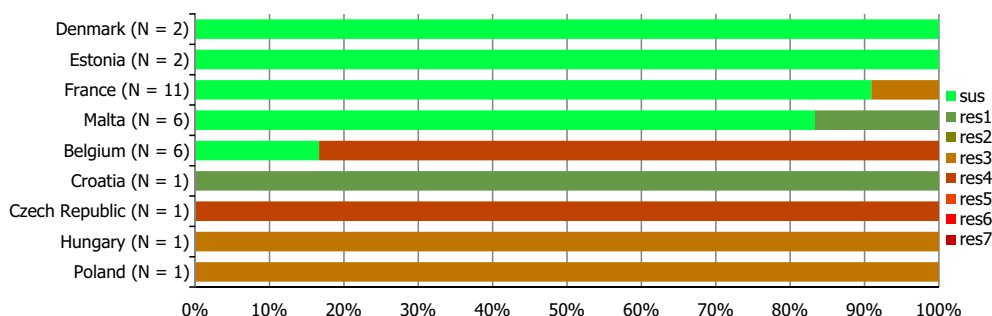
N: total number of isolates tested for susceptibility against the whole harmonised sef of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 25: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in *Salmonella* Infantis from carcases of fattening pigs in MSs in 2015

3.1.2.2. Antimicrobial resistance in *Salmonella* in carcases of bovines under one year of age

Resistance levels in Salmonella *spp. isolates from carcases of bovines under one year of age*

In 2015, seven MSs reported quantitative MIC data in *Salmonella* spp. isolates from carcases of bovines under one year of age (Table 16). Levels of resistance were generally lower than those observed in carcases of fattening pigs. The proportion of multiresistant *Salmonella* spp. isolates varied from none of the isolates tested in Belgium even if only three isolates were tested, to very high levels (54.5–55.6%) in those isolates tested in Croatia and Spain (Figure 26). Co-resistance to ciprofloxacin and cefotaxime was not detected among the multiresistant isolates (seven MSs, N = 80) (Table COMSALMBOVMEAT). *S.* Typhimurium isolates from carcases of bovines under one year of age reported by Croatia (N = 3) and the Czech Republic (N = 2) were multiresistant, whereas only 20% of *S.* Typhimurium isolates from France were multiresistant and all of the Belgium isolates (N = 3) were susceptible to all 11 antimicrobials included in the MDR analysis.
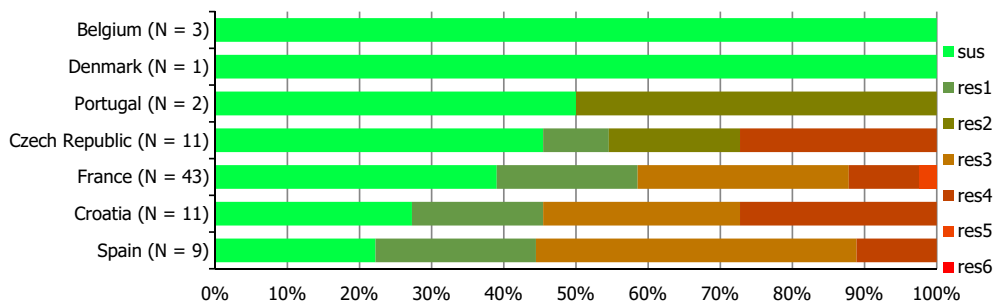
N: total number of isolates tested for susceptibility against the whole harmonised sef of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 26: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobial classes in *Salmonella* spp. from carcases of bovines under one year of age in MSs in 2015

Temporal trends in resistance among Salmonella *spp. meat from bovine animals*

Four MSs provided resistance data on 5 years or more to be included in the statistical analysis. Over the 7 years of data, levels of resistance to ampicillin remained mostly constant for most of the reporting MSs, although slight but statistically significant increases occurred in five MSs, whereas

statistically decreasing trends was observed in one MSs. Within each MS, similar levels of resistance to ciprofloxacin and nalidixic acid were observed from 2009 to 2015. Resistance to cefotaxime is generally very low (Figure 27).

As antimicrobial resistance is associated with particular serovars or clones within serovars, fluctuations in the occurrence of resistance in *Salmonella* spp. isolates within a country may be the result of changes in the proportions of different *Salmonella* serovars which contribute to the total numbers of *Salmonella* spp. isolates.
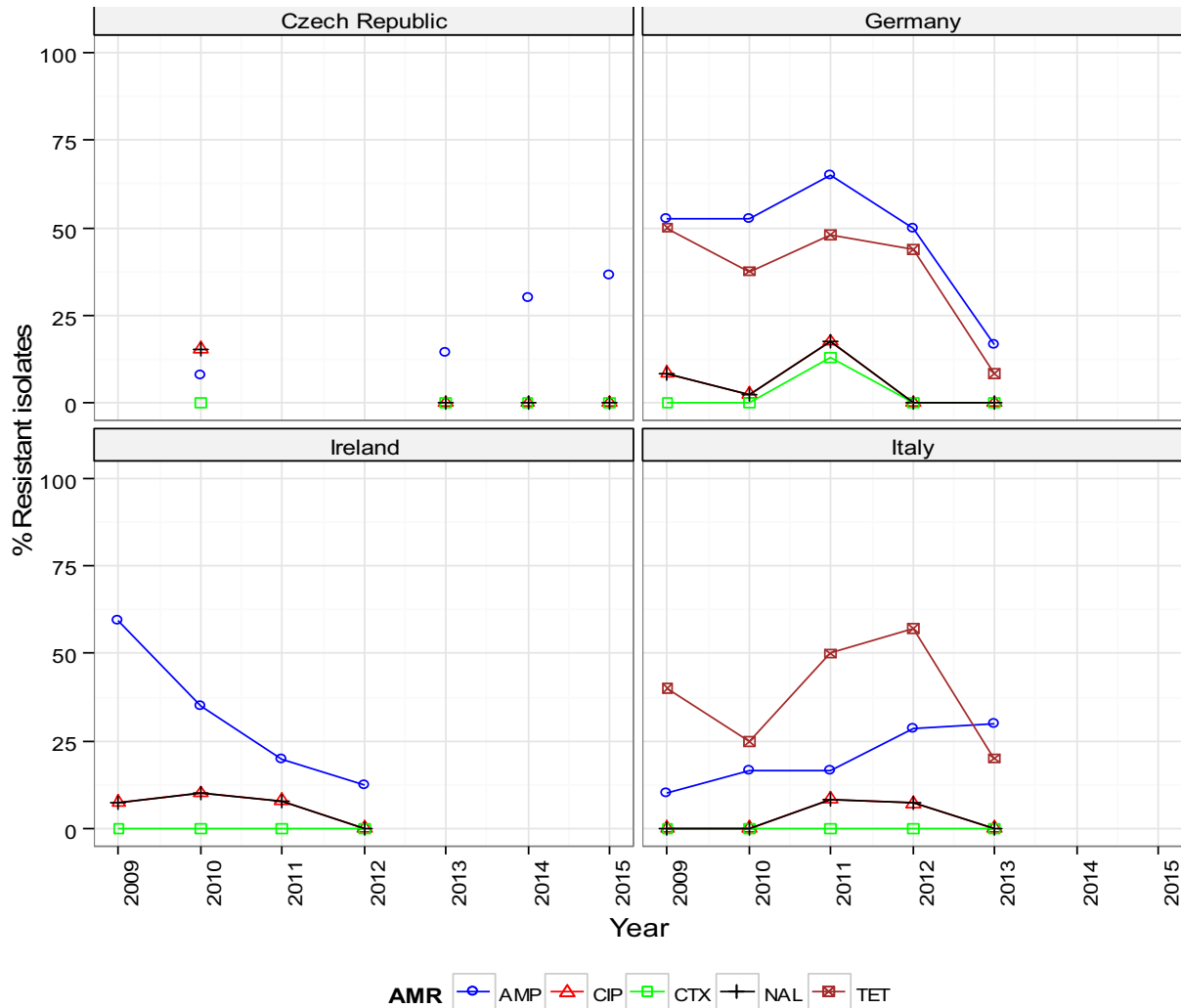
A statistically significant trend for 5 or more years, as tested by a logistic regression model (p ≤ 0.05), was observed in the Germany (↓) for ampicillin.

Figure 27: Trends in ampicillin, cefotaxime, ciprofloxacin nalidixic acid and tetracycline resistance in tested *Salmonella* spp. isolates from meat from bovine animals in reporting MSs, 2009–2015, quantitative data

Table 13: Occurrence of resistance to selected antimicrobials in *Salmonella* spp. isolates from carcases of fattening pigs in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Belgium	183	42.1	183	0.5	183	1.1	183	1.1	183	6.0	183	4.4	183	1.1
Croatia	31	48.4	31	0	31	0	31	0	31	12.9	31	0	31	0
Cyprus	4	75	4	25.0	4	0	4	0	4	25.0	4	25	4	0
Czech Republic	23	26.1	23	0	23	4.3	23	4.3	23	4.3	23	0	23	0
Denmark	78	35.9	78	1.3	78	0	78	0	78	5.1	78	0	78	1.3
Estonia	10	20	10	0	10	0	10	0	10	0	10	0	10	0
France	115	40.9	115	0	115	0	115	0	115	14.8	115	0.9	115	1.7
Germany	51	56.9	51	5.9	51	3.9	51	3.9	51	17.6	51	2	51	0
Hungary	8	87.5	8	0	8	0	8	0	8	25.0	8	12.5	8	0
Latvia	2	0	2	0	2	0	2	0	2	0	2	0	2	0
Malta	16	18.8	16	0	16	0	16	0	16	6.3	16	0	16	6.3
Poland	10	60.0	10	0	10	0	10	0	10	20.0	10	40.0	10	0
Portugal	48	52.1	48	37.5	48	4.2	48	4.2	48	20.8	48	8.3	48	6.3
Romania	23	47.8	23	0	23	0	23	0	23	4.3	23	8.7	23	0
Slovakia	11	27.3	11	0	11	0	11	0	11	0	11	0	11	0
Spain	128	54.7	128	1.6	128	0.8	128	0	128	19.5	128	7	128	0.8
United Kingdom	9	33.3	9	0	9	0	9	0	9	11.1	9	11.1	9	0
Total (17 MSs)	**750**	**44.7**	**750**	**3.5**	**750**	**1.1**	**750**	**0.9**	**750**	**11.9**	**750**	**4.3**	**750**	**1.3**
Iceland	7	28.6	7	0	7	0	7	0	7	0	7	0	7	0

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Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Belgium	183	0.5	183	3.8	183	40.4	183	33.9	183	1.6	183	16.9
Croatia	31	3.2	31	0	31	35.5	31	41.9	31	0	31	16.1
Cyprus	4	50	4	0	4	100	4	100	4	0	4	75.0
Czech Republic	23	0	23	0	23	21.7	23	13.0	23	0	23	4.3
Denmark	78	0	78	0	78	38.5	78	30.8	78	0	78	10.3
Estonia	10	0	10	0	10	20	10	20	10	0	10	10
France	115	1.7	115	0.9	115	53.9	115	54.8	115	0	115	7.8
Germany	51	3.9	51	0	51	56.9	51	62.7	51	3.9	51	17.6
Hungary	8	0	8	12.5	8	75	8	75	8	0	8	0
Latvia	2	0	2	0	2	100	2	100	2	0	2	0
Malta	16	0	16	0	16	62.5	16	25.0	16	0	16	0
Poland	10	0	10	30.0	10	70.0	10	60.0	10	0	10	10.0
Portugal	48	0	48	4.2	48	70.8	48	83.3	48	20.8	48	50.0
Romania	23	4.3	23	4.3	23	30.4	23	34.8	23	0	23	21.7
Slovakia	11	0	11	0	11	27.3	11	18.2	11	0	11	9.1
Spain	128	0.8	128	6.3	128	57.8	128	73.4	128	3.9	128	21.1
United Kingdom	9	11.1	9	11.1	9	44.4	9	33.3	9	0	9	11.1
Total (17 MSs)	**750**	**1.5**	**750**	**3.2**	**750**	**48.5**	**750**	**49.1**	**750**	**2.7**	**750**	**16.8**
Iceland	7	0	7	0	7	28.6	7	28.6	7	0	7	28.6

All *Salmonella* isolates tested were susceptible to meropenem. N: number of isolates tested; % Res: percentage of microbiologically resistant isolates; –: no information available; MSs: Member States.

(a): A number of colistin-resistant isolates are undergoing testing for the presence of *mcr-1* gene. The reported occurrence of colistin resistance is unlikely to equate to the occurrence of *mcr-1*. ECOFF applied 2 mg/L.

(b): ECOFF applied 1 mg/L.

Table 14: Occurrence of resistance to selected antimicrobials in different *Salmonella* Typhimurium and monophasic *S.* Typhimurium from carcases of fattening pigs in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
***Salmonella* Typhimurium**														
Belgium	40	75	40	0	40	2.5	40	2.5	40	10	40	0	40	0
Croatia	7	71.4	7	0	7	0	7	0	7	28.6	7	0	7	0
Czech Republic	3	66.7	3	0	3	0	3	0	3	33.3	3	0	3	0
Denmark	12	50	12	8.3	12	0	12	0	12	16.7	12	0	12	0
Estonia	1	0	1	0	1	0	1	0	1	0	1	0	1	0
France	34	44.1	34	0	34	0	34	0	34	29.4	34	2.9	34	0
Hungary	2	50	2	0	2	0	2	0	2	50	2	0	2	0
Poland	5	60	5	0	5	0	5	0	5	40	5	60	5	0
Romania	7	85.7	7	0	7	0	7	0	7	14.3	7	0	7	0
Spain	22	100	22	0	22	4.5	22	0	22	59.1	22	27.3	22	0
United Kingdom	2	100	2	0	2	0	2	0	2	50	2	0	2	0
Total (11 MSs)	**135**	**68.1**	**135**	**0.7**	**135**	**1.5**	**135**	**0.7**	**135**	**27.4**	**135**	**7.4**	**135**	**0**
Monophasic *Salmonella* Typhimurium														
Belgium	31	87.1	31	3.2	31	0	31	0	31	9.7	31	0	31	0
Croatia	6	83.3	6	0	6	0	6	0	6	16.7	6	0	6	0
Cyprus	2	100	2	50.0	2	0	2	0	2	50	2	0	2	0
Czech Republic	2	50	2	0	2	0	2	0	2	0	2	0	2	0
Denmark	24	83.3	24	0	24	0	24	0	24	4.2	24	0	24	0
Estonia	1	100	1	0	1	0	1	0	1	0	1	0	1	0
France	32	90.6	32	0	32	0	32	0	32	15.6	32	0	32	6.3
Germany	28	75	28	0	28	0	28	0	28	21.4	28	3.6	28	0
Hungary	3	100	3	0	3	0	3	0	3	0	3	0	3	0
Malta	4	75	4	0	4	0	4	0	4	25	4	0	4	0
Portugal	13	100	13	0	13	0	13	0	13	7.7	13	30.8	13	15.4
Slovakia	2	100	2	0	2	0	2	0	2	0	2	0	2	0
Spain	39	89.7	39	0	39	0	39	0	39	12.8	39	7.7	39	0
Total (13 MSs)	**187**	**86.6**	**187**	**1.1**	**187**	**0**	**187**	**0**	**187**	**12.8**	**187**	**4.3**	**187**	**2.1**
Iceland	1	0	1	0	1	0	1	0	1	0	1	0	1	0

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Salmonella Typhimurium												
Belgium	40	0	40	0	40	47.5	40	42.5	40	0	40	25.0
Croatia	7	0	7	0	7	57.1	7	71.4	7	0	7	42.9
Czech Republic	3	0	3	0	3	66.7	3	66.7	3	0	3	0
Denmark	12	0	12	0	12	50.0	12	41.7	12	0	12	33.3
Estonia	1	0	1	0	1	0	1	0	1	0	1	0
France	34	0	34	2.9	34	58.8	34	50	34	0	34	8.8
Hungary	2	0	2	0	2	50.0	2	50	2	0	2	0
Poland	5	0	5	40.0	5	60.0	5	60	5	0	5	0
Romania	7	14.3	7	0	7	28.6	7	42.9	7	0	7	28.6
Spain	22	0	22	27.3	22	90.9	22	100	22	4.5	22	0
United Kingdom	2	50.0	2	0	2	100	2	50	2	0	2	50.0
Total (11 MSs)	**135**	**1.5**	**135**	**6.7**	**135**	**58.5**	**135**	**56.3**	**135**	**0.7**	**135**	**17**
Monophasic *Salmonella* Typhimurium												
Belgium	31	3.2	31	0	31	87.1	31	80.6	31	3.2	31	16.1
Croatia	6	0	6	0	6	83.3	6	83.3	6	0	6	16.7
Cyprus	2	100	2	0	2	100	2	100	2	0	2	50.0
Czech Republic	2	0	2	0	2	50.0	2	50.0	2	0	2	0
Denmark	24	0	24	0	24	83.3	24	54.2	24	0	24	8.3
Estonia	1	0	1	0	1	100	1	100	1	0	1	0
France	32	6.3	32	0	32	87.5	32	96.9	32	0	32	9.4
Germany	28	7.1	28	0	28	85.7	28	78.6	28	0	28	21.4
Hungary	3	0	3	0	3	100	3	100	3	0	3	0
Malta	4	0	4	0	4	100	4	100	4	0	4	0
Portugal	13	0	13	15.4	13	100	13	100	13	7.7	13	30.8
Slovakia	2	0	2	0	2	100	2	100	2	0	2	0
Spain	39	2.6	39	5.1	39	79.5	39	92.3	39	0	39	12.8
Total (13 MSs)	**187**	**4.3**	**187**	**2.1**	**187**	**86.1**	**187**	**84.5**	**187**	**1.1**	**187**	**14.4**
Iceland	1	0	1	0	1	0	1	0	1	0	1	0

All *Salmonella* isolates tested were susceptible to meropenem. N: number of isolates tested; % Res: percentage of microbiologically resistant isolates.
(a): A number of colistin-resistant isolates are undergoing testing for the presence of the *mcr-1* gene. The reported occurrence of colistin resistance does not equate to the occurrence of *mcr-1*.
   ECOFF applied 2 mg/L.
(b): ECOFF applied 1 mg/L.

Table 15: Occurrence of resistance to selected antimicrobials in different *Salmonella* Derby and *S.* Rissen from carcases of fattening pigs in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Salmonella Derby														
Belgium	67	3	67	0	67	0	67	0	67	0	67	1.5	67	1.5
Croatia	6	33.3	6	0	6	0	6	0	6	0	6	0	6	0
Cyprus	1	100	1	0	1	0	1	0	1	0	1	100	1	0
Czech Republic	12	8.3	12	0	12	0	12	0	12	0	12	0	12	0
Denmark	34	5.9	34	0	34	0	34	0	34	2.9	34	0	34	0
Estonia	4	0	4	0	4	0	4	0	4	0	4	0	4	0
France	22	0	22	0	22	0	22	0	22	0	22	0	22	0
Germany	7	28.6	7	0	7	28.6	7	28.6	7	0	7	0	7	0
Hungary	1	100	1	0	1	0	1	0	1	100	1	0	1	0
Latvia	2	0	2	0	2	0	2	0	2	0	2	0	2	0
Portugal	4	0	4	0	4	0	4	0	4	0	4	0	4	0
Romania	3	66.7	3	0	3	0	3	0	3	0	3	0	3	0
Slovakia	5	20	5	0	5	0	5	0	5	0	5	0	5	0
Spain	20	0	20	0	20	0	20	0	20	0	20	0	20	0
United Kingdom	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Total (15 MSs)	**189**	**7.4**	**189**	**0**	**189**	**1.1**	**189**	**1.1**	**189**	**1.1**	**189**	**1.1**	**189**	**0.5**
Iceland	2	0	2	0	2	0	2	0	2	0	2	0	2	0
Salmonella Rissen														
Belgium	7	42.9	7	0	7	0	7	0	7	42.9	7	0	7	0
Croatia	1	0	1	0	1	0	1	0	1	0	1	0	1	0
France	4	0	4	0	4	0	4	0	4	0	4	0	4	0
Germany	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Portugal	20	40	20	65	20	0	20	0	20	30	20	0	20	5
Romania	3	33.3	3	0	3	0	3	0	3	0	3	0	3	0
Spain	17	29.4	17	11.8	17	0	17	0	17	5.9	17	0	17	0
Total (7 MSs)	**53**	**32.1**	**53**	**28.3**	**53**	**0**	**53**	**0**	**53**	**18.9**	**53**	**0**	**53**	**1.9**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline[(b)]		Tigecycline		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Salmonella Derby												
Belgium	67	0	67	0	67	6	67	4.5	67	0	67	4.5
Croatia	6	0	6	0	6	0	6	33.3	6	0	6	0
Cyprus	1	0	1	0	1	100	1	100	1	0	1	100
Czech Republic	12	0	12	0	12	0	12	0	12	0	12	0
Denmark	34	0	34	0	34	11.8	34	17.6	34	0	34	5.9
Estonia	4	0	4	0	4	0	4	0	4	0	4	0
France	22	0	22	0	22	45.5	22	40.9	22	0	22	0
Germany	7	0	7	0	7	0	7	0	7	0	7	0
Hungary	1	0	1	0	1	0	1	100	1	0	1	0
Latvia	2	0	2	0	2	100	2	100	2	0	2	0
Portugal	4	0	4	0	4	75	4	100	4	0	4	50
Romania	3	0	3	0	3	66.7	3	33.3	3	0	3	33.3
Slovakia	5	0	5	0	5	20	5	0	5	0	5	20
Spain	20	0	20	0	20	30	20	40	20	0	20	20
United Kingdom	1	0	1	0	1	0	1	0	1	0	1	0
Total (15 MSs)	**189**	**0**	**189**	**0**	**189**	**17.5**	**189**	**19.6**	**189**	**0**	**189**	**7.4**
Iceland	2	0	2	0	2	0	2	0	2	0	2	0
Salmonella Rissen												
Belgium	7	0	7	0	7	71.4	7	57.1	7	14.3	7	42.9
Croatia	1	0	1	0	1	0	1	0	1	0	1	0
France	4	0	4	0	4	0	4	75	4	0	4	0
Germany	1	0	1	0	1	0	1	0	1	0	1	0
Portugal	20	0	20	0	20	70	20	95	20	30.0	20	70
Romania	3	0	3	0	3	33.3	3	66.7	3	0	3	0
Spain	17	0	17	0	17	35.3	17	94.1	17	17.6	17	35.3
Total (7 MSs)	**53**	**0**	**53**	**0**	**53**	**49.1**	**53**	**83.0**	**53**	**18.9**	**53**	**43.4**

All *Salmonella* isolates tested were susceptible to meropenem. N: number of isolates tested; % Res: percentage of microbiologically resistant isolates.
(a): A number of colistin-resistant isolates are undergoing testing for the presence of the *mcr-1* gene. The reported occurrence of colistin resistance does not equate to the occurrence of *mcr-1*.
  ECOFF applied 2 mg/L.
(b): ECOFF applied 1 mg/L.

Table 16: Occurrence of resistance to selected antimicrobials in *Salmonella* spp. isolates from carcases of bovines under one year of age in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin(a)	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Belgium	3	0	3	0	3	0	3	0	3	0	3	0	3	0
Croatia	11	54.5	11	0	11	0	11	0	11	0	11	18.2	11	0
Czech Republic	11	36.4	11	0	11	0	11	0	11	18.2	11	0	11	0
Denmark	1	0	1	0	1	0	1	0	1	0	1	0	1	0
France	43	34.9	43	0	43	0	43	0	43	11.6	43	0	43	2.3
Portugal	2	50	2	50	2	0	2	0	2	50.0	2	0	2	0
Spain	9	66.7	9	0	9	0	9	0	9	0	9	0	9	0
Total (7 MSs)	80	40.0	80	1.3	80	0	80	0	80	10.0	80	2.5	80	1.3

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline(b)		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Belgium	3	0	3	0	3	0	3	0	3	0	3	0
Croatia	11	0	11	0	11	54.5	11	54.5	11	0	11	27.3
Czech Republic	11	9.1	11	0	11	45.5	11	36.4	11	0	11	9.1
Denmark	1	0	1	0	1	100	1	100	1	0	1	0
France	43	0	43	0	43	51.2	43	51.2	43	4.7	43	4.7
Portugal	2	0	2	0	2	50	2	100	2	0	2	50.0
Spain	9	0	9	0	9	55.6	9	66.7	9	0	9	11.1
Total (7 MSs)	80	1.3	80	0	80	50.0	80	51.3	80	2.5	80	10.0

All *Salmonella* isolates tested were susceptible to meropenem. N: number of isolates tested; % Res: percentage of microbiologically resistant isolates; –: no information available; MSs: Member.
(a): A number of colistin-resistant isolates are undergoing testing for the presence of the *mcr-1* gene. The reported occurrence of colistin resistance does not equate to the occurrence of *mcr-1*.
ECOFF applied 2 mg/L.
(b): ECOFF applied 1 mg/L.

Table 17: Occurrence of resistance to selected antimicrobials in different *Salmonella* serovars from carcases of bovines under one year of age in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
***Salmonella* Typhimurium**														
Belgium	3	0	3	0	3	0	3	0	3	0	3	0	3	0
Croatia	3	100	3	0	3	0	3	0	3	0	3	0	3	0
Czech Republic	2	100	2	0	2	0	2	0	2	100	2	0	2	0
France	5	40	5	0	5	0	5	0	5	20	5	0	5	0
Total (4 MSs)	**13**	**53.8**	**13**	**0**	**13**	**0**	**13**	**0**	**13**	**23.1**	**13**	**0**	**13**	**0**
Monophasic *Salmonella* Typhimurium														
Croatia	1	100	1	0	1	0	1	0	1	0	1	0	1	0
Denmark	1	0	1	0	1	0	1	0	1	0	1	0	1	0
France	6	66.7	6	0	6	0	6	0	6	16.7	6	0	6	0
Spain	6	100	6	0	6	0	6	0	6	0	6	0	6	0
Total (4 MSs)	**14**	**78.6**	**14**	**0**	**14**	**0**	**14**	**0**	**14**	**7.1**	**14**	**0**	**14**	**0**
***Salmonella* Derby**														
Croatia	2	0	2	0	2	0	2	0	2	0	2	50	2	0
Czech Republic	2	0	2	0	2	0	2	0	2	0	2	0	2	0
France	8	12.5	8	0	8	0	8	0	8	0	8	0	8	0
Portugal	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Total (4 MSs)	**13**	**7.7**	**13**	**0**	**13**	**0**	**13**	**0**	**13**	**0**	**13**	**7.7**	**13**	**0**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Salmonella Typhimurium												
Belgium	3	0	3	0	3	0	3	0	3	0	3	0
Croatia	3	0	3	0	3	100	3	100	3	0	3	33.3
Czech Republic	2	0	2	0	2	100	2	100	2	0	2	0
France	5	0	5	0	5	60.0	5	20	5	0	5	0
Total (4 MSs)	**13**	**0**	**13**	**0**	**13**	**61.5**	**13**	**46.2**	**13**	**0**	**13**	**7.7**
Monophasic *Salmonella* Typhimurium												
Croatia	1	0	1	0	1	100	1	100	1	0	1	0
Denmark	1	0	1	0	1	100	1	100	1	0	1	0
France	6	0	6	0	6	83.3	6	100	6	0	6	16.7
Spain	6	0	6	0	6	83.3	6	83.3	6	0	6	16.7
Total (4 MSs)	**14**	**0**	**14**	**0**	**14**	**85.7**	**14**	**92.9**	**14**	**0**	**14**	**14.3**
Salmonella Derby												
Croatia	2	0	2	0	2	0	2	0	2	0	2	0
Czech Republic	2	50	2	0	2	50	2	0	2	0	2	0
France	8	0	8	0	8	50	8	50.0	8	25.0	8	0
Portugal	1	0	1	0	1	0	1	100	1	0	1	0
Total (4 MSs)	**13**	**7.7**	**13**	**0**	**13**	**38.5**	**13**	**38.5**	**13**	**15.4**	**13**	**0**

All *Salmonella* isolates tested were susceptible to meropenem. N: number of isolates tested; % Res: percentage of microbiologically resistant isolates.

(a): A number of colistin-resistant isolates are undergoing testing for the presence of the *mcr-1* gene. The reported occurrence of colistin resistance does not equate to the occurrence of *mcr-1*. ECOFF applied 2 mg/L.

(b): ECOFF applied 1 mg/L.

3.1.2.3. Antimicrobial resistance in *Salmonella* spp. in fattening pigs

Resistance levels in Salmonella spp. isolates from fattening pigs

In 2015, six MSs reported on *Salmonella* spp. in fattening pigs (Table 18). Most MSs recorded high to extremely high resistance to ampicillin, sulfamethoxazole and tetracycline, with overall resistance at 45.3%, 52.6% and 53.5%, respectively. Overall resistance to trimethoprim was moderate at 17.2%. Resistance to chloramphenicol, ciprofloxacin, nalidixic acid, gentamicin and tigecycline was overall low, although resistance levels varied markedly from none to 22.7% between reporting MSs. Resistance to cefotaxime and ceftazidime was detected only by Italy at low levels. Resistance to azithromycin was detected only by Denmark at very low level. Colistin resistance was not detected by any of the MSs reporting 2016 data.

Multidrug resistance in Salmonella spp. isolates from fattening pigs

Six MSs submitted isolate-based data included in the MDR analysis (N = 424). Situations varied markedly between MSs, as from 27.3.6% to 100% of the *Salmonella* spp. isolates were multiresistant, and none to 51.1% of them were fully susceptible to the nine antimicrobial classes considered (Figure 28) (Table COMSALMFATPIG). 'Microbiological' co-resistance to ciprofloxacin and cefotaxime was observed at low level (2.2%) in only one MS of the six MSs and the 'clinical' resistance to both ciprofloxacin and cefotaxime was not detected.
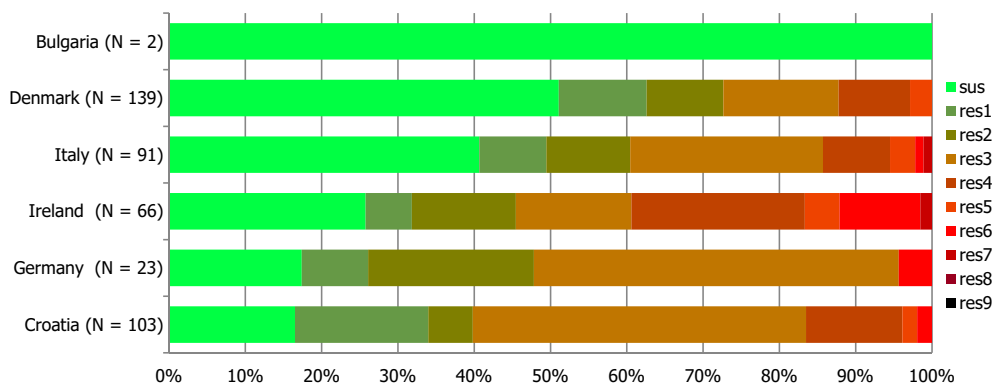
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 28: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobials classes in *Salmonella* spp. from fattening pigs in MSs in 2015

*Spatial trends in resistance among* Salmonella *spp. from fattening pigs*

Ciprofloxacin resistance was reported by only three MSs from southern and western Europe (Croatia, Italy and Ireland) (Figure 29). Low resistance to cefotaxime was reported in one MS (Figure 30).

Figure 29: Spatial distribution of ciprofloxacin resistance among *Salmonella* spp. from fattening pigs in countries reporting MIC data in 2015

Figure 30: Spatial distribution of cefotaxime resistance among *Salmonella* spp. fattening pigs reporting MIC data in 2015

Temporal trends in resistance among Salmonella *spp. from pigs*

Eight MSs provided resistance data on 5 years or more to be included in the statistical analysis. Over the 7 years of data, levels of resistance to ampicillin remained mostly constant for most of the reporting MSs, although slight but statistically significant increases occurred in the Netherlands. Statistically significant decreasing trends in resistance to ciprofloxacin and nalidixic acid were registered in Italy, whereas statistically significant increasing trend to ciprofloxacin was observed in Estonia. Resistance to cefotaxime is generally very low; however, a statistically significant increasing trend was observed in Italy. Statistically significant increasing trend to tetracycline was observed in the Netherlands and decreasing trend in Italy (Figure 31).

As antimicrobial resistance is associated with particular serovars or clones within serovars, fluctuations in the occurrence of resistance in *Salmonella* spp. isolates within a country may be the result of changes in the proportions of different *Salmonella* serovars which contribute to the total numbers of *Salmonella* spp. isolates. As observed in isolates from pig meat, fluctuations in resistance levels to tetracyclines and ampicillin tended to parallel each other.
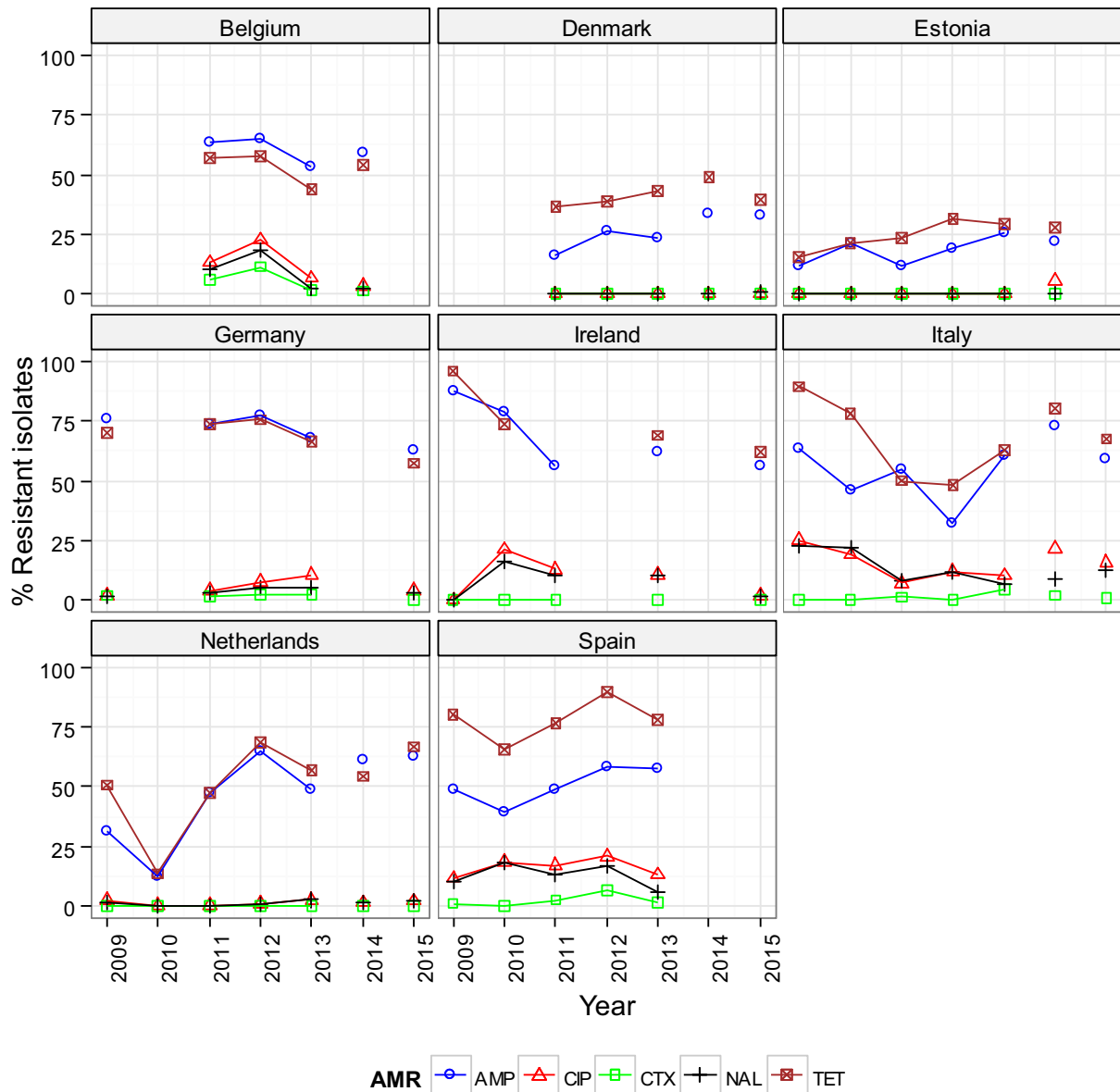
Figure 31: Trends in ampicillin, cefotaxime, ciprofloxacin nalidixic acid and tetracycline resistance in tested *Salmonella* spp. isolates from pigs in reporting MSs, 2009–2015, quantitative data

A statistically significant trend for 5 or more years, as tested by a logistic regression model (p ≤ 0.05), was observed in the Italy (↓) for both ciprofloxacin and nalidixic acid, for ampicillin in the Netherlands(↑), for ciprofloxacin in Estonia(↑), for cefotaxime in Italy (↑), and for tetracycline in Italy (↓) and the Netherlands (↑).

Table 18: Occurrence of resistance to selected antimicrobials in *Salmonella* spp. isolates from fattening pigs in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
2015														
Bulgaria	2	100	2	0	2	0	2	0	2	0	2	0	2	0
Croatia	103	48.5	103	0	103	0	103	0	103	4.9	103	11.7	103	0
Denmark	139	33.1	139	0.7	139	0	139	0	139	5.8	139	0	139	0
Germany	23	73.9	23	0	23	0	23	0	23	4.3	23	0	23	0
Ireland	66	56.1	66	0	66	0	66	0	66	21.2	66	1.5	66	0
Italy	91	44	91	0	91	3.3	91	2.2	91	11	91	7.7	91	0
Total (6 MSs)	**424**	**45.3**	**424**	**0.2**	**424**	**0.7**	**424**	**0.5**	**424**	**9**	**424**	**4.7**	**424**	**0**
2014														
Finland	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Netherlands	70	61.4	70	0	70	0	70	0	70	10	70	1.4	70	7.1
Total (2 MSs)	**71**	**60.6**	**71**	**0**	**71**	**0**	**71**	**0**	**71**	**9.9**	**71**	**1.4**	**71**	**7**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
2015												
Bulgaria	2	0	2	0	2	100	2	100	2	0	2	0
Croatia	103	1	103	3.9	103	64.1	103	65	103	1	103	35.9
Denmark	139	3.6	139	0.7	139	36	139	39.6	139	0	139	10.1
Germany	23	0	23	0	23	69.6	23	65.2	23	4.3	23	4.3
Ireland	66	22.7	66	1.5	66	71.2	66	62.1	66	7.6	66	24.2
Italy	91	2.2	91	6.6	91	46.2	91	51.6	91	0	91	5.5
Total (6 MSs)	**424**	**5.4**	**424**	**2.8**	**424**	**52.6**	**424**	**53.5**	**424**	**1.7**	**424**	**17.2**
2014												
Finland	1	0	1	0	1	0	1	0	1	0	1	0
Netherlands	70	2.9	70	1.4	70	58.6	70	54.3	70	2.9	70	12.9
Total (2 MSs)	**71**	**2.8**	**71**	**1.4**	**71**	**57.7**	**71**	**53.5**	**71**	**2.8**	**71**	**12.7**

All *Salmonella* isolates tested were susceptible to meropenem.
N: number of isolates tested; % Res: percentage of microbiologically resistant isolates; –: no information available; MSs: Member States.
(a): A number of colistin-resistant isolates are undergoing testing for the presence of *mcr-1* gene. The reported occurrence of colistin resistance is unlikely to equate to the occurrence of *mcr-1*.
ECOFF applied 2 mg/L.
(b): ECOFF applied 1 mg/L..

3.1.2.4. Antimicrobial resistance in certain *Salmonella* serovars in fattening pigs

Resistance levels in S. *Derby isolates from fattening pigs*

S. Derby was the first most frequently reported serovars in fattening pigs, accounting for 34.9% of the *Salmonella* isolates serotyped (N = 416) (Table SERFATPIGSD). In *S.* Derby isolates from fattening pigs (5 MSs, Table 19), resistance to sulfamethoxazole and tetracycline varied considerably from none to extremely high and overall was at high levels (28.3% and 38.6%, respectively), whereas resistance to ampicillin overall was low (7.6%). Only two MSs observed resistance to chloramphenicol (overall 2.1%). Croatia recorded resistance to moderate resistance to ciprofloxacin (18.2%), but without any resistance to nalidixic acid. It is notable that isolates from Denmark comprised 52.4% of the *S.* Derby isolates.

Multidrug resistance in S. *Derby isolates from fattening pigs*

Only 20.0% of the *S.* Derby isolates, reported by five MSs, from fattening pigs (5 MSs, N = 145) included in the MDR analysis were multiresistant (Figure 32). 'Microbiological' co-resistance to ciprofloxacin and cefotaxime was not detected by any MS (Table COMDERBYFATPIG).
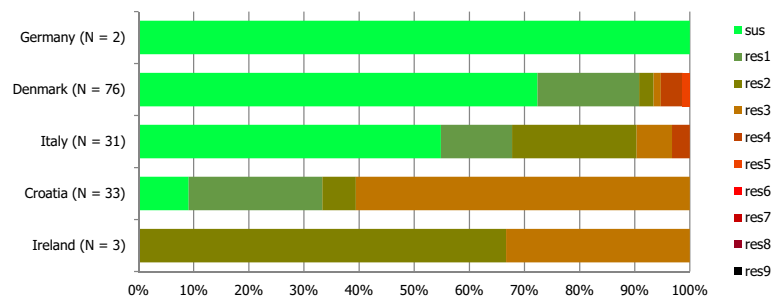
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 32: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobials classes in *Salmonella* Derby from fattening pigs in MSs in 2015

Resistance levels in monophasic S. *Typhimurium isolates from fattening pigs*

Monophasic S. Typhimurium was the second most frequently reported serovar in fattening pigs, accounting for 31.3%, of the *Salmonella* isolates serotyped (N = 416) (Table SERFATPIGSD). Among monophasic *S.* Typhimurium isolates from fattening pigs (5 MSs, Table 19), the overall resistance to ampicillin, sulfamethoxazole and tetracycline was at extremely high levels (92.3%, 92.3% and 85.4%, respectively). High levels of resistance to gentamicin were reported by Ireland. Resistance to nalidixic acid and ciprofloxacin was reported in monophasic *S.* Typhimurium at moderate levels (17.9%) only by Italy.

Multidrug resistance in monophasic S. *Typhimurium isolates from fattening pigs*

Most of the monophasic *S.* Typhimurium isolates (82.3%) were multiresistant (5 MSs, N = 130) (Figure 33). 'Microbiological' resistance to cefotaxime and ceftazidime was only reported by Italy in a single isolate of monophasic *S.* Typhimurium (Table COMMOTYPHIPIG).
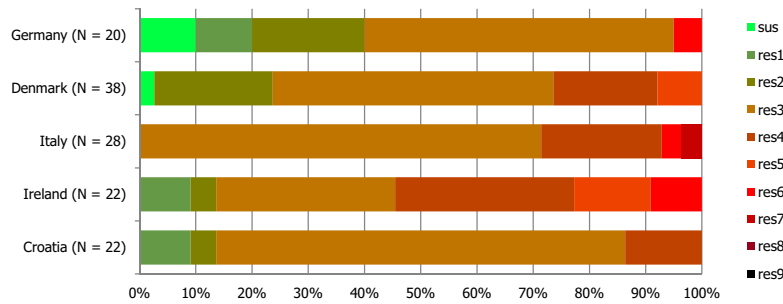
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 33: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobials classes in monophasic *Salmonella* Typhimurium from fattening pigs in MSs in 2015

Resistance levels in S. *Typhimurium isolates from fattening pigs*

S. Typhimurium was the third most frequently reported serovar in fattening pigs, accounting for 15.1% of the *Salmonella* isolates serotyped (N = 416) (Table SERFATPIGSD). In *S.* Typhimurium isolates from fattening pigs (5 MSs, Table 19), the overall levels of resistance to ampicillin, sulfamethoxazole and tetracycline were lower than in monophasic *S.* Typhimurium and higher than in *Salmonella* spp. Azithromycin resistance was not detected in any MS. As in the case of monophasic *Salmonella* Typhimurium, resistance to cefotaxime and ceftazidime was reported only by Italy. It is of note that Croatia accounted for 34.9% of the *S.* Typhimurium isolates analysed.

Multidrug resistance in S. *Typhimurium isolates from fattening pigs*

In *S.* Typhimurium isolates from fattening pigs (5 MSs, N = 63) 52.4% of the isolates included in the MDR analysis were multiresistant (Figure 34, Table COMTYPHIFATPIG). 'Microbiological' co-resistance to ciprofloxacin and cefotaxime was detected in one isolate in Italy (20.0%) (Table COMTYPHIFATPIG). However, when the resistance to ciprofloxacin and cefotaxime was interpreted using CBPs, no isolates displayed 'clinical' resistance.
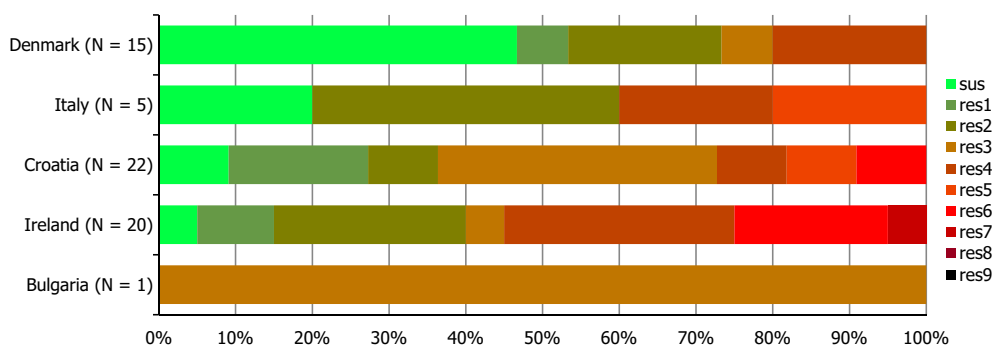
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 34: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobials classes in *Salmonella* Typhimurium from fattening pigs in MSs in 2015

Table 19: Occurrence of resistance to selected antimicrobials in different *Salmonella* serovars from fattening pigs in 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[(a)]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
***Salmonella* Typhimurium**														
Bulgaria	1	100	1	0	1	0	1	0	1	0	1	0	1	0
Croatia	22	86.4	22	0	22	0	22	0	22	18.2	22	18.2	22	0
Denmark	15	33.3	15	0	15	0	15	0	15	20	15	0	15	0
Ireland	20	70	20	0	20	0	20	0	20	45	20	5	20	0
Italy	5	80	5	0	5	40	5	20	5	80	5	20	5	0
Total (5 MSs)	**63**	**68.3**	**63**	**0**	**63**	**3.2**	**63**	**1.6**	**63**	**31.7**	**63**	**9.5**	**63**	**0**
Monophasic *Salmonella* Typhimurium														
Croatia	22	100	22	0	22	0	22	0	22	4.5	22	0	22	0
Denmark	38	89.5	38	2.6	38	0	38	0	38	7.9	38	0	38	0
Germany	20	85	20	0	20	0	20	0	20	5	20	0	20	0
Ireland	22	86.4	22	0	22	0	22	0	22	18.2	22	0	22	0
Italy	28	100	28	0	28	3.6	28	3.6	28	10.7	28	17.9	28	0
Total (5 MSs)	**130**	**92.3**	**130**	**0.8**	**130**	**0.8**	**130**	**0.8**	**130**	**9.2**	**130**	**3.8**	**130**	**0**
***Salmonella* Derby**														
Croatia	33	3	33	0	33	0	33	0	33	0	33	18.2	33	0
Denmark	76	9.2	76	0	76	0	76	0	76	2.6	76	0	76	0
Germany	2	0	2	0	2	0	2	0	2	0	2	0	2	0
Ireland	3	0	3	0	3	0	3	0	3	0	3	0	3	0
Italy	31	9.7	31	0	31	0	31	0	31	3.2	31	3.2	31	0
Total (5 MSs)	**145**	**7.6**	**145**	**0**	**145**	**0**	**145**	**0**	**145**	**2.1**	**145**	**4.8**	**145**	**0**
***Salmonella* Rissen**														
Croatia	3	0	3	0	3	0	3	0	3	0	3	0	3	0
Denmark	2	0	2	0	2	0	2	0	2	0	2	0	2	0
Italy	4	0	4	0	4	0	4	0	4	0	4	0	4	0
Total (3 MSs)	**9**	**0**	**9**	**0**	**9**	**0**	**9**	**0**	**9**	**0**	**9**	**0**	**9**	**0**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
***Salmonella* Typhimurium**												
Bulgaria	1	0	1	0	1	100	1	100	1	0	1	0
Croatia	22	4.5	22	13.6	22	68.2	22	63.6	22	4.5	22	18.2
Denmark	15	0	15	0	15	53.3	15	20	15	0	15	20
Ireland	20	15	20	5	20	90	20	65	20	20	20	40
Italy	5	0	5	0	5	0	5	20	5	0	5	20
Total (5 MSs)	**63**	**6.3**	**63**	**6.3**	**63**	**66.7**	**63**	**50.8**	**63**	**7.9**	**63**	**25.4**
Monophasic *Salmonella* Typhimurium												
Croatia	22	0	22	0	22	90.9	22	81.8	22	0	22	13.6
Denmark	38	10.5	38	0	38	94.7	38	84.2	38	0	38	18.4
Germany	20	0	20	0	20	75	20	70	20	5	20	5
Ireland	22	45.5	22	0	22	95.5	22	90.9	22	0	22	27.3
Italy	28	7.1	28	17.9	28	100	28	96.4	28	0	28	7.1
Total (5 MSs)	**130**	**12.3**	**130**	**3.8**	**130**	**92.3**	**130**	**85.4**	**130**	**0.8**	**130**	**14.6**
***Salmonella* Derby**												
Croatia	33	0	33	0	33	63.6	33	69.7	33	0	33	63.6
Denmark	76	0	76	1.3	76	7.9	76	23.7	76	0	76	5.3
Germany	2	0	2	0	2	0	2	0	2	0	2	0
Ireland	3	0	3	0	3	100	3	100	3	0	3	33.3
Italy	31	0	31	3.2	31	35.5	31	38.7	31	0	31	0
Total (5 MSs)	**145**	**0**	**145**	**1.4**	**145**	**28.3**	**145**	**38.6**	**145**	**0**	**145**	**17.9**

All *Salmonella* isolates tested were susceptible to meropenem. N: number of isolates tested; % Res: percentage of microbiologically resistant isolates.
(a): A number of colistin-resistant isolates are undergoing testing for the presence of the *mcr-1* gene. The reported occurrence of colistin resistance does not equate to the occurrence of *mcr-1*.
ECOFF applied 2 mg/L.
(b): ECOFF applied 1 mg/L.

3.1.2.5. Antimicrobial resistance in *Salmonella* spp. in calves under one year of age

Resistance levels in Salmonella *spp. isolates from calves under one year of age*

In 2015, three MSs reported data on *Salmonella* spp. in calves under one year of age (Table 20). Italy registered higher levels of resistance to most antimicrobials tested, when compared with Spain. Resistance to cefotaxime and ceftazidime was not detected. The low numbers of isolates tested mean that the results may be subject to the inherent variation associated with small sample sizes.

Multidrug resistance in Salmonella *spp. isolates from calves under one year of age*

More than one-third (37.8%) of the *Salmonella* spp. isolates included in the MDR analysis (3 MSs, N = 45) were multiresistant (Figure 35), at levels of 26.7% in Croatia, 18.8% in Spain and 71.4% in Italy. 'Microbiological' co-resistance to ciprofloxacin and cefotaxime was not detected (Table COMSALMCALV).
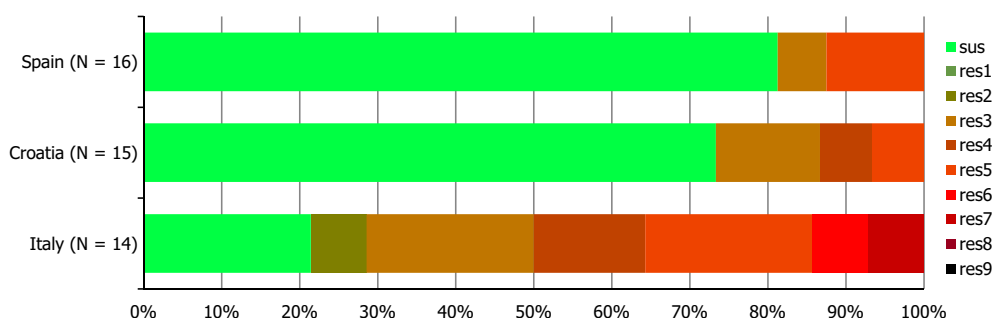
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Salmonella*; sus: susceptible to all antimicrobial classes of the harmonised set for *Salmonella*; res1–res9: resistance to one up to nine antimicrobial classes of the harmonised set for *Salmonella*.

Figure 35: Frequency distribution of completely susceptible isolates and resistant isolates to one to nine antimicrobials classes in *Salmonella* spp. from calves under one year of age in MSs in 2015

Spatial trends in resistance among Salmonella *spp. from calves under one year of age*

The levels of resistance to ciprofloxacin in *Salmonella* spp. from calves under one year of age was high in Italy and not detected by Croatia and Spain (Figure 36). No resistance to cefotaxime was reported the three MSs (Figure 37).

Figure 36: Spatial distribution of ciprofloxacin resistance among *Salmonella* spp. from calves under one year of age in countries reporting MIC data in 2015

Figure 37: Spatial distribution of cefotaxime resistance among *Salmonella* spp. from calves under one year of age in countries reporting MIC data in 2015

Table 20: Occurrence of resistance to selected antimicrobials in *Salmonella* spp. isolates from calves under one year of age in 2015, using harmonised ECOFFs

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Salmonella spp.														
Croatia	15	20	15	0	15	0	15	0	15	6.7	15	0	15	0
Italy	14	71.4	14	0	14	0	14	0	14	50	14	42.9	14	0
Spain	16	18.8	16	0	16	0	16	0	16	12.5	16	0	16	6.3
Total (3 MSs)	**45**	**35.6**	**45**	**0**	**45**	**0**	**45**	**0**	**45**	**22.2**	**45**	**13.3**	**45**	**2.2**
Salmonella Typhimurium														
Croatia	2	100	2	0	2	0	2	0	2	50	2	0	2	0
Italy	5	60	5	0	5	0	5	0	5	60	5	80	5	0
Spain	2	50	2	0	2	0	2	0	2	50	2	0	2	0
Total (3 MSs)	**9**	**66.7**	**9**	**0**	**9**	**0**	**9**	**0**	**9**	**55.6**	**9**	**44.4**	**9**	**0**
Monophasic *Salmonella* Typhimurium														
Italy	7	100	7	0	7	0	7	0	7	57.1	7	28.6	7	0
Salmonella Derby														
Croatia	1	100	1	0	1	0	1	0	1	0	1	0	1	0
Spain	2	0	2	0	2	0	2	0	2	0	2	0	2	0
Total (2 MSs)	**3**	**33.3**	**3**	**0**	**3**	**0**	**3**	**0**	**3**	**0**	**3**	**0**	**3**	**0**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Salmonella spp.												
Croatia	15	6.7	15	0	15	26.7	15	20.0	15	0	15	20.0
Italy	14	7.1	14	28.6	14	71.4	14	78.6	14	0	14	14.3
Spain	16	6.3	16	0	16	18.8	16	18.8	16	0	16	6.3
Total (3 MSs)	**45**	**6.7**	**30**	**13.3**	**30**	**43.3**	**30**	**46.7**	**30**	**0**	**30**	**10.0**
Salmonella Typhimurium												
Croatia	2	50	2	0	2	100	2	100	2	0	2	50
Italy	5	20	5	80	5	60	5	80	5	0	5	20
Spain	2	50	2	0	2	50	2	50	2	0	2	0
Total (3 MSs)	**9**	**33.3**	**9**	**44.4**	**9**	**66.7**	**9**	**77.8**	**9**	**0**	**9**	**22.2**
Monophasic _Salmonella_ Typhimurium												
Italy	7	0	7	0	7	100	7	100	7	0	7	14.3
Salmonella Derby												
Croatia	1	0	1	0	1	100	1	0	1	0	1	100
Spain	2	0	2	0	2	0	2	0	2	0	2	0
Total (2 MSs)	**3**	**0**	**3**	**0**	**3**	**33.3**	**3**	**0**	**3**	**0**	**3**	**33.3**

Note: All _Salmonella_ isolates tested were susceptible to meropenem N: number of isolates tested; % Res: percentage of microbiologically resistant isolates; MSs: Member States.
(a): A number of colistin-resistant isolates are undergoing testing for the presence of _mcr-1_ gene. The reported occurrence of colistin resistance is unlikely to equate to the occurrence of _mcr-1_
    ECOFF applied 2 mg/L.
(b): ECOFF applied 1 mg/L.

3.1.2.6. Analyses of high-level ciprofloxacin and cefotaxime resistance

Fluoroquinolones and third-generation cephalosporins, including the class representatives ciprofloxacin and cefotaxime/ceftazidime included in the panels stipulated by Decision 2013/652/EU, are internationally recognised as highest priority critically important in human medicine (Collignon et al., 2016; WHO, 2016) and often constitute the first-line treatment for invasive salmonellosis, although fluoroquinolones are not recommended for children (Chen et al., 2013). Fluoroquinolones and third- and fourth-generation cephalosporins may be used for treatment of pigs and cattle in Europe. High levels of resistance to either class of antimicrobials if observed among *Salmonella* spp. in some animal species are of concern, because of the importance of these compounds in the treatment of invasive salmonellosis in humans.

Comparison of 'clinical' and 'microbiological' resistance to cefotaxime

In *Salmonella* spp. from fattening pigs an overall low level of 'microbiological' and 'clinical' resistance to cefotaxime (0.7%) was reported, with only Italy recording low levels (Table 21). Resistance to cefotaxime in *Salmonella* spp. from fattening pigs in Italy was shown by monophasic *S.* Typhimurium and *S.* Typhimurium.

> The term 'microbiological' resistance is used in this report when resistance is interpreted using the EUCAST epidemiological cut-off values, whereas the term 'clinical' resistance is noted when resistance is analysed using the EUCAST clinical breakpoints.
>
> Quinolone and fluoroquinolone resistance in the Enterobacteriaceae is mostly attributed to point mutations in the quinolone resistance-determining regions (QRDR) of the gyrase (*gyrA* and *gyrB*) and topoisomerase IV (*parC* and *parD*) genes. Plasmid mediated quinolone resistance (PMQR) can be caused by the action of efflux pumps (*qepA* genes), enzymatic modifications (*aac(6′)-Ib-cr* gene, which also confers resistance to kanamycin), and protection of the DNA gyrase (*qnrA*, *qnrB*, *qnrD* and *qnrS* genes) (Cavaco et al., 2009).
>
> The presence of two single point mutations in the QRDR will usually confer 'clinical' resistance to ciprofloxacin (minimum inhibitory concentration (MIC) > 0.064 mg/L) as well as to nalidixic acid (MIC > 16 mg/L). In contrast, isolates harbouring only one single point mutation in the QRDR will usually show 'clinical' resistance to nalidixic acid, whereas the susceptibility to ciprofloxacin is reduced such that only 'microbiological' resistance is shown. In absence of other mechanisms, the presence of PMQR determinants (i.e. *qnr* genes) in a bacterium will confer only 'microbiological' resistance to ciprofloxacin, but the isolate will be susceptible to nalidixic acid.

Neither 'microbiological' nor 'clinical' resistance to cefotaxime in *Salmonella* spp. from calves under one year of age was found.

Table 21: Occurrence of resistance to cefotaxime among *Salmonella* spp. from fattening pigs and calves under one year of age in 2015, using harmonised ECOFFs and EUCAST CBPs

Country	Fattening pigs					Calves (under one year of age)				
	N	n res ECOFF	% res ECOFF	n res CBP	% res CBP	N	n res ECOFF	% res ECOFF	n res CBP	% res CBP
Bulgaria	2	0	0	0	0	–	–	–	–	–
Croatia	103	0	0	0	0	15	0	0	0	0
Denmark	139	0	0	0	0	–	–	–	–	–
Germany	23	0	0	0	0	–	–	–	–	–
Ireland	66	0	0	0	0	–	–	–	–	–
Italy	91	3	3.3	3	3.3	14	0	0	0	0
Spain	–	–	–	–	–	16	0	0	0	0
Total (MSs 7)	**424**	**3**	**0.7**	**3**	**0.7**	**45**	**0**	**0**	**0**	**0**

ECOFFs: epidemiological cut-off values; EUCAST: European Committee on Antimicrobial Susceptibility Testing; N: number of isolates tested; n: number of isolates resistant; % res: percentage of resistant isolates; CBP: clinical breakpoint.

Analysis of high-level ciprofloxacin resistance

High-level resistance to ciprofloxacin, defined as resistance to MIC values ≥ 4 mg/L, in *Salmonella* of animal and food origin is shown in Tables HIGHSALMPIGMEAT, HIGHSALMBOVMEAT, HIGHSALMFATPIG and HIGHSALMCALV.

The only *Salmonella* isolate that displayed high-level resistance to ciprofloxacin originated from calves under one year of age. This *Salmonella* Typhimurium isolate also showed resistance to nalidixic acid and tetracycline (Table HIGHSALMCALV).

3.1.2.7. Tigecycline resistance in *Salmonella* spp.

Microbiological resistance to tigecycline was reported in 2.7% of 750 *Salmonella* spp. from meat from pigs, 2.5% of 80 *Salmonella* spp. from meat from bovines, 1.7% of 424 *Salmonella* spp. from fattening pigs, and 0% of 45 *Salmonella* spp. from calves under one year of age. Certain features relating to tigecycline resistance are evident when the prevalence of tigecycline resistance is considered for individual reporting countries.

Certain serovars displayed microbiological resistance to tigecycline. This may indicate clonal expansion of microbiologically resistant strains belonging to these serovars and is exemplified by the findings for *Salmonella* Typhimurium from fattening pigs where 4/424 isolates from Ireland were the major contributor to the total of 7 tigecycline resistant isolates reported from all reporting MSs.

Countries reporting results for fewer than 40 isolates did not detect tigecycline resistance in *Salmonella* spp., with the sole exception of fattening pigs in Germany.

Countries detecting tigecycline resistance mostly reported low levels, with the exception of Portugal, which detected resistance in 10/48 isolates in meat from fattening pigs; 6/10 of these isolates were MDR *S.* Rissen, all of which were also resistant to tetracyclines.

The tigecycline MIC distributions for *Salmonella* spp. from fattening pigs, calves under one year of age and meat from these animals are shown in Figure 38. The microbiological cut-off for tigecycline is that resistant isolates have an MIC > 1 mg/L – the distribution shows a significant proportion of isolates with a tigecycline MIC at 1 mg/L. Therefore, given the variation inherent in the MIC method, a proportion of isolates are likely to show microbiological resistance, simply because of the distribution of MICs. Determining the susceptibility of tigecycline is also not entirely straightforward as the method can be affected by oxidation of the test reagents. Several mechanisms of resistance to tigecycline in *Salmonella*/Enterobacteriaceae have been described and these include increased activity of efflux pumps (AcrAB), mutation of the ribosomal protein S10 and modification of the Mla system involved in phospholipid transport in cell membranes (He et al., 2016). The mechanisms of development of microbiological resistance, which may involve upregulation of normal cell pathways or processes, probably also contribute to the occurrence of a 'tail' of isolates on the MIC distribution with values just above the ECOFF.
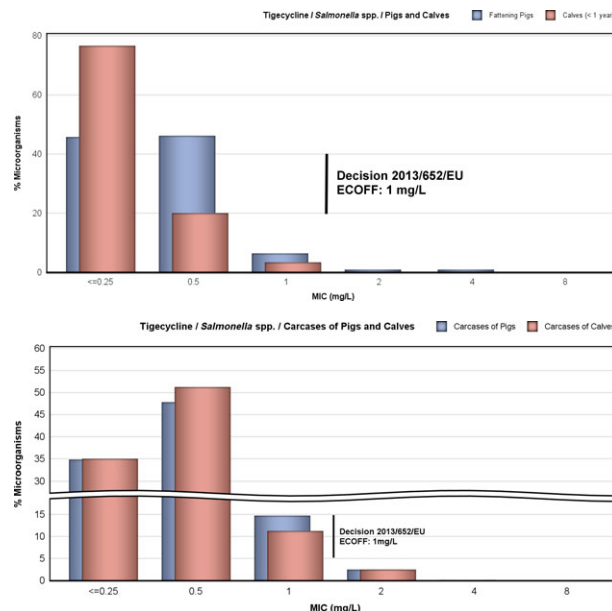
Figure 38: Tigecycline resistance in *Salmonella* spp. from fattening pigs, calves under one year of age and meat from these animals

3.1.2.8. 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. Figure 39 shows the distribution of colistin MICs. As is the case with tigecycline, isolates with an MIC close to the clinical/microbiological thresholds of > 2 mg/L will be subject to the inherent variation of the MIC method.

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.

Table 22: Distribution of MICs of colistin by serovar in *Salmonella* spp. in carcases from fattening pigs

Serovar	MIC			Total
	4	**8**	**16**	
Salmonella 4,12:i:-	–	1	–	1
Salmonella 4,5,12:i:-	–	–	2	2
Salmonella 4,[5],12:i:-	1	–	–	1
Salmonella Derby	1	–	–	1
Salmonella Dublin	–	1	–	1
Salmonella Idikan	1	–	–	1
Salmonella Infantis	1	–	–	1
Salmonella Kedougou	1	–	–	1
Salmonella Rissen	–	–	1	1
Total	5	2	3	10

MIC: minimum inhibitory concentration.

S. Dublin is a group D (serogroup O:9) *Salmonella* and group D *Salmonella* isolates are reported to show higher intrinsic levels of resistance to colistin than other serogroups. The other *Salmonella* serovars in Table 22 do not belong to Serogroup O:9 and while some display resistance only one dilution above the breakpoint, others show higher levels of resistance. Considering *S.* Derby, monophasic *S.* Typhimurium and *S.* Typhimurium there were 189, 187 and 135 isolates reported by MSs from pig carcases, yet only a single *S.* Derby isolate and no *S.* Typhimurium isolates were resistant to colistin, whereas 4/10 colistin-resistant isolates detected were monophasic *S.* Typhimurium, originating from France and Portugal. An Italian study recently reported detection of the transferable colistin resistance gene *mcr-1* in a number of *Salmonella* serovars, of which monophasic *S.* Typhimurium was the most frequent (detected in pigs, pork and man), while *S.* Derby was the second most frequently detected (in pigs) (Carnevali et al., 2016).

The *S.* Rissen and monophasic *S.* Typhimurium isolates, in which the highest colistin MICs of 16 mg/L were observed, originated from Portugal. Portugal reported that 2.5% of 198 indicator *E. coli* from fattening pigs were resistant to colistin (Section 3.3), while Spain reported that 2.9% of 170 indicator *E. coli* from fattening pigs were resistant to colistin and detected a single *S.* Kedougou isolate resistant to colistin with an MIC of 4 mg/L. Belgium detected two *Salmonella* isolates (Derby and Idikan) with colistin resistance at 4 mg/L and Malta detected *S.* Infantis with a colistin MIC of 4 mg/L, while the prevalence of colistin resistance in indicator *E. coli* in Belgium and Malta was 0%. The question therefore arises as to whether correlations might exist between the occurrence of colistin resistance and/or the degree of colistin resistance (MIC value) observed in both *Salmonella* and indicator *E. coli* and whether any such correlations are also associated with the level of use of colistin. The Joint Interagency Antimicrobial Consumption and Resistance Analysis (JIACRA) Report being prepared by ECDC, EFSA and EMA is currently considering resistance to colistin and possible associations with the level of usage.
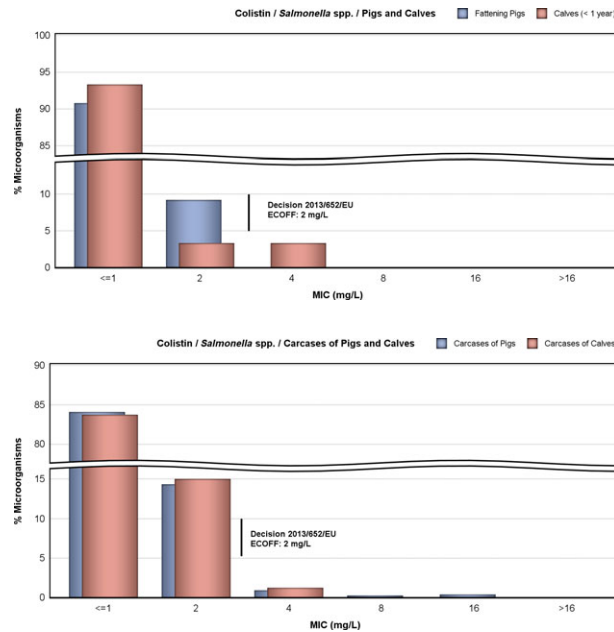
Figure 39: Colistin resistance in *Salmonella* spp. from fattening pigs, calves under one year of age and meat from these animals

3.1.2.9. Multidrug resistance patterns in certain *Salmonella* serovars

The data relating to *Salmonella* spp. from an MS typically cover a variety of different serovars, each of which may have a different propensity to exhibit AMR. Differences in the occurrence of serovars among MSs may account for much of the pronounced variation in the recorded MDR parameters for *Salmonella* spp. For example, *S.* Enteritidis in general exhibited much lower MDR than *S.* Typhimurium; however, there were marked differences between MSs in the occurrence of MDR for each of these serovars.

Salmonella *spp.*

The patterns of AMR exhibited by all reported *Salmonella* isolates revealed numerous combinations of resistance to the nine different antimicrobial agents included in the analysis. The occurrence of specific MDR profiles reported by MSs in meat and animals are presented in the MDR patterns tables. In meat from bovine animals, seven serovars (Infantis, monophasic Typhimurium, Derby, Typhimurium, Anatum, Brandenburg and Rissen) accounted for 84.8% of *Salmonella* spp. (Table SERBOVMEATD). There were a further 10 serovars reported from meat from bovine animals. In calves under one year of age, eight serovars (Typhimurium, Dublin, monophasic Typhimurium, Enteritidis, Derby, Agona, Anatum and Montevideo) accounted for 73.3% of *Salmonella* spp. (Table SERCALVESD). A further 10 serovars were reported from calves under one year of age and 8 of these were represented by only single isolates. In meat from pigs, seven serovars (Derby, monophasic Typhimurium, Typhimurium, Rissen, Infantis, Bredeney and Livingstone) accounted for 85.6% of *Salmonella* spp. (Table SERPIGMEATD). There were a further 37 serovars reported from meat from pigs. In fattening pigs, nine serovars (monophasic Typhimurium, Derby, Typhimurium, Bredeney, Rissen, Infantis, Brandenburg, Enteritidis and London) accounted for 91.3% of *Salmonella* spp. (Table SERFATPIGSD). There were a further 19 serovars reported from fattening pigs.

Detailed analysis of the specific patterns of resistance detected is most useful when performed at the serovar level. However, the overall data from all *Salmonella* spp. have also been examined to determine the pattern most common in highly prevalent sources per country. In meat from pigs, where 305/755 (40.4%) of isolates were MDR (Table MULTISALMPIGMEAT) and fattening pigs where 186/424 (43.9%) of isolates were MDR (Table MULTISALMFATPIG), the most common resistance pattern was a combination of ampicillin, sulfamethoxazole and tetracycline, followed in pig meat by the same pattern with the addition of chloramphenicol, and in fattening pigs by the combination sulfamethoxazole, tetracycline and trimethoprim; both patterns accounting for 20.7% of the meat from pigs isolates and 255% of the fattening pigs isolates included in the analysis. The majority of isolates with the patterns

ampicillin, sulfamethoxazole and tetracycline of resistance both from pig meat (80.0% of isolates with this pattern) and from fattening pigs (82.3% of isolates with this pattern) were monophasic *S.* Typhimurium. This resistant profile (combination of ampicillin, sulfamethoxazole and tetracycline) was predominately reported in meat from pigs by the Czech Republic (50.0%), Denmark (55.6%), France 52.2%, Germany 45.8%, Malta 75%, and Slovakia (66.7%) and in fattening pigs by Denmark (50.0%), Germany (91.7%), and Italy (58.3%).

In meat from bovine animals, where 32/76 (42.1%) of isolates were MDR (Table MULTISALMBOVMEAT), and in calves under one year of age 17/45 (37.8%) of isolates were MDR (Table MULTISALMCALV), monophasic *S.* Typhimurium accounted for 34.4% of the MDR isolates in meat from bovine animals and 41.2% of the MDR isolates in calves under one year of age. The most common pattern in both meat from bovine animals and in calves under one year of age was the combination: ampicillin, sulfamethoxazole and tetracycline.

Monophasic Salmonella *Typhimurium*

The MDR patterns for monophasic *S.* Typhimurium isolates were reported from meat from pigs (138 isolates were MDR out of 187 isolates reported, 73.8%) (Table MULTIMOTYPHIPIGMEAT), fattening pigs (107/130, 82.3%) (Table MULTIMOTYPHIPIG), meat from bovine animals (11/13, 84.6%) (Table MULTIMONTYPHIBOVMEAT) and calves under one year of age (7/7, 100%) (Table MULTISALMCALV). The most frequent pattern of resistance observed was resistance to ampicillin, sulfamethoxazole and tetracycline occurring in all MDR isolates.

Salmonella *Typhimurium*

MDR *S.* Typhimurium isolates were reported in pig meat (54.5%) (73 isolates were MDR out of 134 *S.* Typhimurium isolates reported) (Table MULTIMOTYPHIPIGMEAT), fattening pigs (33 isolates were MDR out of 63 *S.* Typhimurium isolates reported, 52.4%) (Table MULTITYPHIFATPIG), meat from bovine animal 6 isolates were MDR out of 10 *S.* Typhimurium isolates reported, 60.0%) (Table MULTITYPHIBOVMEAT) and calves under one year of age (6 isolates were MDR out of 9 *S.* Typhimurium isolates reported, 66.7%) (Table MULTISALMCALV). A wide range of different MDR patterns were reported in all sources. The most frequent MDR core pattern was resistance to ampicillin, sulfamethoxazole and tetracycline in most sources. However, penta- and hexa-resistance were reported in a few isolates from meat from pigs, fattening pigs and calves under one year of age. Heptavalent resistance was found in one isolate from fattening pigs and one isolate from calves under one year of age. Resistance to cefotaxime/ceftazidime was reported in only one isolate from meat from pigs, two isolates from fattening pigs and was absent in all other sources.

Salmonella *Derby*

The patterns of MDR for *S.* Derby isolates were reported from meat from pigs (14 isolates were MDR out of 135 isolates reported, 10.4%) (Table MULTIDERBYPIGMEAT), fattening pigs (29 isolates were MDR out of 143 isolates reported, 20.3%) (Table MULTIDERBYFATPIG), meat from bovine animals (3 isolates were MDR out of 8 isolates reported, 37.5%) (Table MULTIDERBYBOVMEAT) and calves under one year of age (1 isolate was MDR out of 3 isolates reported, 33.3%) (Table MULTIDERBYCALV). About 71.4% of the isolates from meat from pigs and 79.3% of the isolates from fattening pigs had the core pattern of resistance to sulfamethoxazole, tetracycline and trimethoprim.

Salmonella *Rissen*

The patterns of MDR for *S.* Rissen isolates were reported from meat from pigs (28 isolates were MDR out of 45 isolates reported, 59.6%) (Table MULTIRISSENSPIGMEAT) and fattening pigs (1 isolate was MDR out of 3 isolates reported, 33.3%) (Table MULTIRISSENFATPIG).

Salmonella *Infantis*

The MDR patterns for *S.* Infantis isolates were reported from meat from pigs (9 isolates were MDR out of 20 isolates reported, 45.0%) (Table MULTIINFANTINSPIGMEAT) fattening pigs (1 isolate was MDR out of 1 *S.* Infantis isolate reported) (Table MULTIINFATPIG) and meat from bovine animals (8 isolates were MDR out of 15 isolates reported, 53.3%) (Table MULTIINFANTISBOVMEAT). One *S.* Infantis isolate from meat from pigs was found to be resistant to eight antimictobials.

3.1.3. Discussion

3.1.3.1. Antimicrobial resistance in *Salmonella* in humans

Salmonellosis is the second most commonly reported zoonotic disease in humans in the EU, exceeded only by campylobacteriosis. The decline in incidence since 2004 seems to be mainly attributable to the reduction in the prevalence of *Salmonella* in flocks of laying hens and also in broilers and turkeys, probably as a result of the national control and monitoring programmes implemented by the MSs in the corresponding production sectors (EFSA and ECDC, 2015). In 2014 and 2015, however, reported salmonellosis stabilised within the EU/EEA (EFSA and ECDC, 2016b). While most infections cause mild disease, effective antimicrobials are essential for treatment of severe enteric disease or invasive infections.

In this report, isolates from cases notified as having been acquired while travelling abroad were excluded from the analysis. The rationale is to facilitate assessment of the relationship between antimicrobial resistance in *Salmonella* isolates from food and food-producing animals with antimicrobial resistance in human isolates of *Salmonella* spp. However, as imported or traded food can constitute a large proportion of the food available in some countries, the relationship between resistance in food and food-producing animals and in the human population remains complex.

In 2015, information on AMR in *Salmonella* isolates from human cases was reported by 22 MSs and two non-MS. Resistance in human *Salmonella* isolates was high to ampicillin, sulfamethoxazole and tetracycline, but slightly lower than in 2014, possibly due to the varying subset of countries reporting each year, the number of isolates tested by each country and the serotypes tested. These antimicrobials or other agents of the same class are used commonly for treating infections in animals and humans (although not usually for treating *Salmonella* infections in humans). Resistance to ciprofloxacin, a critical antimicrobial for treating salmonellosis in adults, increased compared to 2014 which may reflect that more countries using disk diffusion have replaced the ciprofloxacin disk with pefloxacin for screening of low-level fluoroquinolone resistance. In addition, the 2014 clinical breakpoint for *Salmonella* and ciprofloxacin from EUCAST, which was significantly lower than the previous one, had been applied by most countries reporting interpreted SIR data. The relatively high resistance to cefotaxime and ceftazidime in Italy (5.6%, all in *S.* Infantis), was most likely due to the continued circulation of a multiresistant ESBL-producing clone of *S.* Infantis in Italy (Franco et al., 2015).

Harmonised with EFSA, multidrug resistance was assessed in isolates tested for at least nine different antimicrobial classes. MDR was high overall in *Salmonella* from humans, but few isolates were clinically resistant to the two antimicrobials regarded as highest priority critically important for human treatment. Twenty-eight isolates (0.4% of the 6,762) were resistant to seven or eight antimicrobial classes, of which half were monophasic *S.* Typhimurium.

Because of the compulsory antimicrobial susceptibility testing of isolates from pigs and calves in 2015, the analysis of human data focused on the three most common serovars in those animal types. The levels of resistance observed in *S.* Typhimurium, monophasic *S.* Typhimurium and *S.* Derby isolated from humans and from pig carcasses were very similar across the range of tested antimicrobial substances. Too few isolates were available from calves at serovar level for such a comparison. More than half of *S.* Typhimurium isolated from humans were resistant to ampicillin, sulfonamides and tetracycline with high to extremely high levels in most reporting MSs. Even higher proportions of resistance were observed in monophasic *S.* Typhimurium from humans where close to 90% of all isolates were resistant to these three antimicrobials. In comparison, much lower proportions of *S.* Derby were resistant to these antimicrobials, particularly to ampicillin. Resistance to ampicillin and tetracycline often followed the same trend over time with increasing trends in *S.* Typhimurium in some MSs and decreasing trends in other MSs in the three-year period studied.

Isolates co-resistant to the two critically important therapeutic antimicrobial classes, fluoroquinolones and 3rd-generation cephalosporins, were rare among human isolates of *Salmonella* overall and also among the studied serovars. A few countries, however, reported high proportions of *S.* Typhimurium isolates resistant to fluoroquinolones and significant increasing trends were observed in fluoroquinolone resistance in two MSs in 2013–2015. Multidrug resistance was high in *S.* Typhimurium and extremely high in monophasic *S.* Typhimurium and had increased by more than 10% at the EU level in both serovars in 2015 compared to 2014. Very high increases were observed in a few MSs, but the reason is not known. Half of the MSs testing isolates for the nine antimicrobial classes included in the MDR analysis reported a few isolates resistant to at least six of the classes, and one MS reported one isolate each of *S.* Typhimurium and monophasic *S.* Typhimurium resistant to

eight classes, only susceptible to meropenem. Considering the high MDR among these very common serovars and others, e.g. *S.* Kentucky (EFSA and ECDC, 2016a), it is important to monitor *Salmonella* for resistance also to reserve agents, such as meropenem, colistin, azithromycin and tigecycline that may need to be considered for treatment of extremely drug-resistant isolates. For 2015, all MSs except two reported data on meropenem, five more than for 2014. Four to six countries reported data on the other last-resort drugs, a few more than for 2014. From June 2016, also colistin, azithromycin and tigecycline are listed as priority antimicrobials for AMR monitoring in human *Salmonella* isolates (ECDC, 2016), which will most likely result in more countries testing these antimicrobials, as was the case for meropenem. In the absence of routine monitoring, resistance to reserve agents may grow and remain undetected. Resistance to reserve agents not used in food-producing animals may be related to cross-resistance to agents used in food-producing animals for some agents, or to antimicrobial use in humans or exposure to sources of *Salmonella* other than those associated with food-producing animals.

The quality of the AMR data for *Salmonella* from humans continues to improve as the result of the agreement on harmonised monitoring and reporting (ECDC, 2014, 2016). For 2015, fourteen of the 24 reporting countries provided data as measured values to which ECOFFs could be applied. These were two countries more than for 2014 and twice as many as for 2013. There was also one more reporting country than for 2013. Ten countries still provided results interpreted with clinical breakpoints. By combining the categories of clinically 'intermediate' resistant and clinically 'resistant', the ECOFF-based category of 'wild type' corresponds closely to the 'susceptible' category and the ECOFF-based category of 'non-wild type' corresponds closely to the 'non-susceptible' category with only one dilution difference across all antimicrobials except meropenem. Thus, this approach further improves the comparability of human and non-human data. The ECOFF for *Salmonella* and meropenem is four dilutions lower than the 'non-susceptible' (based on clinical breakpoints), although EUCAST recommends the use of ECOFF as a screening breakpoint to detect carbapenemase-producing *Enterobacteriaceae* (EUCAST, 2013). For future reports, EFSA and ECDC hope that more countries will report measured values. More harmonisation is also needed regarding the optimal sample of human isolates for inclusion in the monitoring programme at the EU level, as, in many countries, the sampling and the antimicrobials tested for a particular sample are not random, and represent different fractions of all isolates identified in a country.

3.1.3.2. Antimicrobial resistance in *Salmonella* from pigs and cattle and meat thereof

In *Salmonella* isolates from pigs and meat, harmonised isolate-based data were reported by 20 MSs and one non-MS in 2015. The reporting of isolate-based data enabled the analysis of MDR patterns, high level of resistance to ciprofloxacin and co-resistance to ciprofloxacin and cefotaxime, first-line agents critically important for treating human salmonellosis. The levels of resistance are presented by serovar for the different animal production types. The subdivision of resistance data allows for more accurate analysis and as required by the legislation, all MSs included information on serovars and production type. In 2015, MSs collected *Salmonella* isolates for susceptibility testing according to the new harmonised monitoring plan (Commission implementing Decision 2013/652/EU). In line with this decision, the antimicrobial agents included in the test panels were changed; most importantly, testing of resistance to streptomycin was not required, which had an impact on how MDR patterns were interpreted. The animal and meat sections in this chapter focus primarily on *Salmonella* from fattening pigs and cattle under one year of age and meat thereof, reflecting the monitoring plan for 2015 set out in the Decision.

Antimicrobials such as ampicillin, sulfamethoxazole and tetracycline have been widely used for many years in veterinary medicine to treat infections in production animals. Generally, high levels of resistance to these antimicrobials are reported by MSs from producing animals and meat products thereof. The highest levels of resistance to ampicillin, sulfamethoxazole and tetracycline, as well as to chloramphenicol, were recorded in *Salmonella* isolates from fattening pigs. Considering all reporting MSs, isolates from calves under one year of age displayed the lowest levels of resistance to these antimicrobials. The genes conferring resistance to these agents are commonly found in association together on various mobile genetic elements such as class 1 integrons or in the variant *Salmonella* genomic islands which have been described, explaining both their frequent occurrence as well as their frequent occurrence together or in various combinations. Levels of resistance were generally higher in monophasic *S.* Typhimurium from fattening pigs than from meat from pigs.

Colistin-resistant *Salmonella* isolates were not detected by any reporting country in pigs, 10 isolates out of 750 tested originating from carcases from fattening pigs were colistin-resistant and only few from calves under one year of age and meat from bovine animals. Considering these 10 colistin-resistant

isolates the colistin MIC ranged from 4 to 16 mg/L and they belonged to serovars *S.* 4,12:i:-, *S.* 4,5,12:i:-, *S.* 4,[5],12:i:-, *S.* Derby, *S.* Dublin, *S.* Idikan, *S.* Infantis, *S.* Kedougou, *S.* Rissen. Serovar Dublin is Group D (serogroup O:9) *Salmonella* isolates and *Salmonella* belonging to this group, tend to have elevated colistin MICs, a phenomenon which is considered to reflect slightly decreased intrinsic susceptibility of these serovars.

The occurrence of resistance to fluoroquinolones (ciprofloxacin) was in general low. High-level ciprofloxacin resistance was reported in *S.* Typhimurium from calves under one year of age by Italy, which also reported a high prevalence of ciprofloxacin resistance in *Salmonella* spp. from calves, although only a low number of *Salmonella* isolates were detected. The findings might reflect dissemination of a resistant clone or alternatively independent emergence of different strains of *S.* Typhimurium as result of the selective pressure of use of fluoroquinolones.

Third-generation cephalosporins and fluoroquinolones are critically important for the treatment of human salmonellosis. Co-resistance to cefotaxime and ciprofloxacin differed between MSs and was not detected in isolates from the majority of MSs. In the one MSs where it was detected (Italy), co-resistance to these antimicrobials occurred in two *Salmonella* isolate from fattening pigs (monophasic *S.* Typhimurium and *S.* Typhimurium).

S. Rissen was detected by seven MSs in pig meat and was the fourth most common serovar, accounting for 7.3% of *Salmonella* isolates from pig meat. *S.* Rissen also commonly showed multiple drug resistance and these findings are interesting because MDR *S.* Rissen is a common serovar occurring in pigs and causing salmonellosis in man in parts of Asia. The results suggest that MDR *S.* Rissen is also emerging in the European pig population in several MSs.

MDR, defined as resistance to three or more of nine antimicrobial classes, was slightly higher in *Salmonella* spp. from fattening pigs (43.9% of isolates) and calves under one year of age (37.8% of isolates) than in meat from pigs (40.4% of isolates) and meat from bovine animals (40.5%). In fattening pigs, the proportion of all isolates showing MDR, was greatly influenced by the occurrence of MDR monophasic *S.* Typhimurium, this serovar accounting for approximately 57.5% of the MDR isolates in fattening pigs. This serovar has currently spread widely in pigs in Europe. Particular MDR patterns were associated with monophasic *S.* Typhimurium and because this serovar was prevalent in many countries, these patterns greatly influenced the overall resistance figures. This is exemplified by resistance to ampicillin, sulfamethoxazole and tetracycline which occurred as an MDR pattern without additional resistances in 71/130 (54.6%) of monophasic *S.* Typhimurium isolates from fattening pigs; monophasic *S.* Typhimurium represented 130/424 (30.7%) of all *Salmonella* isolates examined from fattening pigs. This pattern of resistance, in some phage types with additional resistance to chloramphenicol, is also commonly present in some strains of *S.* Typhimurium. Generally, the resistance levels varied among serovars that may exhibit particular MDR patterns, so the relative contribution of different serovars in different production types and between MSs should be kept in mind when comparing the situation between the reporting countries.

The analysis of MDR resistance patterns also highlighted multiresistant strains of *Salmonella* occurring in several MSs. The trend analysis showed that tetracycline resistance exceeds ampicillin resistance in many MSs and although tetracycline resistance may show some fluctuations, ampicillin resistance tends to show parallel fluctuations, maintaining the interval between tetracycline and ampicillin resistance. This may be related to the occurrence of the underlying genetic structures and the proportion carrying linked resistance genes to tetracyclines and ampicillin.

There were no *Salmonella* isolates recovered from fattening pigs and calves under one year of age in 2015 which were resistant to carbapenems, a class of antimicrobials which is not used therapeutically in food-producing animals, but which is reserved for use in humans. Supplementary testing of those *Salmonella* isolates which were resistant to the indicator cephalosporins (cefotaxime and ceftazidime) with a further panel of antimicrobials revealed the presence of isolates with ESBL, AmpC and combined ESBL plus AmpC phenotypes.

Within a given MS, any attempt to relate AMR in human *Salmonella* isolates to AMR in isolates from food and food-producing animals in that MS is complicated, because much of the food consumed in an MS may have originated in other MSs or in third countries. *Salmonella* infections can also be associated with foreign travel, other types of animal contact (such as pet reptiles) or the environment. Some human infections can also occur through spread between affected human patients. To improve investigation of these relationships, isolates from cases notified as having been acquired during travel outside of the reporting country were excluded from the analysis, except with respect to the analysis of resistance in different geographical regions. The comparison would further improve if a distinction could be made between food isolates from domestically produced animals and those from other

countries, although this is not currently possible. Certain MDR serovars were detected in different categories of livestock and meat and this may indicate that there is transfer between these different categories of livestock (for example through mixed enterprise farms) or different categories of meat (for example through cross-contamination in meat processing plants). Genetic investigation of isolates could provide useful information on their degree of relatedness.

3.1.3.3. *Salmonella* Rissen – an emerging MDR *Salmonella* serovar in pigs

S. Rissen isolates from carcases of fattening pigs (7 MSs, N = 53) were frequently multidrug resistant, especially considering isolates from the Iberian peninsula, although multidrug resistance was also encountered in Belgium and Romania, with resistance to ampicillin, sulfonamides, tetracyclines and trimethoprim frequently detected. *S.* Rissen has been a common serovar in Spain where a dominant clone has been identified in pigs, pork and man for the last 10 years, which has shown resistance to ampicillin, chloramphenicol, streptomycin, sulfonamides, tetracyclines and trimethoprim (García-Fierro et al., 2016). *S.* Rissen is also a common serovar in pigs, chicken, pork and man in some parts of Asia where is it is frequently multidrug resistant to those antimicrobials listed above (Pornsukarom et al., 2015). This serovar has therefore been highlighted because of its potential for epidemic spread in livestock, particularly pigs, its penetration along the food chain to affect man and its tendency to display MDR.

3.2. Antimicrobial resistance in *Campylobacter*

Human infections with *Campylobacter*

Campylobacter causes many human cases of gastroenteritis, and despite a lot of underreporting (Haagsma et al., 2013; Havelaar et al., 2013; Gibbons et al., 2014) campylobacteriosis has been the most frequently reported cause of human food-borne zoonoses in the EU since 2004 (EFSA and ECDC, 2016b). In 2015, 229,213 laboratory-confirmed cases of campylobacteriosis were reported in the EU/EEA. *C. jejuni* and *C. coli* accounted for 99% of cases with species information. Patients may experience mild to severe illness. Symptoms may include (bloody) diarrhoea, abdominal pain, fever, headache and nausea. The mean duration of illness is 2–5 days but can be up to 10 days. The majority of campylobacteriosis enteric infections are self-limiting; however, infection can be associated with serious complications. Campylobacteriosis is an important trigger for autoimmune inflammatory conditions of the central nervous system, heart and joints, which can result in prolonged and debilitating illness (e.g. Guillain–Barré syndrome, acute transverse myelitis and reactive arthritis). Blood stream infection with *Campylobacter* spp. is very rare, except for infections with *Campylobacter fetus*.

Antimicrobial treatment is usually not required, but effective treatment may shorten the duration of illness. Resistance to antimicrobials in *Campylobacter* is of concern because of the large number of human infections and the fact that some cases require treatment. Treatment of enteric infections in humans may involve administration of macrolides, such as erythromycin, or fluoroquinolones (e.g. ciprofloxacin), as the first- and second-choice drugs (ECDC et al., 2009). With ciprofloxacin, resistance may develop rapidly.

3.2.1. Antimicrobial resistance in *Campylobacter* isolates from humans

Seventeen MSs, Iceland and Norway provided AMR data from human *Campylobacter* isolates for 2015. Twelve countries (Austria, Cyprus, Denmark, Estonia, Finland, Italy, Luxembourg, Norway, Portugal, Romania, Slovenia and Spain) reported quantitative isolate-based AST results as measured values of either inhibition zone diameters or MICs. Seven countries reported case-based or isolate-based AST results interpreted as susceptible (S), intermediate (I) or resistant (R) according to the CBPs applied. Countries reporting resistance in *Campylobacter* from humans in 2015 are presented in Tables CAMPJEOVERVIEW and CAMPCOOVERVIEW.

Since resistance levels differ substantially between *C. jejuni* and *C. coli*, data are reported separately for the two species. Results are presented for the four-first-priority antimicrobials currently included in the harmonised panel of antimicrobials to be tested with *Campylobacter* isolates from humans (ciprofloxacin, erythromycin, tetracycline and, since June 2016, gentamicin) and for one optional agent (co-amoxiclav) (ECDC, 2016).

The MDR analysis presented here included the four priority antimicrobials. The number of antimicrobials tested per isolate varied by country: all countries except one tested the three original priority antimicrobials, seven also tested gentamicin and five tested co-amoxiclav in addition.

Interpretation of data should take account of the wide variation in the numbers of *Campylobacter* isolates reported by MSs. While this may in part be related to true differences in the incidence of campylobacteriosis, it is also likely to be greatly influenced by practices related to referral of isolates from primary clinical laboratories to the national public health reference laboratory/ies or by reporting of AST data from the primary laboratories to the national public health institutes.

3.2.1.1. Antimicrobial resistance in *Campylobacter coli*[14] from humans

Resistance levels in C. coli *from human cases*

With 8,615 human cases, *C. coli* was the second most common *Campylobacter* species reported in the EU/EEA in 2015. AST data were reported for 21.5% of these cases in 2015 by 17 MSs and Norway. Very high proportions of resistance were observed for ciprofloxacin (70.6%) and tetracyclines (68.8%), with extremely high proportions (79.8–100.0%) resistant to ciprofloxacin in 11 of the 17 reporting countries (Table 23). Proportions of isolates resistant to erythromycin and gentamicin were markedly higher in *C. coli* than in *C. jejuni* (14.4% vs 1.5% and 1.6% vs 0.8%, respectively). Portugal, Italy and Spain reported the highest levels of resistance to erythromycin (53.5%, 42.9% and 38.2%, respectively).

Methods and interpretive criteria used for antimicrobial susceptibility testing of *Campylobacter* isolates from humans

The method of testing for antimicrobial susceptibility and the selection of the isolates to be tested varied between countries. The methods and interpretive criteria used for antimicrobial susceptibility testing of *Campylobacter* are presented in Table 5. Quantitative data were interpreted by ECDC based on the EUCAST epidemiological cut-off (ECOFF) values, where available. In the absence of ECOFFs, CBPs from the French Society for Microbiology (CA-SFM) were applied. For the qualitative SIR data, the intermediate and resistant results were combined into a 'non-susceptible' category. For the four antimicrobials reported for both human and animal/food isolates, the commonly used interpretive criteria were aligned (Figure 40). For this purpose, 'susceptible' isolates were aligned with wild-type isolates based on ECOFFS, and 'non-susceptible' isolates ('intermediate' and 'resistant') were aligned with non-wild-type isolates. This resulted in total concordance across interpretive categories, except for the EUCAST CBP for *C. jejuni* for tetracyclines, which is one dilution step higher than the EUCAST ECOFF.
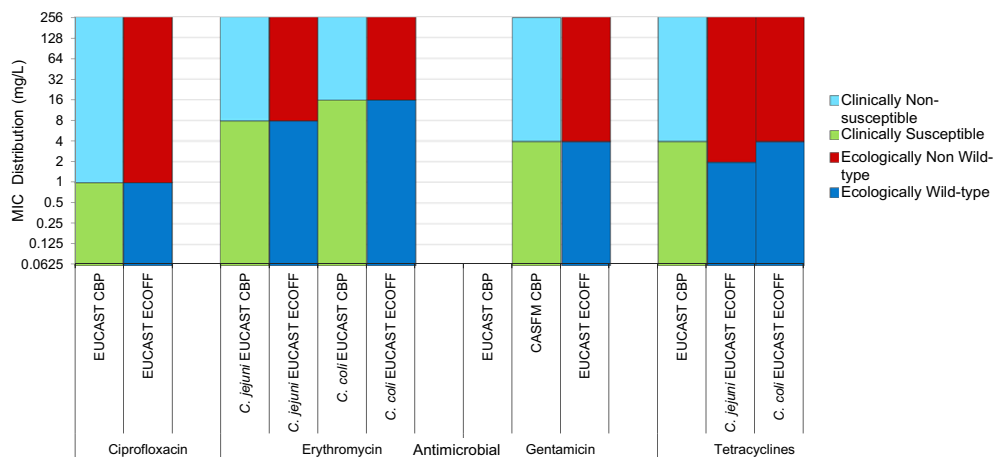
Figure 40: Comparison of clinical breakpoints (CBPs) and epidemiological cut-off values (ECOFFs) used to interpret MIC data reported for *Campylobacter* spp. from humans, animals or food

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[14] Due to the focus of the AST monitoring in 2015 of pigs, data on *C. coli* are presented before *C. jejuni* in the human sections.

Table 23: Antimicrobial resistance in *Campylobacter coli* from humans per country in 2015

Country	Ciprofloxacin		Co-amoxiclav		Erythromycin		Gentamicin		Tetracyclines	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	39	87.2	–	–	39	5.1	39	0	39	59.0
Cyprus	10	80.0	–	–	10	0	–	–	10	80.0
Denmark	6	NA	–	–	6	NA	6	NA	6	NA
Estonia	21	81.0	–	–	21	33.3	–	–	21	76.2
Finland[a]	277	83.4	–	–	260	24.2	–	–	142	71.1
France[b]	870	65.7	870	1.6	869	9.4	788	1.1	844	71.6
Italy	14	92.9	–	–	14	42.9	–	–	14	78.6
Lithuania[b]	19	89.5	–	–	20	15.0	–	–	18	66.7
Luxembourg	22	81.8	22	18.2	22	27.3	–	–	22	86.4
Malta[b]	57	57.9	3	NA	57	10.5	–	–	5	NA
Netherlands[b]	145	60.0	–	–	121	14.9	–	–	87	64.4
Portugal	43	100.0	–	–	43	53.5	43	2.3	43	95.3
Romania	17	82.4	17	0	17	5.9	17	0	17	29.4
Slovakia[b]	52	36.5	23	17.4	55	12.7	–	–	61	44.3
Slovenia	94	79.8	–	–	94	3.2	–	–	94	38.3
Spain	55	92.7	51	37.3	55	38.2	55	9.1	55	92.7
United Kingdom[b]	13	38.5	–	–	23	4.3	–	–	4	NA
Total (17 MSs)	**1,754**	**70.6**	**986**	**4.4**	**1,726**	**14.4**	**948**	**1.6**	**1,482**	**68.8**
Norway	2	NA	–	–	2	NA	2	NA	2	NA

N: number of isolates tested; % Res: percentage of resistant isolates (either non-wild type by ECOFFs or clinically non-susceptible by combining resistant and intermediate categories); –: no data reported; NA: not applicable (if less than 10 isolates were tested, the percentage of resistance was not calculated).

(a): Travel-associated cases, accounting for 75% of *Campylobacter* infections in Finland in 2015, could not be excluded from the Finnish AST data.

(b): Data interpreted with clinical breakpoints.

Temporal trends in resistance in C. coli *from human cases*

Temporal trend analysis was performed for the 3 years 2013–2015 following the agreement on harmonised data collection (ECDC, 2014) and for the three antimicrobials tested by the majority of countries. Twelve MSs provided resistance data for a minimum of 2 years in this period and a minimum of ten isolates (Figure 10). Statistical tests were only performed when data were available for all 3 years. For ciprofloxacin resistance in *C. coli*, statistically significant increases were observed in Austria and Slovenia. Resistance to erythromycin decreased significantly in France and Malta. No significantly increasing or decreasing trends were observed for tetracycline resistance.
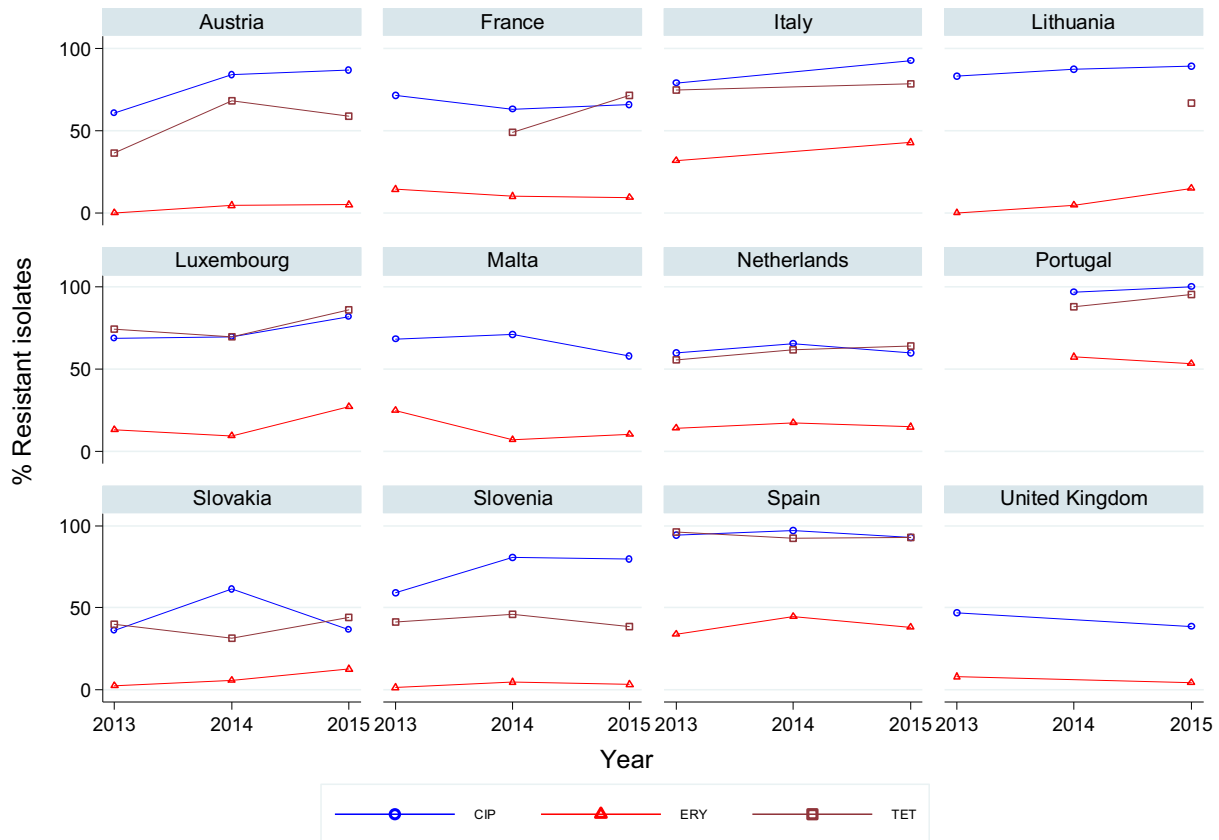
Statistically significant increasing trends over 3 years, as tested by logistic regression (p ≤ 0.05), were observed for ciprofloxacin in Austria and Slovenia (↑). Statistically significant decreasing trends over 3 years were observed for erythromycin in France and Malta (↓). Only countries testing at least 10 isolates per year were included in the analysis.

Figure 41: Trends in ciprofloxacin, erythromycin and tetracycline resistance in *Campylobacter coli* from humans in reporting countries, 2013–2015

Spatial distribution of resistance in C. coli *from human cases*

The highest proportions of resistance to ciprofloxacin in *C. coli* isolates from humans (Figure 42) were reported by southern and eastern European countries, whereas northern and central European countries reported lower levels. The proportions of erythromycin resistance was markedly higher in some countries in southern Europe (Portugal, Italy and Spain) (Figure 43). Travel-associated cases in Finland, accounting for 75% of *Campylobacter* infections in the country in 2015, could not be excluded from the Finnish AST data.
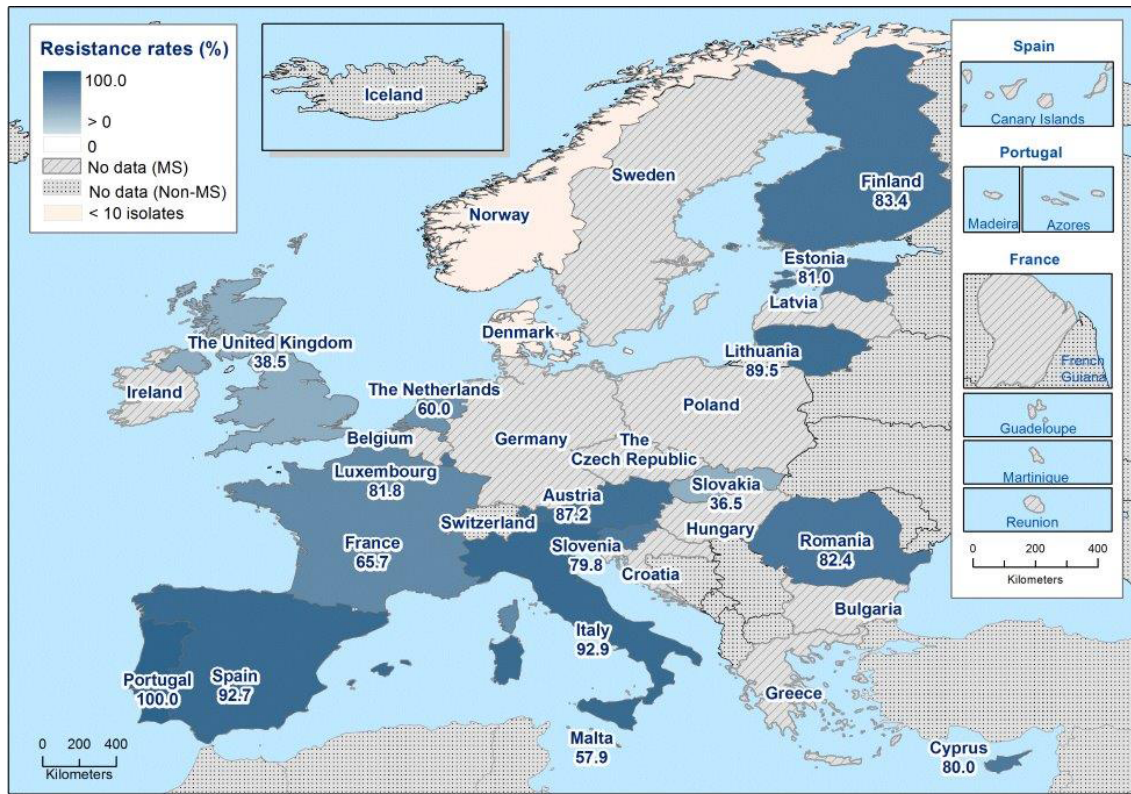
Figure 42: Spatial distribution of ciprofloxacin resistance among *Campylobacter coli* from human cases in reporting countries in 2015
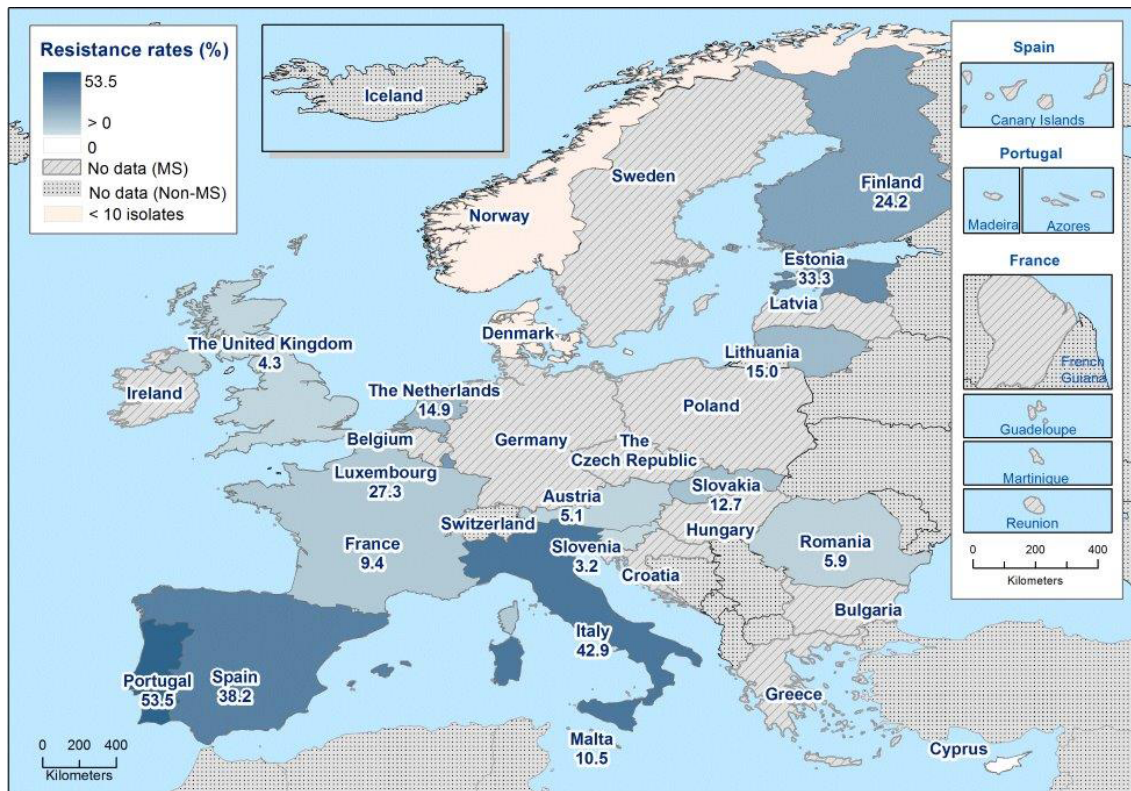
Figure 43: Spatial distribution of erythromycin resistance among *Campylobacter coli* from human cases in reporting countries in 2015

MDR in C. coli *from human cases*

Overall, 15.0% of the human *C. coli* isolates were susceptible to all four antimicrobial classes, with no susceptible isolates reported by Portugal (Figure 44, Table COMCAMPCOHUM). The level of MDR was moderate overall (11.5%) but ranged from 5.1% to 53.5% between countries, with a country average of 22.1%. The overall level of microbiological and clinical co-resistance to ciprofloxacin and erythromycin was 11.7% but almost 40% in Spain and over 50% in Portugal. Portugal, France and Spain reported one, three and five isolates, respectively, resistant to all four antimicrobial classes (Figure 44).
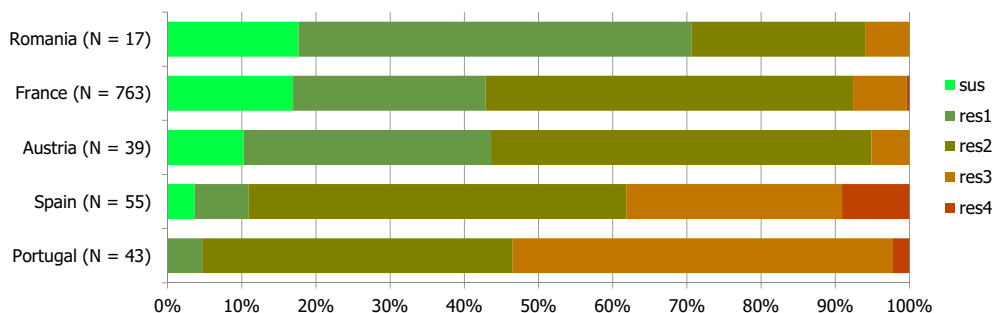
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Campylobacter*; sus: susceptible to all antimicrobial classes of the harmonised set for *Campylobacter*; res1-res4: resistance to one up to four antimicrobial classes of the harmonised set for *Campylobacter*.

Figure 44: Frequency distribution of *Campylobacter coli* isolates from humans completely susceptible or resistant to one to four antimicrobial classes in 2015

Considering the high proportion of MDR among *C. coli*, combined resistance to the three antimicrobials most commonly used for treatment, ciprofloxacin, erythromycin and tetracycline, was analysed in all reporting countries. Fourteen per cent (199 isolates of 1,447) of the *C. coli* isolates tested from humans were resistant to all three classes in 2015 with an average among the 16 MSs of 23.9% (Table 24). In five of 16 MS, combined resistance was found in at least a third of the tested isolates with the highest rates in Portugal (53.5%).

Table 24: Proportion of *C. coli* isolates from humans resistant to ciprofloxacin, erythromycin and tetracycline in 2015

Country	Res to CIP, ERY & TET	
	N	% Res
Austria	39	5.1
Cyprus	10	0
Denmark	6	NA
Estonia	21	33.3
Finland[a]	142	32.4
France[b]	843	7.6
Italy	14	35.7
Lithuania[b]	18	16.7
Luxembourg	22	27.3
Malta[b]	5	NA
Netherlands[b]	79	11.4
Portugal	43	53.5
Romania	17	5.9
Slovakia[b]	39	12.8
Slovenia	94	2.1
Spain	55	38.2

Country	Res to CIP, ERY & TET	
	N	% Res
Total (16 MSs)	1,447	13.8
Norway	2	NA

(a): Travel-associated cases, accounting for 75% of *Campylobacter* infections in Finland in 2015, could not be excluded from the Finnish AST data.
(b): Data interpreted with clinical breakpoints.

3.2.1.2. Antimicrobial resistance in *Campylobacter jejuni* from humans

Resistance levels in C. jejuni *from human cases*

As in previous years, *C. jejuni* was the most common *Campylobacter* species identified in 2015, with 83,350 cases reported in the EU/EEA. AST data were reported for 17.7% of these cases in 2015 by 17 MSs, Iceland and Norway. A very high proportion (60.8%) of human isolates were resistant to ciprofloxacin in 2015 (17 MSs, Table 25) with extremely high proportions observed in several countries, most noticeably in Portugal (96.6%), Spain (90.4%), Estonia (86.5%) and Lithuania (85.0%). The lowest proportions of isolates resistant to ciprofloxacin were reported by Norway (27.4%) and Denmark (42.1%). Similar observations were made regarding the levels of resistance to tetracyclines which were high overall (44.6%) with the highest proportion of resistance reported by Portugal (81.9%), Spain (78.5%), Estonia (68.9%) and Lithuania (65.2%) and the lowest reported by Norway (13.2%). The level of resistance to erythromycin was overall relatively low, at 1.5%, but varied between countries. The highest proportion of erythromycin-resistant isolates was reported by Romania (8.7%), Portugal (8.1%) and Italy (5.7%). Resistance to gentamicin was overall very low (0.8%) but higher in Slovakia (5.6%) and Spain (2.2%).

Table 25: Antimicrobial resistance in *Campylobacter jejuni* from humans per country in 2015

Country	Ciprofloxacin		Co-amoxiclav		Erythromycin		Gentamicin		Tetracyclines	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Austria	393	73.0	–	–	393	0.5	393	0	393	39.2
Cyprus	31	71.0	–	–	31	0	–	–	31	45.2
Denmark	145	42.1	–	–	145	4.1	145	1.4	145	22.8
Estonia	193	86.5	–	–	193	0	–	–	193	68.9
Finland[a]	2,810	60.1	–	–	2,684	2.6	–	–	1,102	43.1
France[b]	4,627	56.2	4,630	0.6	4,629	0.4	4,115	0.8	4,472	48.3
Italy	53	71.7	–	–	53	5.7	–	–	51	58.8
Lithuania[b]	267	85.0	–	–	322	2.5	–	–	244	65.2
Luxembourg	224	62.1	224	4.9	224	0	–	–	224	38.8
Malta[b]	194	62.4	–	–	192	2.1	–	–	1	NA
Netherlands[b]	2,479	60.5	–	–	2,237	2.0	–	–	1,739	40.4
Portugal	149	96.6	–	–	149	8.1	149	0.7	149	81.9
Romania	23	73.9	23	0	23	8.7	23	0	23	34.8
Slovakia[b]	638	51.6	165	2.4	682	1.9	36	5.6	659	29.0
Slovenia	1,005	65.2	–	–	1,005	0.7	–	–	1,005	31.2
Spain	228	90.4	199	21.1	227	2.2	228	2.2	228	78.5
United Kingdom[b]	237	52.3	–	–	202	1.5	6	NA	14	28.6
Total (17 MSs)	**13,696**	**60.8**	**5,241**	**1.6**	**13,391**	**1.5**	**5,095**	**0.8**	**10,673**	**44.6**
Iceland[b]	58	8.6	–	–	58	0.0	–	–	–	–
Norway	106	27.4	–	–	106	1.9	106	1.9	106	13.2

N: number of isolates tested; % Res: percentage of resistant isolates (either non-wild type by ECOFFs or clinically non-susceptible by combining resistant and intermediate categories); –: no data reported; NA: not applicable – if fewer than 10 isolates were tested resistance was not calculated.
(a): Travel-associated cases, accounting for 75% of *Campylobacter* infections in Finland in 2015, could not be excluded from the Finnish AST data.
(b): Data interpreted with clinical breakpoints.

Temporal trends in resistance in C. jejuni *from human cases*

Temporal trend analysis was performed for the 3 years 2013–2015 for the three antimicrobials tested by the majority of countries. Fifteen MSs and one non-MS provided resistance data for a minimum of 2 years in this period and a minimum of ten isolates tested (Figure 45); however, statistical testing was only performed when data had been submitted for all 3 years. For ciprofloxacin resistance, statistically significant increases were observed in Austria, Estonia, France, the Netherlands and Slovakia. Resistance to erythromycin in *C. jejuni* remained relatively stable at low levels over the study period, with significantly increasing resistance observed only in Slovakia and significant decreasing resistance observed in Luxembourg and Malta. Tetracycline resistance increased significantly in Austria, Estonia, Italy, the Netherlands and Slovakia.
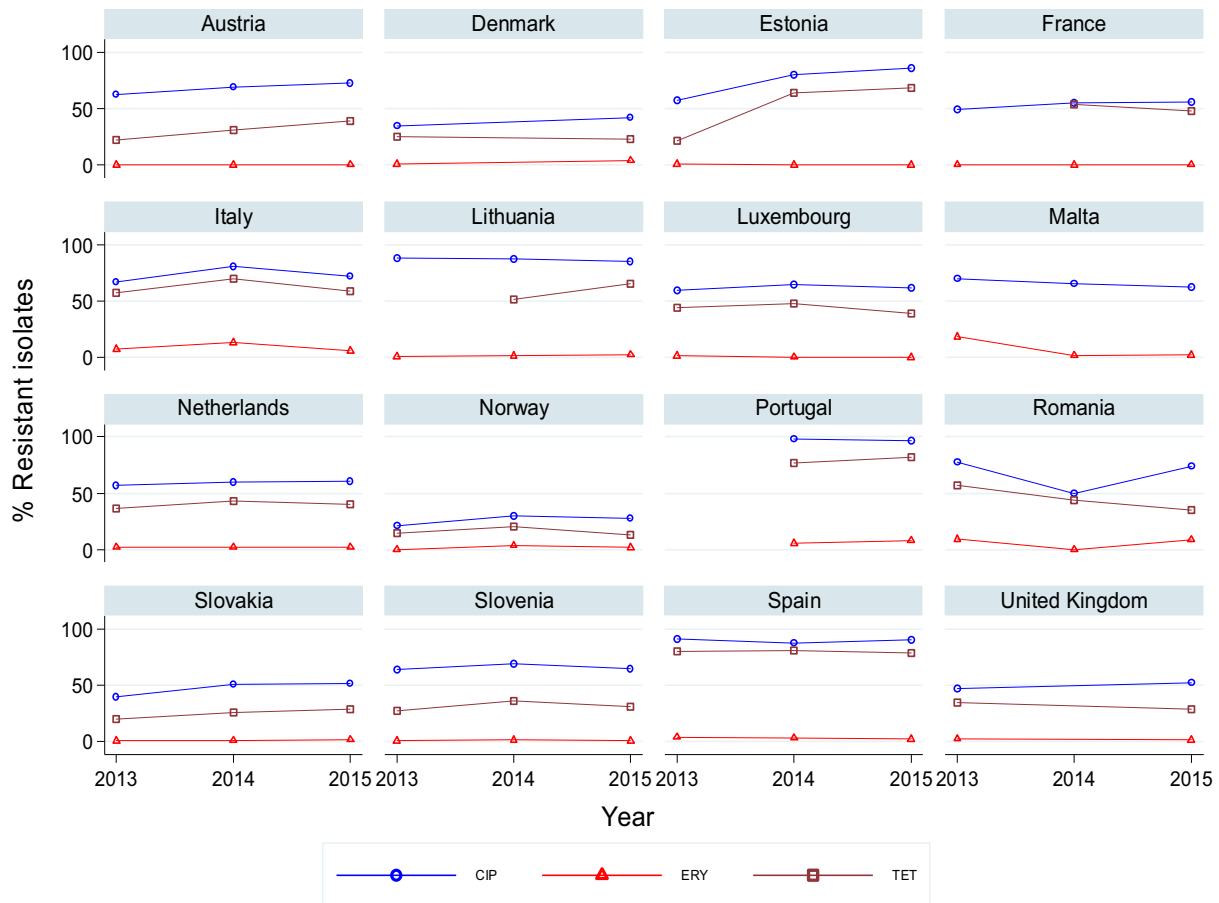
Statistically significant increasing trends over 3 years, as tested by logistic regression (p ≤ 0.05), were observed for ciprofloxacin in Austria, Estonia, France, the Netherlands and Slovakia (↑), for erythromycin in Slovakia (↑) and for tetracycline in Austria, Estonia, Italy, the Netherlands and Slovakia (↑). Statistically significant decreasing trends over 3 years were observed for erythromycin in Luxembourg and Malta (↓). Only countries testing at least 10 isolates per year were included in the analysis.

Figure 45: Trends in ciprofloxacin, erythromycin and tetracycline resistance in *Campylobacter jejuni* from humans in reporting countries, 2013–2015

Spatial distribution of resistance in C. jejuni *from human cases*

The spatial distribution of ciprofloxacin resistance in *C. jejuni* isolates from human cases (Figure 46) shows that the highest proportion of resistance was reported by southern European and Baltic countries, whereas northern and central European countries reported lower levels. Travel-associated cases, accounting for 75% of *Campylobacter* infections in Finland in 2015, could not be excluded from the Finnish AST data. The levels of erythromycin resistance did not show any clear geographical trend, but a few countries in southern and eastern Europe (Italy, Portugal and Romania) reported higher levels (Figure 47).
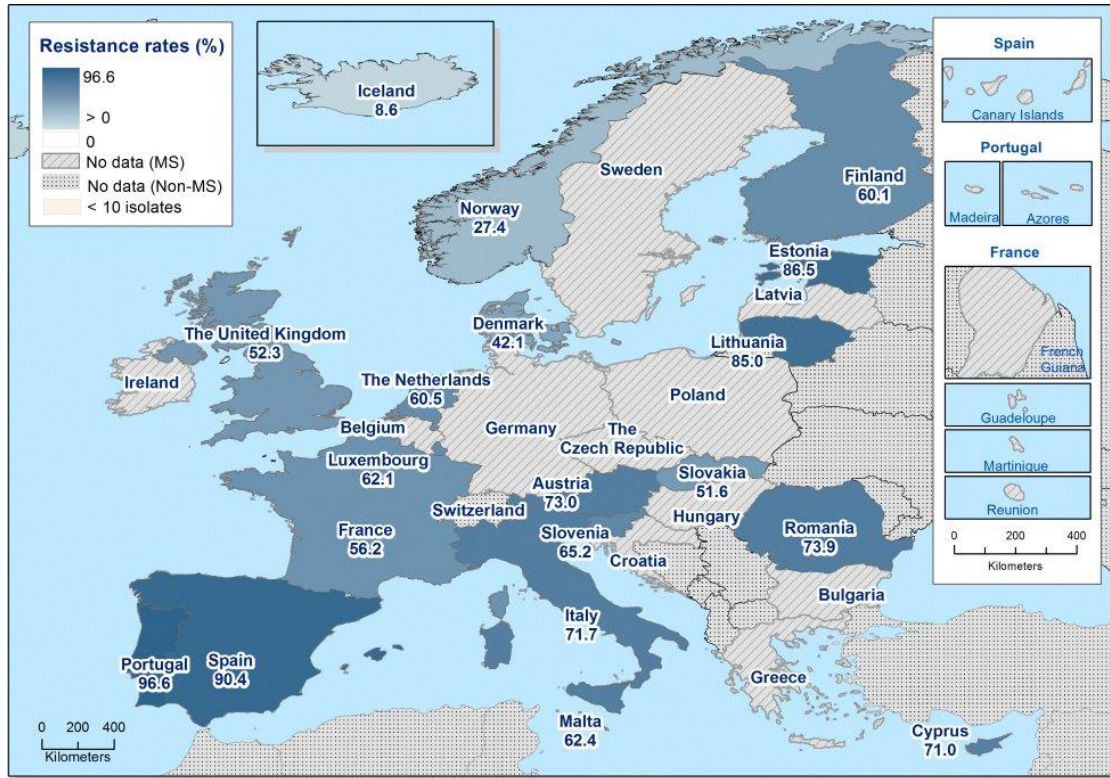
Figure 46: Spatial distribution of ciprofloxacin resistance among *Campylobacter jejuni* from human cases in reporting countries in 2015
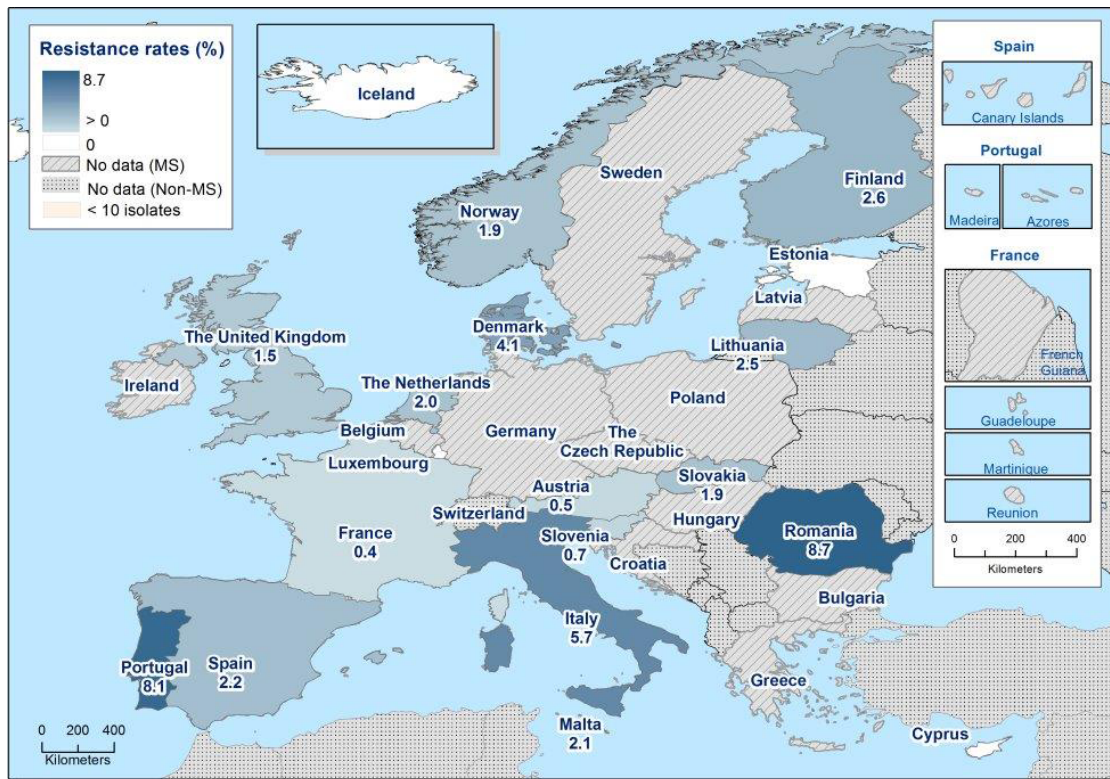
Figure 47: Spatial distribution of erythromycin resistance among *Campylobacter jejuni* from human cases in reporting countries in 2015

MDR in C. jejuni *from human cases*

Six MSs and Norway tested at least ten isolates of *C. jejuni* for resistance to the four antimicrobial classes included in the MDR analysis. Overall, 31.9% of human *C. jejuni* isolates in the six reporting MSs were susceptible to all four antimicrobial classes (6 MSs, Table COMCAMPJEHUM). Particularly low levels of susceptibility were reported from Portugal (1.3%) and Spain (6.2%) (Figure 48). MDR was very low overall (0.8%) but higher when assessing the country average (4.1%). The highest proportions of MDR were observed in Portugal (8.7%) and Romania (8.7%). An increase in MDR was observed in all reporting countries compared to 2014. A very low proportion of isolates (0.8% and 0.6%, respectively) in the six MSs exhibited 'microbiological' as well as 'clinical' resistance to both ciprofloxacin and erythromycin, but higher levels were observed in Portugal and Romania. France reported one isolate and Spain two isolates resistant to all four antimicrobial classes.
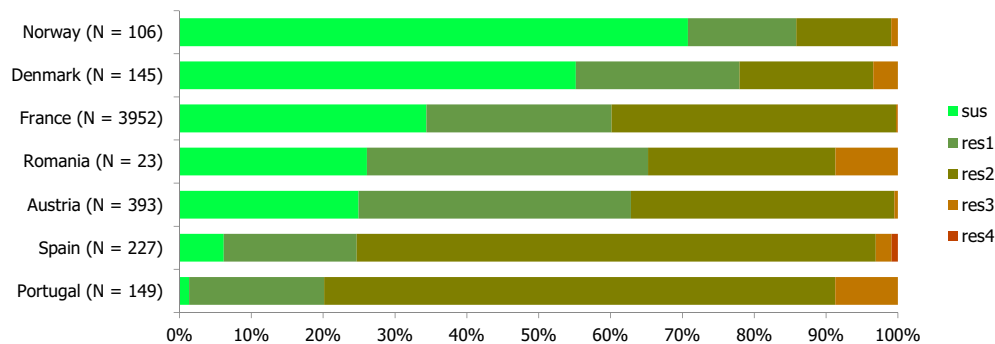
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Campylobacter*; sus: susceptible to all antimicrobial classes of the harmonised set for *Campylobacter*; res1-res4: resistance to one up to four antimicrobial classes of the harmonised set for *Campylobacter*.

Figure 48: Frequency distribution of *Campylobacter jejuni* isolates from humans completely susceptible or resistant to one to four antimicrobial classes in 2015

3.2.2. Antimicrobial resistance in *Campylobacter* isolates from animals and food

The monitoring programmes of AMR in *Campylobacter* from food-producing animals and food in the MSs usually cover only the species *C. jejuni* and *C. coli*. Under the framework of Decision 2013/652/EU, for 2015, quantitative isolate-based MIC data on *Campylobacter* were primarily collected and reported on *C. coli* from fattening pigs and meat derived thereof by seven MSs and two non-MSs, Norway and Switzerland, on a voluntary basis. As data on *C. coli* from pork reported by Germany and Portugal only concerned a very limited number of isolates, they were not examined in this report, as data on the few *C. jejuni* isolates from calves under one year of age reported by Romania.

A more general overview of the countries reporting *Campylobacter* resistance from various animal and food sampling origins in 2015 are presented in Tables CAMPCOOVERVIEW and CAMPJEOVERVIEW. In addition to data reported on pigs, pork and calves, in 2015, Austria, the Netherlands and Portugal monitored AMR in *C. jejuni* and *C. coli* from broiler meat; Austria and Portugal in *C. coli* from turkey meat, Austria and the Netherlands in *C. jejuni* from turkey meat. Croatia, Denmark and Finland monitored *C. jejuni* from broilers and Croatia *C. coli* from broilers. Since the AMR monitoring in 2015 concentrates on fattening pigs and calves under one year of age, the AST results in *C. jejuni* and *C. coli* from poultry and meat derived thereof will be analysed and presented in the 2016 EU Summary Report, which will focus on poultry.

3.2.2.1. Antimicrobial resistance in *Campylobacter* isolates from fattening pigs

Representative monitoring

Detailed information on the harmonised representative sampling of caecal samples from healthy fattening pigs at slaughter, and the harmonised methodology for AST may be found in the Material and methods section.

Resistance levels in C. coli *from fattening pigs*

The occurrence of resistance in *C. coli* to the antimicrobials studied varied greatly between the reporting countries in 2015 (Table 26). In general, the overall observed levels of resistance to streptomycin (overall 79.4%), tetracyclines (overall 66.6%), nalidixic acid (overall 60.8%) and ciprofloxacin (overall 62.1%) were high to extremely high.

Those levels of resistance to erythromycin (overall 21.6%) were highly variable from low to high and those to gentamicin (overall 3.6%) were low or absent. Exceptions to this general pattern of resistance to these substances were observed for isolates from Estonia, Sweden and Norway which reported the lowest occurrence of resistance (at low levels), and for the isolates from Spain, which exhibited a very high level of resistance to erythromycin (62.4%).

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.

Spatial distribution of resistance among Campylobacter coli *isolates from fattening pigs*

The spatial distributions of ciprofloxacin resistance in *C. coli* isolates from fattening pigs (Figures 49 and 50) show that the highest levels of resistance to this substance were reported in eastern and southern Europe, whereas northern European countries tended to report lower resistance levels. Although erythromycin resistance was generally registered at low to very low levels across the reporting countries, much higher resistance was observed in south-western Europe.

Table 26: Occurrence of resistance to selected antimicrobials in *C. coli* from fattening pigs in reporting MSs in 2015, using harmonised ECOFFs

Country	Ciprofloxacin		Erythromycin		Gentamicin		Nalidixic acid		Streptomycin		Tetracycline	
	N	%	N	%	N	%	N	%	N	%	N	%
Croatia	72	81.9	72	12.5	72	1.4	72	80.6	72	87.5	72	87.5
Estonia	33	24.2	33	3	33	3	33	24.2	33	72.7	33	36.4
Germany	243	42.8	243	10.7	243	0	243	37.9	243	79	243	72
Luxembourg	30	76.7	30	23.3	30	6.7	30	86.7	30	83.3	30	93.3
Slovenia	49	81.6	49	6.1	49	6.1	49	81.6	49	81.6	49	40.8
Spain	170	93.5	170	62.4	170	10.6	170	93.5	170	92.4	170	99.4
Sweden	107	41.1	107	0	107	0	107	42.1	107	54.2	107	1.9
Total (7 MSs)	**704**	**62.1**	**704**	**21.6**	**704**	**3.6**	**704**	**60.8**	**704**	**79.4**	**704**	**66.6**
Norway	217	12	217	0	217	0	217	12.4	217	29.5	217	0.5
Switzerland	156	46.8	156	4.5	156	0.6	156	46.8	156	86.5	156	63.5

ECOFFs: epidemiological cut-off values; N: number of isolates tested; %: percentage of resistant isolates per category of susceptibility or multiple resistance; MSs: Member States.
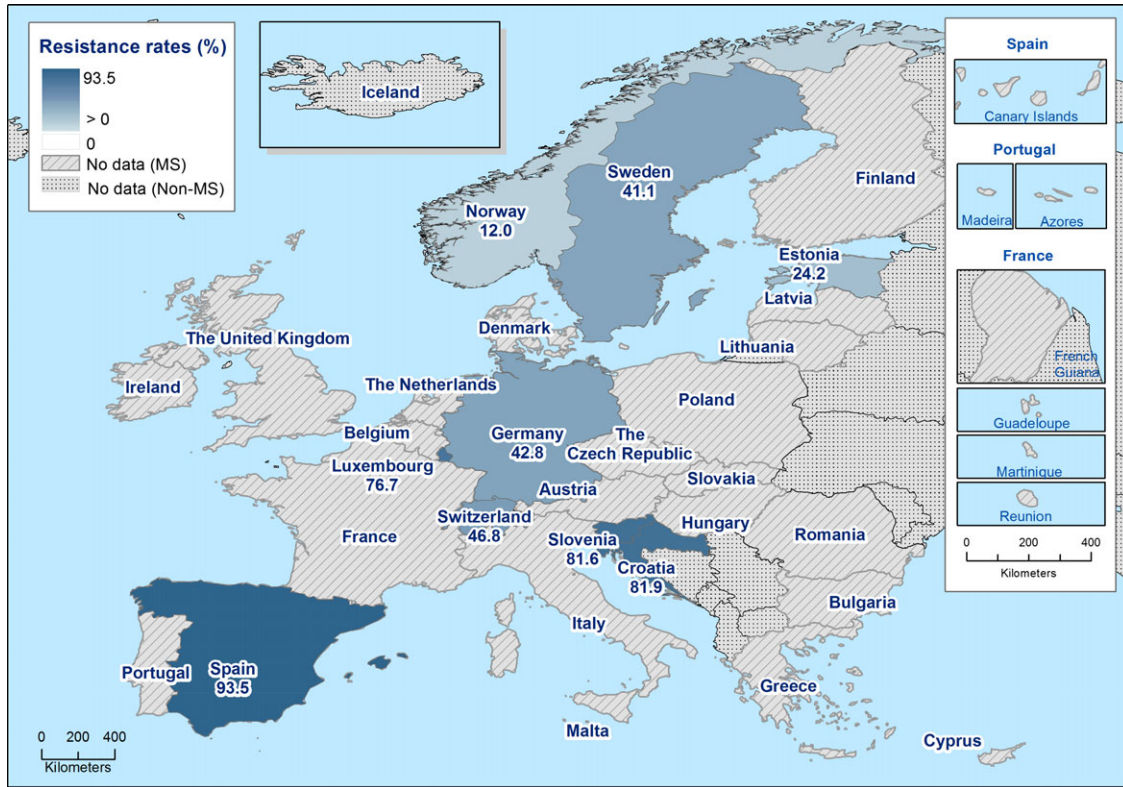
Figure 49: Spatial distribution of ciprofloxacin resistance *in C. coli* from fattening pigs in reporting countries in 2015, using harmonised ECOFFs

Figure 50: Spatial distribution of erythromycin resistance *in C. coli* from fattening pigs in reporting countries in 2015, using harmonised ECOFFs
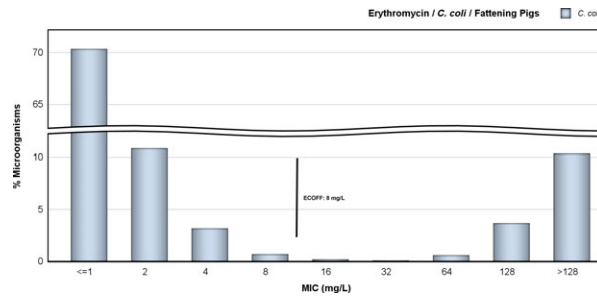
Figure 51: Distribution of MICs of erythromycin in *C.-coli* from fattening pigs - 1,005 isolates, 8 countries, 2015

High-level erythromycin resistance among C. *spp. from fattening pigs*

Mechanism of high-level erythromycin resistance in *Campylobacter* spp.

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) from 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.

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 antibiotic 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.

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. The acquisition of the *erm*(B) gene by successful circulating tetracycline resistance plasmids in *C. coli* from fattening pigs could provide a rapid means of dissemination of macrolide resistance, since such plasmids would confer resistance to both macrolides and tetracyclines and be subject to co-selection.

A MIC distribution can be used to assess the proportion of isolates exhibiting higher levels of resistance to the substance in question. The MIC distribution for erythromycin for *C. coli* isolates from fattening pigs in 2015 (Figure 51) shows that isolates of *C. coli* from fattening pigs with MICs > 128 mg/L have been detected.

The distribution by reporting country of isolates which have an erythromycin MIC higher than the highest erythromycin concentration tested (MIC > 128 mg/L) – in accordance with the harmonised method set out in Decision 2013/652/EU – is showed in Table 27. Spain was the MS which detected most high-level resistance to erythromycin; Spain and Germany together accounted for 91.3% of high-level erythromycin-resistant *C. coli* isolates which were detected.

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, although still above the ECOFF, dependent on the particular mutations having occurred (see text box above). Those isolates exhibiting MICs > 128 mg/L therefore have an erythromycin resistance phenotype consistent with either possession of transferable – *erm*(B) – or mutational resistance. Genetic investigation of isolates will be necessary for definitive characterisation of the resistance mechanisms which are present. Any fluctuation observed in the MIC proportions observed in the distribution may provide an early indication of changes in the occurrence of high-level macrolide resistance in *Campylobacter*.

Table 27: Occurrence of high-level resistance to erythromycin (MIC > 128 mg/L) in *C. coli* from fattening pigs in reporting countries in 2015

Country	N	High-level resistance to erythromycin (MIC > 128 mg/L)	
		n	%
Estonia	33	1	3.0
Germany	243	20	8.2
Luxembourg	30	4	13.3
Slovenia	49	1	2.0
Spain	170	75	44.1
Sweden	107	0	0.0
Total (6 MSs)	**632**	**101**	**16.0**
Norway	217	0	0.0
Switzerland	156	3	1.9

Co-resistance to ciprofloxacin and erythromycin among C. coli from fattening pigs

The important co-resistance[15] for public health to both ciprofloxacin and erythromycin in *C. coli* was detected in seven out of nine reporting countries, with Spain reporting the highest occurrence of co-resistance corresponding to 61.2% of the isolates tested. The overall occurrence of co-resistance to ciprofloxacin and erythromycin in *C. coli* was 13.3% considering all reporting MSs.

Temporal trends in resistance among C. coli *from fattening pigs*

None of MSs provided resistance data for *C. coli* from fattening pigs isolates on 5 years or more for inclusion in the statistical analysis (Figure 52).

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[15] The term co-resistance has been defined as two or more resistance genes which are genetically linked, i.e. located adjacent or close to each other on a mobile genetic element (Chapman, 2003). For brevity, the term is used slightly more loosely in this report and indicates two or more phenotypic resistances to different classes of antimicrobials, exhibited by the same bacterial isolate.
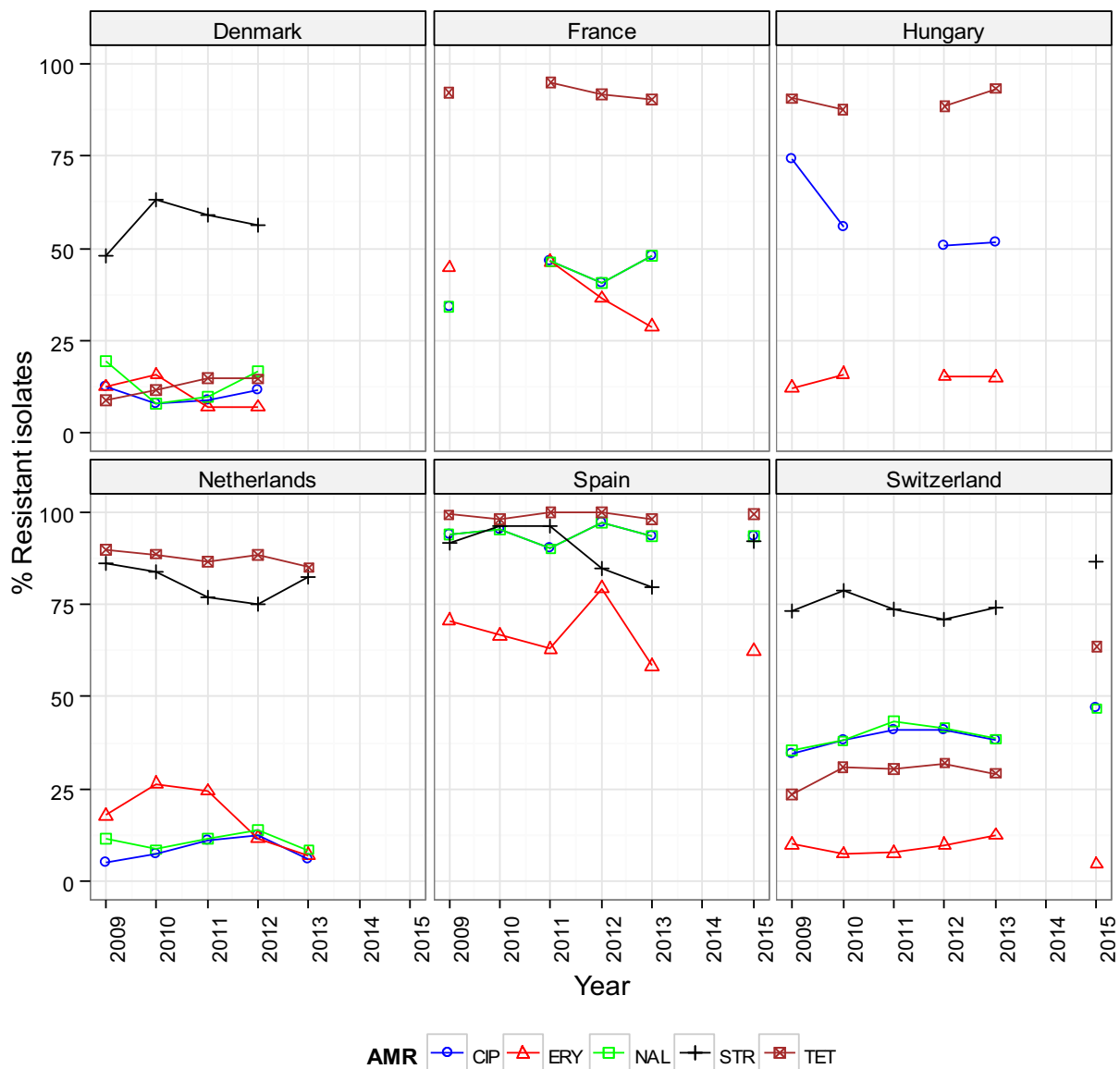
Statistical significance of temporal trends over 5 or more years was assessed by using a logistic regression model (p ≤ 0.05).

Statistically significant **increasing** trends were observed for **ciprofloxacin** in France (↑) and Switzerland (↑), and for **streptomycin** and **tetracycline** in Switzerland (↑).

Statistically significant **decreasing** trends were observed for **erythromycin** and **streptomycin** in the Netherlands (↓).

Figure 52: Trends in ciprofloxacin (CIP), erythromycin (ERY), nalidixic acid (NAL), streptomycin (STR) and tetracycline (TET) resistance in *Campylobacter coli* from fattening pigs in reporting countries, 2009–2015, using harmonised ECOFFs

Full susceptibility and multidrug resistance in C. coli *from fattening pigs*

A large variation in the levels of complete susceptibility to the common set of antimicrobials for *Campylobacter* (four antimicrobials) was observed among the reporting countries (Figure 53). Complete susceptibility was generally found in more than 30.0% of the *C. coli* isolates tested in the reporting countries, and reached 87.6% in Norway and 57.6% in Estonia, whereas in Croatia and Slovenia the proportion of fully susceptible isolates was much lower (under 10.0%). Luxembourg and Spain did not report any isolate fully susceptible.

The frequency distributions of the numbers of antimicrobials to which individual isolates were resistant (Figure 53) showed that Sweden and Norway did not report any isolates exhibiting MDR,[16] whereas the seven remaining countries (out of nine reporting data) reported MDR up to levels of in 26.7% in Luxembourg and 62.9% in Spain (Figure 53). The overall MDR of the *C. coli* isolates from fattening pigs was assessed at 13.6%. (Table COMCAMPCOFATPIG).

Patterns of multidrug resistance in C. coli *from fattening pigs*

The isolate-based data on *C. coli* were available from seven contributing MSs and two non-MSs, which in total reported details of 1,077 isolates. The isolates reported by one MS Sweden and one non-MS Norway (30.1% from the total number of the isolates reported) were not addressed in Table MULTICAMPCOFATPIG, as they were not multiresistant.

Among the 753 *C. coli* isolates from fattening pigs from the reporting countries submitting isolates, 19.5% (n = 147) exhibited MDR (Table MULTICAMPCOFATPIG). Testing of streptomycin susceptibility of *Campylobacter* is voluntary and results were not included in the MDR analysis. The most common pattern of MDR was resistance to ciprofloxacin/nalidixic acid, erythromycin and tetracyclines, occurring in 123 out of 147 resistant isolates (and constituting the core resistance pattern in a further 14 isolates, which also showed gentamicin resistance) reported by submitting reporting countries.
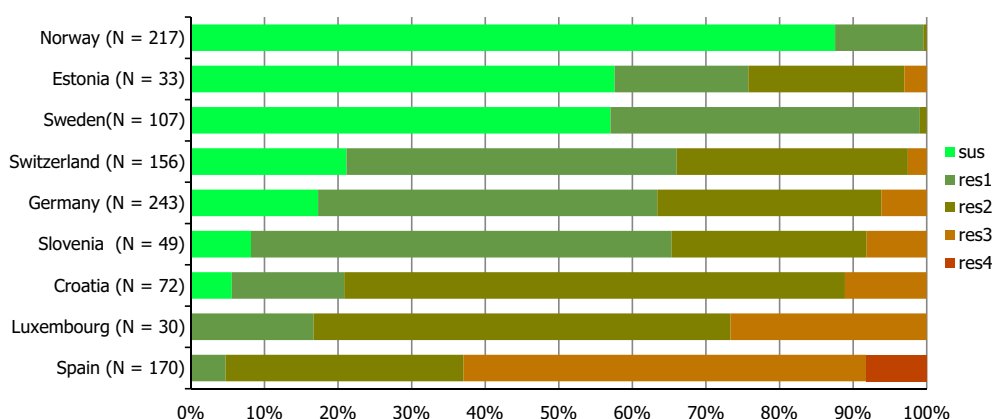
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Campylobacter*; sus: susceptible to all antimicrobial classes of the harmonised set for *Campylobacter*; res1–res4: resistance to one up to four antimicrobial classes of the harmonised set for Campylobacter.

Figure 53: Frequency distribution of *C. coli* isolates completely susceptible and resistant to one to four antimicrobials, in fattening pigs in the reporting countries, 2015, using harmonised ECOFFs

3.2.2.2. Prevalence of antimicrobial resistance in *Campylobacter* isolates from fattening pigs

Prevalence of resistance among C. coli *from fattening pigs*

The prevalence of resistance to selected antimicrobials in *C. coli* from fattening pigs in 2015, using harmonised ECOFFs is presented in Table 29. The occurrence of resistance in *C. coli* in fattening pigs describes the proportion of all *C. coli* isolates tested showing microbiological resistance to each antimicrobial (Table 26). The prevalence of resistant *C. coli* in fattening pigs (Table 29) describes the proportion of *C. coli* showing microbiological resistance to each antimicrobial as a percentage of all caecal samples cultured for *C. coli*.

Attempt at assessing the prevalence of C. coli *in caecal samples of fattening pigs within the framework of the AMR monitoring*

The estimates of the prevalence of *C. coli* in caecal samples of fattening pigs are presented in Table 28. The number of colonies tested may have affected the *C. coli* prevalence estimates, because testing multiple colonies, increases the likelihood of detecting a positive *C. coli* sample, especially in cases where *C. coli* is a minor component of the *Campylobacter* flora.

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[16] MDR is defined as resistance to three antimicrobial classes or more of the harmonised panel. The testing of streptomycin susceptibility of *Campylobacter* is voluntary, and results were not included in the MDR analysis.

Table 28: Number and proportions (%) of *Campylobacter coli*-positive caecal samples of fattening pigs, EU monitoring of AMR, 2015

Country	Total Caecal Samples	*Campylobacter coli*	
		Positive caecal samples	%
Croatia	409	293	72
Estonia	87	33	38
Germany	379	269	71
Luxembourg	134	103	77
Slovenia	100	93	93
Spain	373	170	46
Sweden	140	107	76
Total (7 MSs)	**1,622**	**1,068**	**66**
Norway	270	217	80
Switzerland	298	156	52

Attempt of assessing the prevalence of antimicrobial resistance in C. coli *from fattening pigs*

The prevalence of *C. coli* resistant to particular antimicrobials in fattening pigs at slaughter is shown in Table 29. This prevalence of *C. coli* resistant is the product of the prevalence of *C. coli* in caecal samples (Table 28) and the occurrence of resistance in the *C. coli* isolates tested for susceptibility (Table 26).

Table 29: Prevalence of resistance to selected antimicrobials in *Campylobacter coli* from fattening pigs in 2015, using harmonised ECOFFs[a]

Country	Ciprofloxacin		Erythromycin		Gentamicin	
	%prev.	%95CI	%prev.	%95CI	%prev.	%95CI
Croatia	58.7	53.0–63.4	9.0	5.7–11.7	1.0	0.27–2.0
Estonia	9.2	4.05–15.2	1.1	0.03–3.4	1.1	0.03–3.4
Germany	30.4	24.9–35.0	7.6	4.4–10.3	0.0	0.0–0.0
Luxembourg	59.0	49.5–67.3	17.9	10.5–24.4	5.2	0.9–8.9
Slovenia	75.9	67.2–84.3	5.7	1.0–10.2	5.7	1.0–10.2
Spain	42.6	35.2–47.6	28.4	21.7–33.0	4.8	1.6–7.0
Sweden	31.4	22.6–39.1	0.0	0.0–0.0	0.0	0.0–0.0
Norway	9.6	5.7–13.2	0.0	0.0–0.0	0.0	0.0–0.0
Switzerland	24.5	17.8–29.4	2.4	0.0–4.1	0.3	0.008–0.9

Country	Nalidixic acid		Streptomycin		Tetracycline	
	%prev.	%95CI	%prev.	%95CI	%prev.	%95CI
Croatia	57.7	52.1–62.5	62.7	57.1–67.4	62.7	57.1–67.4
Estonia	9.2	4.05–15.2	27.6	12.3–37.0	13.8	2.0–21.1
Germany	26.9	21.6–31.4	56.1	50.1–61.1	51.1	45.1–56.1
Luxembourg	66.6	57.5–74.6	64.0	54.8–72.2	71.7	63.0–79.3
Slovenia	75.9	67.2–84.3	75.9	67.2–84.3	37.9	28.1–47.5
Spain	42.6	35.2–47.6	42.1	34.7–47.1	45.3	37.8–50.4
Sweden	32.2	23.3–39.9	41.4	32.1–49.6	1.5	0.17–3.4
Norway	10.0	6.0–13.5	23.7	18.1–28.8	0.4	0.009–1.2
Switzerland	24.5	17.8–29.4	45.3	37.5–50.9	33.2	25.8–38.6

(a): Because of the possible influence of methodological variations on the results for different countries, caution is advised when comparing results between different countries. Further harmonisation of the methods for isolation and speciation used is required to enable valid comparison between results.

Methodological consideration on the isolation and speciation of C. coli *from fattening pigs*

Although the over-arching principle of the monitoring is that only one *C. coli* isolate from each epidemiological unit should be included in the sampling frame, variations in methods used for isolation and speciation of *C. coli* from fattening pigs have occurred, as they are not fully harmonised between MSs, conversely to the susceptibility testing method. When primary culture plates are examined for suspect *Campylobacter* colonies, either one or several suspect *C. coli* isolates can be selected for further examination and confirmation of bacterial identification. Four of the countries submitting results (Germany, Sweden, Norway and Spain) selected a single suspect *Campylobacter* colony from primary culture plates, whereas the remaining countries selected between two and five colonies. Conversely, the culture methods performed by reporting countries tended to be similar.

The methodology applied may have affected *C. coli* prevalence estimates and subsequently, the estimates of prevalence of resistant *C. coli*. In general, it may be assumed that MSs using methods with increased intensity of effort to detect *C. coli* will report a higher relative prevalence. Table 29 presents results obtained using the available data which should be interpreted with the caveat that the intensity of sampling effort is not equal between MSs. Further refinement and harmonisation of the methods and procedures is required and the figures in Table 29 should be regarded as provisional and possibly subject to variation, resulting from these methodological differences between MSs.

3.2.3. Discussion

3.2.3.1. Antimicrobial resistance in *Campylobacter* in humans

Information on antimicrobial resistance in *Campylobacter* isolates from human cases of campylobacteriosis was available from 17 MSs, Iceland and Norway in 2015. Very high to extremely high (> 70.0%) 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 for the period 2013–2015, in two MSs. For *C. jejuni*, increasing trends of fluoroquinolone resistance were observed in five MSs. The level of acquired resistance to fluoroquinolones is so high in some MSs that this antimicrobial 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 (24.2–54.5%) proportions of *C. coli* being resistant in a third of the reporting countries. Decreasing trends of erythromycin resistance were observed in two MSs for both *C. jejuni* and *C. coli* from humans. Clinical and microbiological co-resistance to ciprofloxacin and erythromycin which are both 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. Fourteen per cent of the tested *C. coli* isolates were resistant to all three antimicrobials (ciprofloxacin, erythromycin and tetracycline), possibly due to the presence of the efflux pump CmeABC, see below. 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. This is worrying since these three are the most commonly used antimicrobials to treat campylobacteriosis. In Portugal, carbapenems are sometimes used for treating multidrug-resistant invasive *Campylobacter* infections.

In this report, isolates from cases notified as having been acquired while travelling abroad were excluded from the analysis. The rationale was to assess the relationship between antimicrobial resistance in *Campylobacter* isolates from food and food-producing animals with antimicrobial resistance in human isolates of *Campylobacter* spp. However, as imported or traded food can constitute a large proportion of the food available in some countries, the relationship between resistance in food and food-producing animals and in the human population is complex.

While *C. jejuni* is the *Campylobacter* species causing most of the infections in humans, resistance to antimicrobials important for clinical treatment is a larger problem in *C. coli*. *C. coli* accounted for almost 9,000 laboratory-confirmed human infections reported to ECDC for 2015. The poultry reservoir as a whole, including environmental transmission and direct animal contact in addition to preparation and consumption of poultry meat, has been estimated to account for up to 80% of campylobacteriosis cases (Wagenaar et al., 2013). *C. coli* has previously mostly been associated with the pig reservoir but in several EU countries, *C. coli* is now as prevalent, or even more prevalent, in poultry than *C. jejuni* (Wieczorek et al., 2013; Torralbo et al., 2015; Stella et al., 2016). In order to assess the most important sources for MDR *Campylobacter*, it is therefore important that countries report on *Campylobacter* findings in animals and food by species.

The quality of the AMR data for *Campylobacter* from humans continues to improve as the result of harmonised monitoring and reporting (ECDC, 2014, 2016). In 2015, two-thirds of the reporting countries provided the data as measured values to which ECOFFs could be applied. This compares to half of the countries in 2014 and a third in 2013. The number of reporting countries has also increased during this period, from 16 in 2013 to 19 in 2015. Seven countries still provided results interpreted with clinical breakpoints. By combining the categories of clinically 'intermediate' resistant and clinically 'resistant', the ECOFF-based category of 'wild type' corresponds fully to the 'susceptible' category and the ECOFF-based category of 'non-wild type' corresponds closely to the 'non-susceptible' category with only one exception for tetracyclines and *C. jejuni*. Thus, this approach further improves the comparability of human and non-human data. For future reports, EFSA and ECDC hope that more countries will report measured values. More harmonisation is also needed regarding the optimal sample of human isolates for inclusion in the monitoring programme at the EU level, as, in many countries, the sampling and the antimicrobials tested for a particular sample are not random and represent different fractions of all isolates identified in a country.

3.2.3.2. Antimicrobial resistance in *Campylobacter* in fattening pigs

Commission Implementing Decision 2013/652/EU provides for voluntary monitoring of resistance in *C. coli* from fattening pigs. The data relating to the susceptibility of *Campylobacter* reported were well harmonised with almost all MSs satisfying the requirements of the Decision. Typically, the resistance exhibited by *C. coli* isolates to ciprofloxacin, erythromycin and tetracyclines varied very widely between the reporting countries.

Presumptive mechanisms of resistance

Resistance to gentamicin in *Campylobacter* was uncommon in fattening pig isolates, occurring in 3.6% of isolates. In previous years, where gentamicin occurred in MDR *C. coli* isolates, streptomycin resistance was also observed. Streptomycin is now tested on a voluntary basis and was not included in the MDR analysis for 2015. A cluster of aminoglycoside-modifying enzymes was reported in *C. coli* from broiler chickens in China (Qin et al., 2012), indicating that co-selection of aminoglycoside resistance can occur in *Campylobacter*.

The frequently high levels of **tetracycline resistance** observed in *Campylobacter* may in part be a consequence of the presence of the tetracycline resistance gene *tet(O)* on a transferable plasmid facilitating dissemination of tetracycline resistance (Wieczorek and Osek, 2013), although *tet*(O) may also be chromosomally located in *Campylobacter* (Piddock et al., 2008). *tet*(O) encodes a protein promoting the release of tetracycline from its binding site (Connell et al., 2003).

Resistance to ciprofloxacin in *C. coli* isolates from humans was assessed at 70.6% for all contributing MSs (range: 38.5–100%) and 62.1% in fattening pigs (range: 24.2–93.5%) in 2015. A single mutation can result in resistance to ciprofloxacin and nalidixic acid in *Campylobacter* and this probably accounts for the widespread and frequently high levels of resistance detected in countries. The picture is clearly complex in relation to the vehicles of human infections, because these may be related to consumption of pork, chicken or turkey meat, as well as other sources, such as waterborne infection. International trade also means that consumers may be exposed to meat produced in a number of different countries; cross-contamination between products may also occur, including in the home.

Regarding **resistance to erythromycin** – in all reporting MSs, erythromycin resistance in *C. coli* from fattening pigs was 21.6%, particular resistance mutations have been associated with high-level erythromycin resistance. Transferable macrolide resistance, which also confers high-level macrolide resistance, has been detected recently, taking the form of a transferable plasmid bearing the macrolide resistance gene *erm*(B) (Wang et al., 2015). This is an important development, because macrolide resistance up to this point appears to have been mutational rather than related to transferable, plasmid-mediated resistance mechanisms in *Campylobacter* and the occurrence of plasmid-mediated resistance may allow the much wider dissemination of macrolide resistance than has previously been observed. As the *erm*(B) gene confers erythromycin MICs of ≥ 512 mg/L, it may be necessary in the future to review the dilution range of erythromycin which is tested. In 2015, 104/1,077 (9.7%) *C. coli* isolates from fattening pigs had an MIC > 128 mg/L, so if *erm*(B) is present in these *Campylobacter* isolates, from the current monitoring, an upper ceiling of 9.7% can be placed on the proportion of the total number of isolates which might carry this gene. It is likely that both mutational resistance and transferable resistance to macrolides may contribute to this total, because transferable macrolide resistance has now been described in broilers in Spain (Florez-Cuadrado et al., 2016).

Campylobacter can develop **multiple resistance** to several of the different antimicrobials in the common test panel by different mechanisms conferring either resistance against the different individual compounds or resistance against combinations of compounds. This complicates the process of trying to infer the genotype from the phenotype and account for the multiple resistance patterns detected. Resistance to ciprofloxacin and erythromycin in *Campylobacter* is usually the result of mutation with or without the additional action of efflux pumps (Piddock et al., 2003; Ge et al., 2005; Luangtongkum et al., 2009). The efflux pump CmeABC acting alone has also been shown to confer a degree of resistance to erythromycin, ciprofloxacin and tetracyclines (Ge et al., 2005). In 2015, certain isolates of *C. coli* from animals and humans, showed resistance to erythromycin, ciprofloxacin and tetracyclines, raising the possibility that CmeABC may have been responsible for or contributed to the observed pattern of resistance. Only two isolates of *C. coli* from fattening pigs were resistant to the combination erythromycin, ciprofloxacin and tetracyclines, without showing nalidixic acid resistance. CmeABC may also have contributed to the MDR patterns of resistance shown by isolates which were resistant to erythromycin, ciprofloxacin, nalidixic acid and tetracyclines, but in which *gyrA* mutations were also present conferring both ciprofloxacin and nalidixic acid resistance.

Possible further assessment

The molecular basis for the observed patterns of MDR was not reported for the isolates, but molecular investigation and characterisation of selected isolates, representative of particular patterns of importance or interest, would assist greatly in determining significance and assessing the potential for further dissemination through, for example, co-selection or the occurrence of resistance on conjugative plasmids. Future reviews of the AMR monitoring programme should consider expanding the range of erythromycin concentrations tested to facilitate the detection of possible transferable macrolide resistance and flag those isolates which might be subjected to further testing using appropriate genotyping methods.

The range of dilutions over which erythromycin is currently tested is limited and thus, an analysis of resistance occurring at higher levels above the ECOFF was not completely possible from the present data. Further evaluation of the resistance detected to erythromycin could include such an evaluation of higher levels of resistance. This might be particularly relevant in those MSs where resistance is already high, as a possible indication of on-going high selective pressure. Screening for high-level macrolide resistance would assist in providing an early warning that transferable macrolide resistance may be present.

3.3. Antimicrobial resistance in indicator *Escherichia coli*

> **Rationale for monitoring AMR in indicator *E. coli* in food-producing animals and food**
>
> Commensal *E. coli* is typically chosen as the representative indicator of antimicrobial resistance in Gram-negative bacteria, as it is commonly present in animal faeces, may be relevant to human medicine and can often acquire conjugative plasmids, which can carry resistance determinants and are transferable between enteric bacteria. Commensal *E. coli*, which are resistant and present in the intestines of food-producing animals, constitutes a reservoir of resistance genes that can spread horizontally to zoonotic and other bacteria present in the food chain. The monitoring of antimicrobial resistance in indicator *E. coli*, isolated from either randomly selected healthy animals or carcases and meat derived thereof, and chosen to be representative of the general population, provides valuable data on resistance occurring in that population. Determining the occurrence of resistance to antimicrobials in a representative sample of indicator *E. coli* provides data useful for investigating the relationship between the occurrence of resistance and the selective pressure exerted by the use of antimicrobials on the intestinal population of bacteria in food-producing animals. Indicator *E. coli* is also helpful as a representative of the Enterobacteriaceae to monitor the emergence and changes in the proportion of bacteria producing ESBLs. Since 2014, the monitoring of AMR in indicator *E. coli* from food-producing animals and food thereof has been mandatory under the EU legislation.

For 2015, in total, 27 MSs and two non-MSs reported quantitative MIC data in commensal (indicator) *E. coli* isolates from fattening pigs (Table ESCHEOVERVIEW). Antimicrobial susceptibility data to the harmonised set of substances[17] were interpreted using ECOFFs laid down in Commission

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[17] For further information on antimicrobials tested by the reporting countries and the reported MIC distributions for *E. coli* in 2015, please refer to Tables 6 and 8 in the material and methods chapter and to the submitted and validated MS data published on the EFSA website, respectively.

implementing Decision 2013/652/EC to determine organisms exhibiting reduced susceptibility, i.e. showing 'microbiological' resistance (as opposed to 'clinical' resistance).[18]

3.3.1. Antimicrobial resistance in indicator *Escherichia coli* isolates from animals

3.3.1.1. Antimicrobial resistance in indicator *Escherichia coli* from fattening pigs

For 2015, 27 MSs – all MSs except Luxembourg – and two non-MSs provided data on indicator *E. coli* isolates from fattening pigs (Table 30) based on the requirements laid down in Decision 2013/652/EC. Denmark and the Netherlands also provided data on fattening pigs for 2014.

Resistance levels among indicator E. coli isolates from fattening pigs

The occurrence of resistance in *E. coli* isolates from fattening pigs varied markedly between reporting countries. Resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim was high to very or extremely high in most reporting countries (overall resistance equalling 39.3%, 44.2%, 54.7%, 35.3%, respectively), with the striking exception of some Nordic countries (Finland, Norway and Sweden) which registered lower occurrences of resistance to the above mentioned antimicrobials (Table 30). Resistance to chloramphenicol ranged widely from low to very high, whereas gentamicin resistance was generally reported at very low to low levels, with the exception of Cyprus, recording high resistance.

Resistance to ciprofloxacin and nalidixic acid varied markedly between the reporting countries (overall resistance equalling 10.5% and 6.0%, respectively). Finland, Sweden and Norway reported very low resistance for both substances. The comparison of resistance to ciprofloxacin and nalidixic acid in each reporting country shows that the levels of resistance to ciprofloxacin were generally slightly higher (Table 30).

Resistance to cefotaxime and ceftazidime was either not detected in 11 MSs or reported at low levels in reporting countries (overall resistance equalling 1.4% and 1.3%, respectively). Cefotaxime and ceftazidime resistance were either similar or cefotaxime resistance slightly exceeded ceftazidime resistance in most countries, although, in one MS (Poland), ceftazidime resistance exceeded cefotaxime resistance. For more comprehensive analyses of resistance to third-generation cephalosporins and carbapenems, see Section 3.5.

Resistance to azithromycin was generally very low to low among the reporting countries (overall resistance equalling 2.8%), with the exception of Portugal which reported moderate resistance (14.6%) and Cyprus which reported high resistance of 45.5% to azithromycin.

Resistance to colistin was overall very low at 0.4%, and was not recorded in 18 of the 29 reporting countries. None of the reporting countries reported meropenem resistance.

Tigecycline resistance was reported only by two MSs (Cyprus 14.5% and Malta 1.5%), overall resistance equalling 0.2%.

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[18] Of particular note is that 'microbiological' resistance to ciprofloxacin was addressed using ECOFF CIP > 0.064 mg/L in this report.

Resistance to tigecycline

Resistance to tigecycline was reported by Cyprus, Malta and Norway at MICs of 2 and 4 mg/L of tigecycline. The ECOFF for tigecycline and *E. coli* was resistant > 1 mg/L when Commission implementing Decision 2013/652/EU was published but has been revised by EUCAST very recently and is currently resistant (non-wild-type) > 0.5 mg/L. Susceptibility testing of tigecycline is not straightforward because the method can be affected by oxidation of the test reagents. Several mechanisms of resistance to tigecycline in Enterobacteriaceae have been described and these include increased activity of efflux pumps (AcrAB), mutation of the ribosomal protein S10 and modification of the Mla system involved in phospholipid transport in cell membranes (He et al., 2016). The mechanisms of development of microbiological resistance, which may involve upregulation of normal cell pathways or processes, therefore, probably also contributes to the occurrence of a 'tail' of isolates on the MIC distribution with values just above the ECOFF (Figure 54).
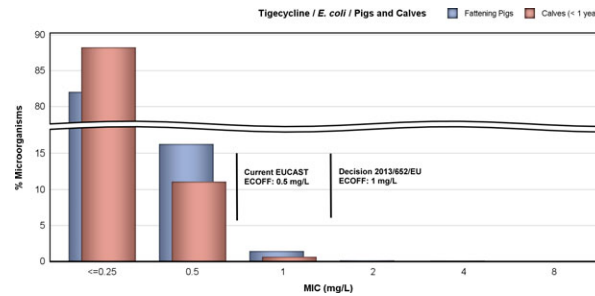
Figure 54: Distribution of MICs of tigecycline in indicator *E. coli* from fattening pigs and calves under one year of age, 2015

Spatial distribution of resistance among indicator E. coli *from fattening pigs*

The spatial distributions of ciprofloxacin and cefotaxime resistance in *E. coli* from fattening pigs are shown in Figures 55 and 56. All countries reported resistance to ciprofloxacin with the highest levels of resistance reported in southern European countries. Resistance to cefotaxime was low, very low or was not detected in fattening pigs across Europe.

Table 30: Occurrence of resistance to selected antimicrobials in indicator *E. coli* from fattening pigs in reporting MSs in 2015, using harmonised ECOFFs

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
2015														
Austria	163	12.9	163	0	163	2.5	163	1.8	163	3.7	163	4.9	163	0.6
Belgium	186	35.5	186	0	186	1.1	186	1.1	186	17.7	186	2.2	186	0
Bulgaria	21	57.1	21	4.8	21	0	21	0	21	52.4	21	47.6	21	0
Croatia	85	32.9	85	0	85	0	85	0	85	10.6	85	7.1	85	0
Cyprus	55	89.1	55	45.5	55	5.5	55	5.5	55	69.1	55	43.6	55	0
Czech Republic	187	34.8	187	1.1	187	2.1	187	2.6	187	8.6	187	2.1	187	0
Denmark	174	31.6	174	0.6	174	0	174	0	174	2.3	174	1.1	174	0.6
Estonia	85	31.8	85	1.2	85	1.2	85	1.2	85	9.4	85	7.1	85	0
Finland	217	14.3	217	0	217	0	217	0	217	0.9	217	0.5	217	0
France	200	19.5	200	0.5	200	0.5	200	0.5	200	12	200	4.5	200	0
Germany	212	33	212	2.4	212	3.3	212	3.3	212	6.6	212	4.2	212	0
Greece	116	57.8	116	2.6	116	5.2	116	5.2	116	36.2	116	12.1	116	0
Hungary	170	39.4	170	0.6	170	1.2	170	1.2	170	11.2	170	8.2	170	0
Ireland	147	25.2	147	1.4	147	0.7	147	0.7	147	10.2	147	2.7	147	0
Italy	168	63.7	168	1.8	168	0.6	168	0	168	32.7	168	14.9	168	0.6
Latvia	150	26.7	150	0	150	0	150	0	150	8	150	5.3	150	0.7
Lithuania	89	34.8	89	2.2	89	0	89	0	89	11.2	89	10.1	89	2.2
Malta	68	25	68	0	68	0	68	0	68	10.3	68	5.9	68	0
Netherlands	298	28.9	298	1	298	0.3	298	0.3	298	9.4	298	0.7	298	0
Poland	170	35.9	170	0	170	4.1	170	4.7	170	12.4	170	15.9	170	0
Portugal	198	74.7	198	14.6	198	5.1	198	5.1	198	52	198	20.7	198	2.5
Romania	399	67.2	399	7.8	399	1.5	399	1.5	399	40.9	399	29.6	399	0.5
Slovakia	85	31.8	85	1.2	85	0	85	0	85	15.3	85	7.1	85	0
Slovenia	85	22.4	85	1.2	85	0	85	0	85	7.1	85	2.4	85	0
Spain	170	82.4	170	2.9	170	0.6	170	0.6	170	40	170	49.4	170	2.9
Sweden	200	20.5	200	0.5	200	1	200	0	200	3	200	2.5	200	0
United Kingdom	170	35.3	170	1.2	170	0	170	0	170	28.2	170	2.4	170	0.6
Total (27 MSs)	**4,268**	**39.3**	**4,268**	**2.8**	**4,268**	**1.4**	**4,268**	**1.3**	**4,268**	**18.3**	**4,268**	**10.5**	**4,268**	**0.4**
Norway	270	11.1	270	0	270	0.7	270	0.4	270	2.2	270	0.7	270	0

EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2015

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Switzerland	182	17.0	182	0	182	0.5	182	0.5	182	8.2	182	3.3	182	0
2014														
Denmark	82	36.6	82	0	82	0	82	0	82	2.4	82	1.2	82	0
Netherlands	392	24.0	392	0	392	0.5	392	1.0	392	12.0	392	0	392	0
Total (2 MSs)	**474**	**26.2**	**474**	**0**	**474**	**0.4**	**474**	**0.8**	**474**	**10.3**	**474**	**0.2**	**474**	**0**

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
2015												
Austria	163	2.5	163	3.1	163	22.7	163	47.2	163	0	163	10.4
Belgium	186	1.6	186	1.6	186	43.0	186	40.3	186	0	186	38.2
Bulgaria	21	0	21	23.8	21	90.5	21	76.2	21	0	21	28.6
Croatia	85	3.5	85	10.6	85	40.0	85	56.5	85	0	85	21.2
Cyprus	55	21.8	55	21.8	55	98.2	55	100	55	14.5	55	94.5
Czech Republic	187	3.2	187	1.1	187	36.9	187	48.1	187	0	187	25.1
Denmark	174	1.1	174	0.6	174	35.6	174	35.6	174	0	174	24.1
Estonia	85	1.2	85	4.7	85	34.1	85	41.2	85	0	85	25.9
Finland	217	0.9	217	0.5	217	17.1	217	21.2	217	0	217	15.2
France	200	2.0	200	4.5	200	41.0	200	54.5	200	0	200	34.5
Germany	212	3.3	212	2.4	212	35.4	212	44.8	212	0	212	25.9
Greece	116	3.4	116	8.6	116	64.7	116	79.3	116	0	116	56.9
Hungary	170	2.4	170	6.5	170	30.0	170	68.2	170	0	170	17.1
Ireland	147	2.0	147	2.0	147	44.2	147	59.2	147	0	147	36.7
Italy	168	4.2	168	6.5	168	63.1	168	72.0	168	0	168	58.3
Latvia	150	4.0	150	4.0	150	29.3	150	44.0	150	0	150	20.7
Lithuania	89	3.4	89	7.9	89	43.8	89	51.7	89	0	89	29.2
Malta	68	4.4	68	4.4	68	42.6	68	69.1	68	1.5	68	41.2
Netherlands	298	0.7	298	0.7	298	40.3	298	45.3	298	0	298	35.9
Poland	170	1.8	170	6.5	170	36.5	170	48.2	170	0	170	18.8
Portugal	198	2.0	198	9.1	198	76.8	198	89.4	198	0	198	68.7
Romania	399	9.0	399	16.0	399	63.4	399	74.2	399	0	399	47.6

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Slovakia	85	3.5	85	7.1	85	34.1	85	48.2	85	0	85	22.4
Slovenia	85	0	85	0	85	15.3	85	40.0	85	0	85	14.1
Spain	170	3.5	170	25.9	170	75.9	170	89.4	170	0	170	74.7
Sweden	200	0.5	200	2.0	200	25.0	200	10.0	200	0	200	19.5
United Kingdom	170	7.6	170	1.2	170	54.7	170	67.6	170	0	170	47.1
Total (27 MSs)	**4,268**	**3.3**	**4,268**	**6.0**	**4,268**	**44.2**	**4,268**	**54.7**	**4,268**	**0.2**	**4,268**	**35.3**
Norway	270	0	270	0.7	270	14.1	270	9.6	270	1.1	270	9.6
Switzerland	182	1.6	182	3.3	182	41.8	182	29.7	182	0	182	22.0
2014												
Denmark	82	1.2	82	1.2	82	35.4	82	41.5	82	0	82	31.7
Netherlands	392	3.6	392	0.3	392	41.3	392	49.2	392	0	392	30.9
Total (2 MSs)	**474**	**3.2**	**474**	**0.4**	**474**	**40.3**	**474**	**47.9**	**474**	**0**	**474**	**31**

All *E. coli* isolates tested were susceptible to meropenem. MSs: Member States; N: number of isolates tested; % Res: percentage of resistant isolates.
(a): The reported occurrence of colistin resistance is unlikely to equate to the occurrence of *mcr-1/mcr-2* genes.
(b): ECOFF applied 1 mg/L.
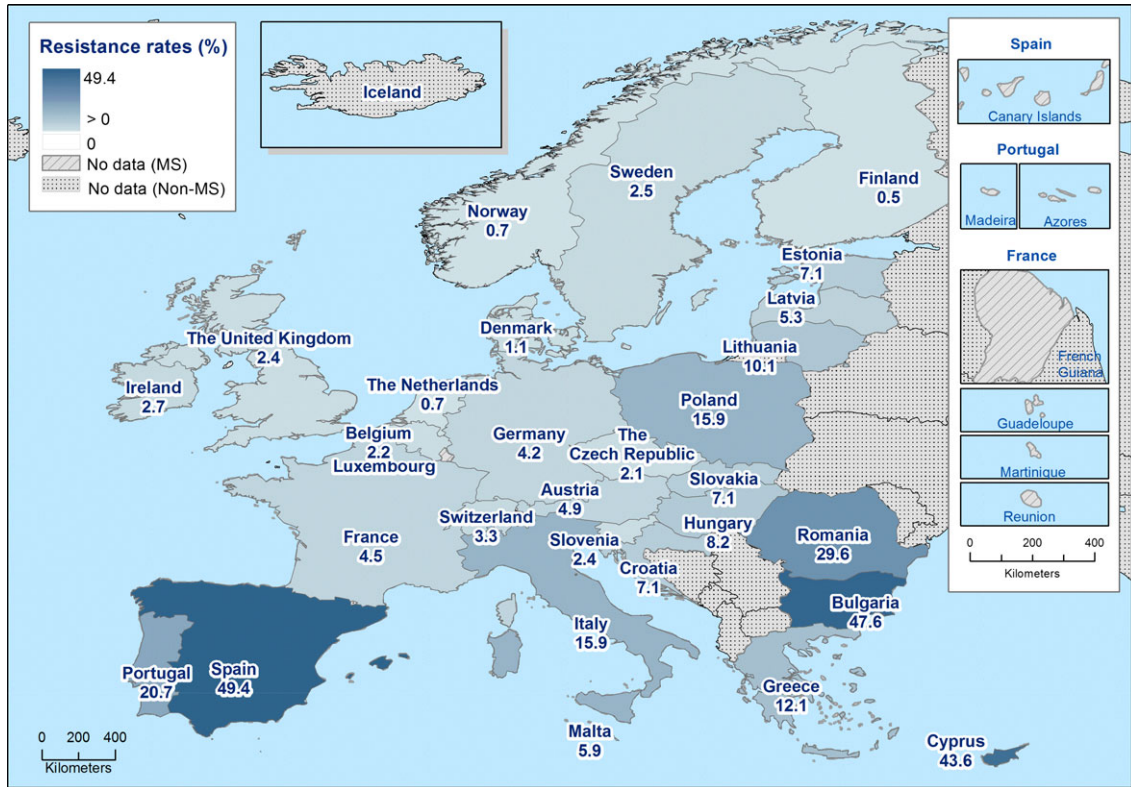
Figure 55: Spatial distribution of ciprofloxacin resistance among indicator *E. coli* from fattening pigs in reporting countries in 2015, using harmonised ECOFF
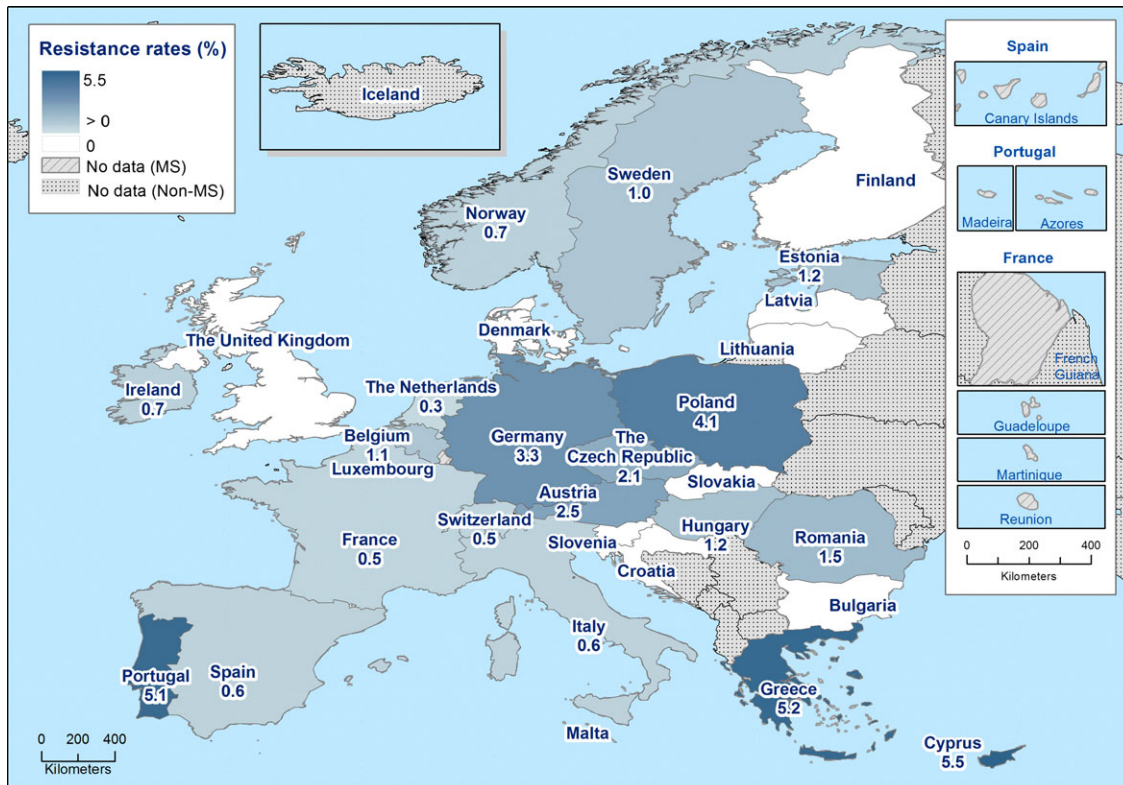
Figure 56: Spatial distribution of cefotaxime resistance among indicator *E. coli* from fattening pigs in reporting countries in 2015, using harmonised ECOFF

Co-resistance to cefotaxime and ciprofloxacin among indicator E. coli *from fattening pigs*

At the EU level, 0.5% (24/4,720) of all indicator *E. coli* isolates, originating from nine MSs showed co-resistance using microbiological cut-offs, whereas 0.3% (12/4,720) from seven MSs were resistant when clinical breakpoints were applied (Table COMESCHEPIG, Table 31). The clinical breakpoints for cefotaxime (> 2 mg/L) and ciprofloxacin (> 1 mg/L) are higher than the corresponding microbiological cut-offs (> 0.25 mg/L, > 0.064 mg/L, respectively) accounting for this difference. Cyprus, Greece and Portugal reported the highest percentages of isolates co-resistant to ciprofloxacin and cefotaxime using the microbiological cut-offs, although figures were low for all three countries at 2.6–3.6%. In those countries where multiple isolates were co-resistant to ciprofloxacin and cefotaxime, the isolates frequently had differing MDR patterns, pointing against simple clonal expansion.

Temporal trends in resistance among indicator E. coli *from fattening pigs*

Temporal trends in resistance to selected antimicrobials in indicator *E. coli* isolates from fattening pigs over the 7-year study period from 2009 to 2015 are displayed in Figure 57. Four MSs and Switzerland provided resistance data for 5 years or more, which facilitated statistical analysis.

Marked differences in resistance levels between reporting countries were observed for many of the antimicrobials. The highest levels of resistance were shown to tetracyclines, with lower levels of resistance to ampicillin, then much lower levels of resistance to ciprofloxacin and cefotaxime and this ranking tended to be maintained in all MSs for which data were available over the study period. Resistance to cefotaxime and ciprofloxacin was generally low to both compounds but where differences were observed, cefotaxime was usually lower than ciprofloxacin. Spain consistently showed higher levels of resistance to ciprofloxacin than the other reporting MSs with an upward trend to 2015, with ciprofloxacin resistance in fattening pigs having increased from 30.6% in 2011 to 49.4% in 2015. A close similarity in resistance levels to ciprofloxacin and nalidixic acid was observed in most MSs.

Although resistance to many of the antimicrobials was broadly stable or had shown only gradual increases or decreases over the study period, statistically significant trends in resistance to some of the antimicrobials over 5 or more years were discerned. Statistically significant decreasing trends were noted in the occurrence of resistance to tetracyclines in Austria, Belgium, France and the Netherlands and to ampicillin in Belgium and the Netherlands, while Denmark recorded an increasing trend of resistance to ampicillin. It is also of special note that statistically significant decreasing trends over 5 or more years were observed for cefotaxime, ciprofloxacin and nalidixic acid in Belgium and the Netherlands.

Assessing the relationship between antimicrobial consumption and resistance

The Netherlands and France (Ecoantibio plan), as well as many other European countries, have initiatives underway to reduce the use of antimicrobials in food-producing animals. Decreasing trends are therefore of interest from several perspectives, including, (1) The outcome of national initiatives in reducing the occurrence of antimicrobial resistance, (2) The ability of the monitoring programme to detect changes in the occurrence of resistance, and (3) The complexity of the epidemiology of antimicrobial resistance, where relationships are not always simple. The Joint Interagency Antimicrobial Consumption and Resistance Analysis (JIACRA) Report (ECDC et al., 2015) examined associations between antimicrobial consumption and the occurrence of resistance and a further JIACRA report is currently in preparation.

Figure 57: Trends in ampicillin (AMP), cefotaxime (CTX), ciprofloxacin (CIP), nalidixic acid (NAL) and tetracyclines (TET) resistance in indicator *E. coli* from fattening pigs in reporting countries, 2009–2015, using harmonised ECOFFs
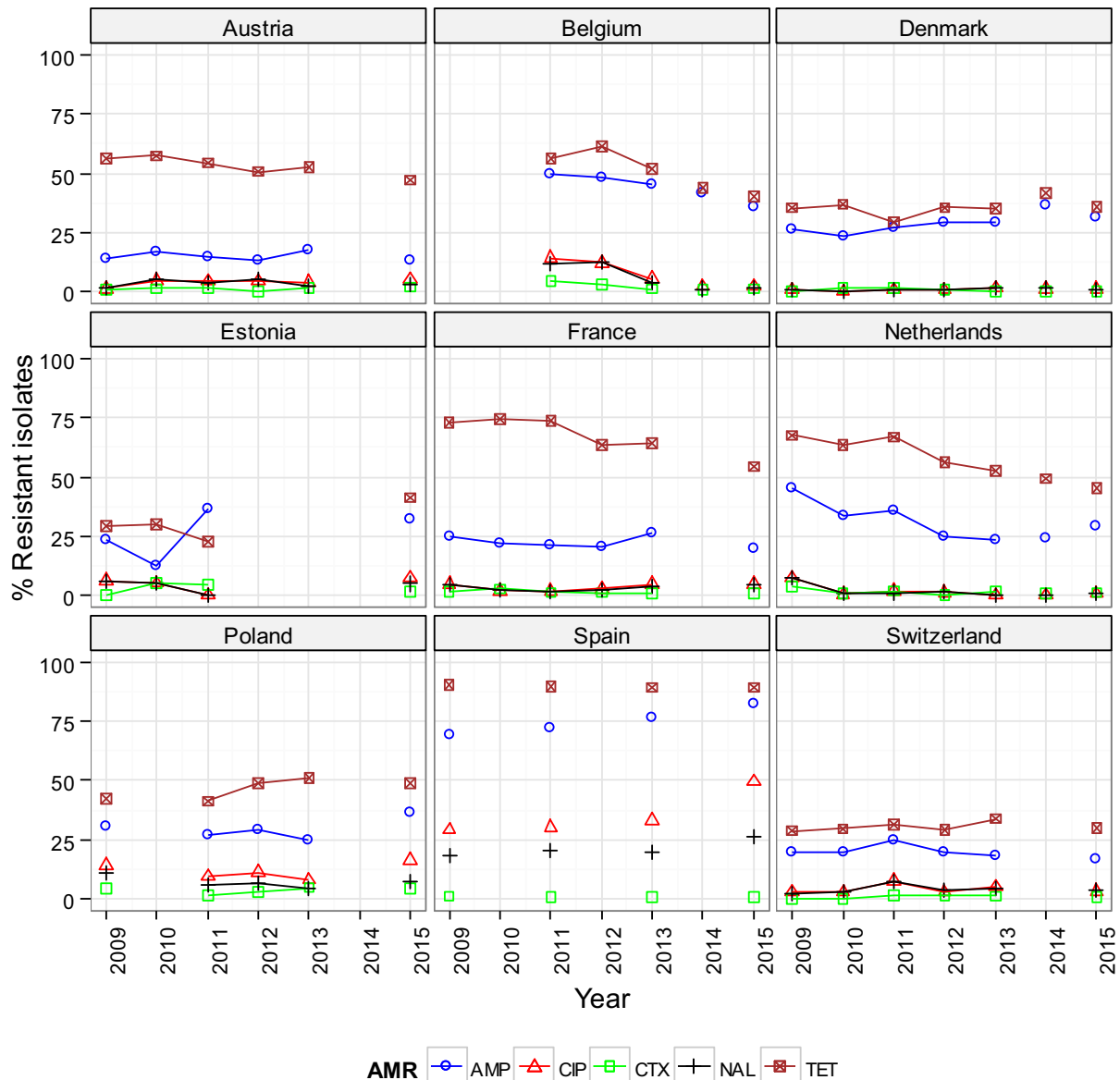
Statistically significance of trends over four/five or more years was tested by a logistic regression model (p ≤ 0.05). Statistically significant ***increasing*** trends were observed for **ampicillin** in Denmark (↑) and Spain (↑), as well as for **ciprofloxacin** in Poland (↑) and Spain (↑). Statistically significant ***decreasing*** trends were observed for **ampicillin** in Belgium (↓) and the Netherlands (↓), for **tetracycline** in Austria (↓), Belgium (↓), France (↓) and the Netherlands (↓), as well as for **cefotaxime**, **ciprofloxacin** and **nalidixic acid** in Belgium (↓) and the Netherlands (↓).

Multiple resistance among indicator E. coli *from fattening pigs*

For 2015, 29 countries provided data at the isolate level regarding resistance in indicator *E. coli* in fattening pigs (Figure 58). Although all reporting countries recorded multiresistant isolates, the proportion differed substantially between them, reaching up to 98.2% in Cyprus (Table COMESCHEPIG). The frequency distributions (Figure 58) showed that isolates resistant to five antimicrobials were reported from all reporting countries, except Finland, and three MSs reported a few isolates resistant to eight substances and one isolate reported by Cyprus was resistant up to nine substances. The maximum multidrug resistance count possible is resistance to eleven substances and this was not detected.
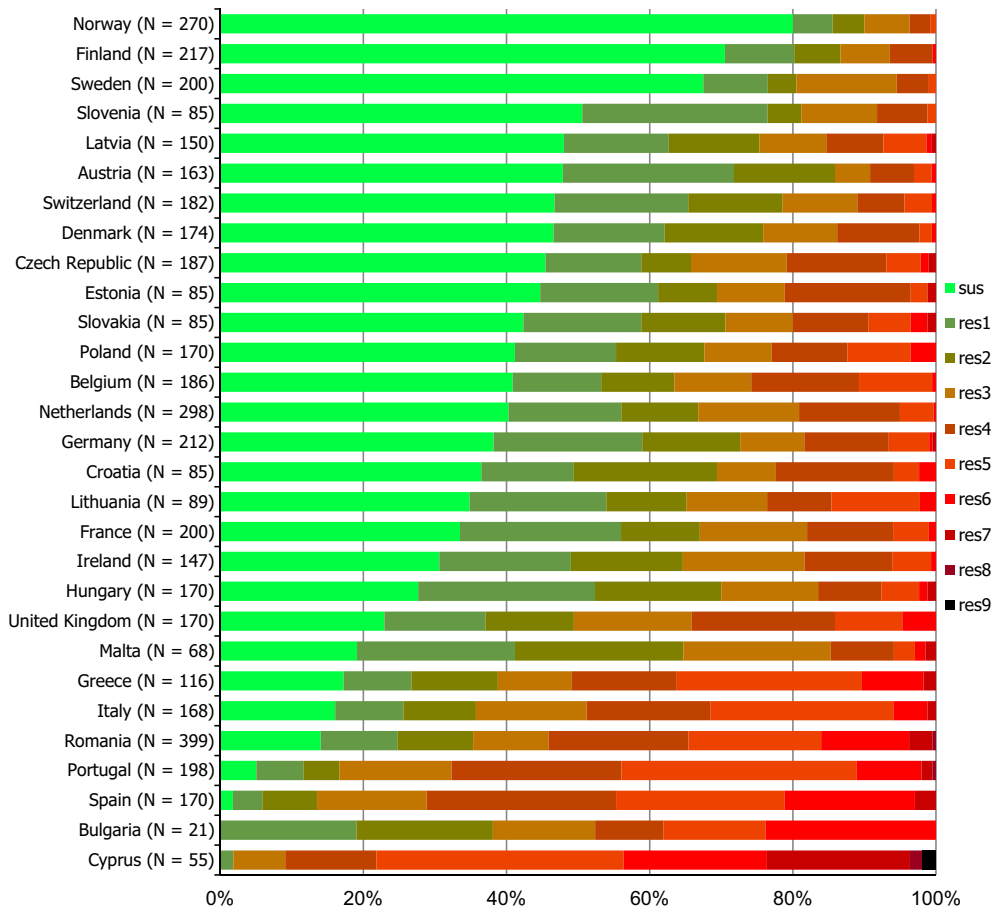
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Escherichia coli*; sus: susceptible to all antimicrobial classes of the harmonised set for *Escherichia coli*; res1–res9: resistance to one up to eleven antimicrobial classes of the harmonised set for *Escherichia coli*.

Figure 58: Frequency distribution of *E. coli* isolates completely susceptible and resistant to 1–11 classes of antimicrobials in fattening pigs in reporting countries, 2015, using harmonised ECOFFs

Spatial distribution of full susceptibility among indicator E. coli *from fattening pigs*

The spatial distribution of full susceptibility to the panel of antimicrobial substances tested in indicator *E. coli* from fattening pigs in 2015 is shown in Figure 59. The susceptibility to each individual antimicrobial was determined using epidemiological cut-off values (ECOFFs); all isolates were tested against the same mandatory panel of antimicrobials. Among the reporting countries, marked variations were observed in the percentages of completely susceptible isolates, which ranged from none in Bulgaria and Cyprus, 1.8% and 5.1% in Spain and Portugal, up to 70.5% in Finland and nearly 80.0% in Norway. The highest levels of full susceptibility were shown by isolates from Norway, Finland and Sweden, and the levels of full susceptibility globally decrease in a north to south gradient.
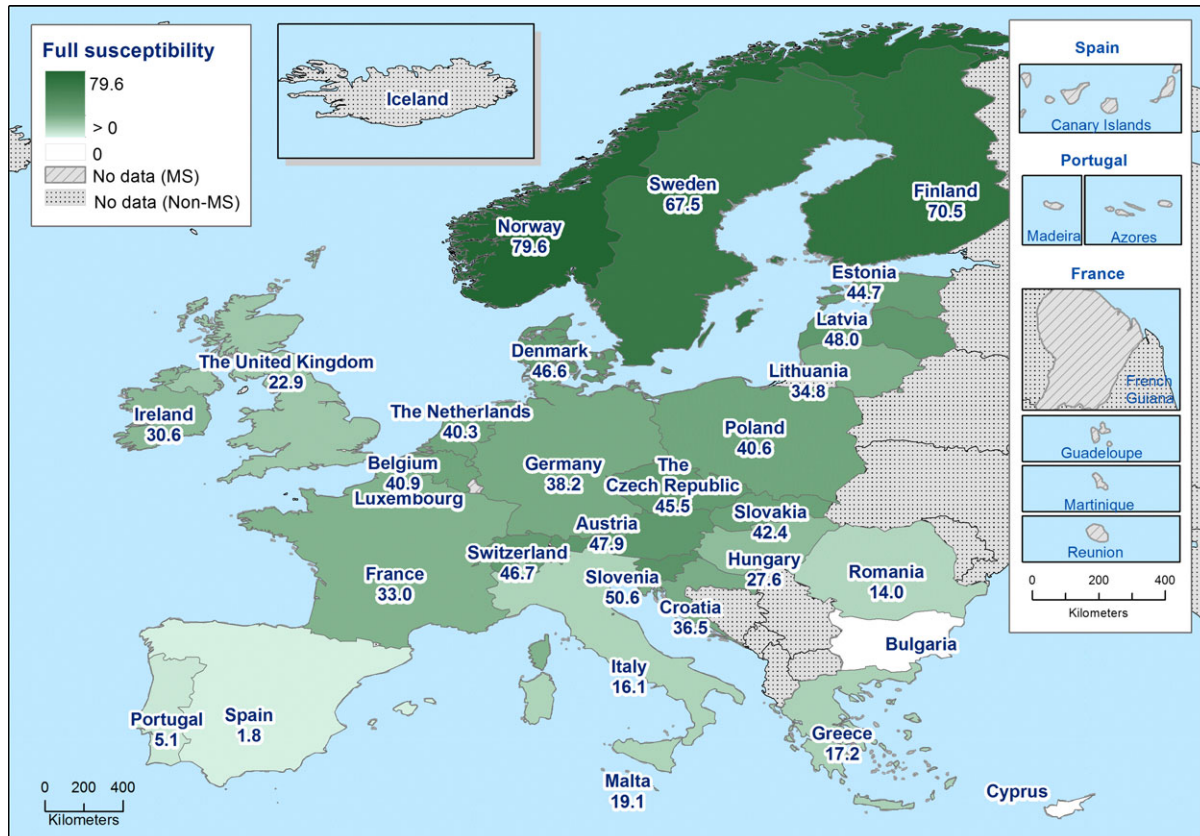
Figure 59: Spatial distribution of full susceptibility to the panel of antimicrobials tested among indicator *E. coli* from fattening pigs in reporting countries, 2015, using harmonised ECOFFs

Multi/co-resistance patterns among indicator E. coli *from fattening pigs*

As expected, most isolates resistant to ciprofloxacin were also resistant to nalidixic acid when using ECOFFs as interpretive thresholds of resistance. Similarly, isolates which were resistant to ceftazidime were usually also resistant to cefotaxime. Considering the resistance patterns of isolates co-resistant to ciprofloxacin and cefotaxime (24 isolates), a number of isolates (19 out of 24 or 79.2%) were also resistant to ampicillin, sulfamethoxazole and tetracyclines, with or without additional resistances. Trimethoprim resistance (18 out of 24 or 75.0%) was also commonly observed in isolates co-resistant to ciprofloxacin and cefotaxime, whereas resistance to nalidixic acid and ampicillin was expected in such co-resistant isolates. A variety of resistance patterns was observed in co-resistant isolates, each pattern occurring at a low frequency. Analysing the occurrence of higher levels of resistance to ciprofloxacin in *E. coli* revealed marked differences between MSs (Table CIPESCHEPIG); high-level ciprofloxacin resistance was most frequently observed in countries with a high proportion of isolates exhibiting 'microbiological' resistance. A wide variety of resistance patterns was observed in high-level ciprofloxacin resistant isolates, each pattern occurring at a low frequency.

Table 31: Co-resistance to (fluoro)quinolones and third-generation cephalosporins in indicator *E. coli* from fattening pigs in MSs, 2015

Country	N	MDR patterns of isolates resistant to both CIP and CTX (number of isolates)	Resistant to both CIP and CTX, applying ECOFFs		Resistant to both CIP and CTX, applying CBPs	
			N	% Res	N	% Res
Austria	163	CTX-CAZ-CIP-AMP-NAL(1)	2	1.2	1	0.6
		CTX-CAZ-CIP-AMP-TET(1)				
Cyprus	55	CHL-CTX-CIP-AMP-NAL-SMX-TET-TMP(1)	2	3.6	1	1.8
		GEN-CHL-CTX-CAZ-CIP-TGC-AMP-NAL-SMX-TET-TMP(1)				
Czech Republic	187	GEN-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	1	0.5	1	0.5
Germany	212	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	1	0.5	1	0.5
Greece	116	CHL-CTX-CAZ-CIP-AMP-SMX-TET-TMP(1)	3	2.6	0	0
		CTX-CAZ-CIP-AMP-NAL-TET(1)				
		CTX-CAZ-CIP-AMP-SMX-TET-TMP(1)				
Hungary	170	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	2	1.2	0	0
		CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)				
Portugal	198	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(2)	7	3.5	6	3
		CHL-CTX-CAZ-CIP-AMP-SMX-TET-TMP(1)				
		CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(2)				
		CTX-CAZ-CIP-AMP-NAL-TET(1)				
		GEN-CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)				
Romania	399	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET(1)	5	1.3	1	0.3
		CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)				
		CTX-CAZ-CIP-AMP-NAL-TET-TMP(1)				
		CTX-CAZ-CIP-AMP-SMX-TET(1)				
		GEN-CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)				
Spain	170	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	1	0.6	1	0.6
Total (9 MSs)	**1,670**		**24**	**1.4**	**12**	**0.7**

N: number of isolates tested; CIP: ciprofloxacin; CTX: cefotaxime; ECOFFs: epidemiological cut-off values; % Res: percentage of resistant isolates; CBPs: clinical breakpoints; CAZ: ceftazidime; NAL: nalidixic acid; AMP: ampicillin; TET: tetracycline; GEN: gentamicin; CHL: chloramphenicol; COL: colistin; SMX: sulfamethoxazole; TMP: trimethoprim; MSs: Member States.

A 'new' summary indicator of resistance in fattening pigs at the EU level

The fattening pig population in each MS can differ in size, and therefore, partly because of this size difference, may have a different relative influence on resistance issues at the European level. A summary indicator of resistance ($R_{SUMMARY}$) in indicator *E. coli* from fattening pigs at the EU level was calculated taking account of such differences on the basis of the weighted mean by 'population correction unit-fattening pigs' (PCU-fattening pigs) of the proportions of resistant isolates observed in each of the 27 reporting MSs (Table 32).

The population correction unit (PCU) is a specific indicator of animal population size which has been developed by the EMA primarily to estimate sales corrected by the animal population in individual countries. PCU is used as a proxy for the size of the animal population domestically produced at risk of being treated and is purely a technical unit of measurement. The data sources used and the methodology for the calculation of PCU are comprehensively described in Appendix 2 to EMA's report 'Trends in the sales of veterinary antimicrobial agents in nine European countries: 2005–2009' (EMA and ESVAC, 2011). The PCU-fattening pigs were computed by the EMA based on data reported by the MSs and provided to EFSA (Table 1, Appendix A).

Compared with the proportion of resistant isolates at the EU level (computed as the fraction of the total number of resistant isolates out of the total number of tested isolates in the group of reporting MSs) typically presented in this EU Summary Report, the $R_{SUMMARY}$ better accounts for the structure of the fattening pig populations within the EU i.e. the distribution of the fattening pig population per reporting MS. More weight is therefore given to the resistance observed in the major fattening pig populations.

Table 32 presents the resistance to the substances of the mandatory panel assessed by using 'Total' and the 'summary indicator of resistance', $R_{SUMMARY}$ expressed in percentages of resistant indicator *E. coli* isolates from fattening pigs. Similar results are generally obtained, although $R_{SUMMARY}$ is slightly higher than 'Total' for a number of substances.

Table 32: Resistance in indicator *E. coli* from fattening pigs assessed by the percentage of resistant isolates (Total) and 'summary indicator of resistance' ($R_{SUMMARY}$) (weighted mean of the proportions of resistant isolates in the reporting MSs) in the EU, 27 MSs, 2015, using harmonised ECOFFs

EU 27 MSs	Ampicillin	Azithromycin	Cefotaxime	Ceftazidime	Chloramphenicol	Ciprofloxacin	Colistin
Total (in %)	39.3	2.8	1.4	1.3	18.3	10.5	0.4
$R_{SUMMARY}$ (in %)	42.9	1.9	1.5	1.5	17.9	14.12	0.8

EU 27 MSs	Gentamicin	Nalidixic acid	Sulfamethoxazole	Tetracycline	Tigecycline[a]	Trimethoprim
Total (in %)	3.3	6.0	44.2	54.7	0.2	35.3
$R_{SUMMARY}$ (in %)	2.8	7.6	47.4	57.1	0.03	39.6

MSs: Member States.
(a): ECOFF applied 1 mg/L.

3.3.1.2. Antimicrobial resistance in indicator *Escherichia coli* isolates from bovines under one year of age

In 2015, ten MSs and two non-MSs provided antimicrobial resistance data on 2,187 indicator *E. coli* isolates from bovines under one year of age which were addressed in the following analyses (Table 33).

> **Monitoring AMR in indicator *E. coli* in calves under one year of age**
>
> Cattle of different production types are farmed in Europe, including dairy cattle, beef cattle and veal calves. The relative importance of each production type of cattle differs between the different MSs. There are also differences in the relative amounts of usage of antimicrobials between the different cattle production types and differences in age when the different production types (or their products, in the case of milk) enter the food chain. The Commission implementing Decision 2013/652/EC stipulates that indicator *E. coli* should be monitored in bovines under one year of age in those MSs where the production of meat of those bovines in the MS is greater than 10,000 tonnes slaughtered per year, and thereby removes a potential source of variation between MSs relating to the type of cattle being monitored. The inclusion of calves of less than one year of age captures veal calves of less than the mandatory monitoring. It has been well-recognised for many years that young animals and those kept more intensively tend to show greater levels of resistance than mature animals or animals kept more extensively, relating to differences in their relative exposure to antimicrobials, including historical exposure (Hinton, 1986). Calves are also likely to receive colostrum or milk from their dam and this may contain antimicrobials if the dam has been treated for mastitis (including dry cow treatment) or other ailments. The EFSA BIOHAZ Panel has recently addressed this issue in a Scientific Opinion on the 'Risk for the development of Antimicrobial Resistance (AMR) due to feeding of calves with milk containing residues of antibiotics' (EFSA BIOHAZ Panel, 2017).

Resistance levels among indicator E. coli *from calves under one year of age*

In 2015, overall resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethroprim in *E. coli* isolates from calves of less than one year of age was high at the reporting MSs level, (31.0%, 36.6%, 45.4%, 24.7%, respectively), whereas overall resistance to chloramphenicol and ciprofloxacin was moderate at the reporting MSs level (15.4% and 11.4%, respectively). The overall resistance to all the other antimicrobials tested was low, with the exception of resistance to meropenem, which was not reported by any MSs.

Resistance to ciprofloxacin and nalidixic acid showed marked variation between reporting countries, ranging between 0.4% and 35.9%. Ciprofloxacin resistance, where detected, slightly exceeded resistance to nalidixic acid.

Resistance to cefotaxime and ceftazidime was either not detected or reported at low levels in all reporting countries. Resistance to cefotaxime and ceftazidime was generally similar within a MS, although resistance to one of the compounds often slightly exceeded resistance to the other.

Resistance to azithromycin was either not detected or was low or very low; tigecycline resistance was not detected in any isolate. Most reporting countries (8/12) did not detect colistin resistance and resistance levels were low or very low in the remaining reporting countries.

Spatial distribution of resistance among indicator E. coli *from calves under one year of age*

The spatial distribution of ciprofloxacin and cefotaxime resistance in indicator *E. coli* from calves under one year of age is shown in Figures 60 and 61, respectively. For ciprofloxacin, most countries reported no resistance or low to moderate levels of resistance; Belgium and Italy reported high levels of resistance. Figure 61 illustrates the occurrence of cefotaxime resistance in *E. coli* across the EU; levels of resistance were low, very low or resistance was not detected.

Table 33: Occurrence of resistance to selected antimicrobials in indicator *E. coli* from calves under one year of age in reporting MSs, in 2015, using harmonised ECOFFs

Country	Ampicillin		Azithromycin		Cefotaxime		Ceftazidime		Chloramphenicol		Ciprofloxacin		Colistin[a]	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
2015														
Belgium	196	57.7	196	4.1	196	3.1	196	3.1	196	27.6	196	24.0	196	2
Croatia	85	22.4	85	0	85	0	85	0	85	12.9	85	9.4	85	0
Denmark	144	8.3	144	0	144	0.7	144	0	144	6.3	144	0	144	0
France	194	52.6	194	7.2	194	1.5	194	2.1	194	19.6	194	12.9	194	1.5
Germany	191	31.9	191	6.3	191	2.6	191	2.1	191	9.4	191	10.5	191	0.5
Italy	170	61.2	170	2.4	170	3.5	170	1.8	170	31.2	170	35.9	170	4.7
Netherlands	293	18.8	293	0	293	0	293	0	293	11.6	293	3.4	293	0
Portugal	218	15.6	218	0.9	218	3.7	218	3.2	218	8.3	218	9.6	218	0
Spain	169	21.9	169	0.6	169	0	169	0	169	18.9	169	3.0	169	0
Sweden	74	1.4	74	1.4	74	0	74	0	74	0	74	0	74	0
Total (10 MSs)	**1,734**	**31.0**	**1,734**	**2.4**	**1,734**	**1.7**	**1,734**	**1.4**	**1,734**	**15.4**	**1,734**	**11.4**	**1,734**	**0.9**
Norway	263	1.9	263	0	263	0	263	0	263	0	263	0.4	263	0
Switzerland	190	36.3	190	0.5	190	3.2	190	3.2	190	11.6	190	6.3	190	0
2014														
Netherlands	292	22.3	292	1.7	292	1.0	292	0.7	292	13.4	292	6.5	292	0

Country	Gentamicin		Nalidixic acid		Sulfamethoxazole		Tetracycline		Tigecycline[b]		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
2015												
Belgium	196	6.6	196	21.9	196	56.1	196	61.2	196	0	196	40.3
Croatia	85	1.2	85	5.9	85	27.1	85	34.1	85	0	85	4.7
Denmark	144	0.7	144	0	144	10.4	144	9	144	0	144	5.6
France	194	5.7	194	11.9	194	62.9	194	71.6	194	0	194	40.2
Germany	191	0.5	191	9.9	191	37.2	191	38.7	191	0	191	26.2
Italy	170	15.9	170	19.4	170	63.5	170	80.6	170	0	170	60.6
Netherlands	293	0.7	293	3.1	293	23.5	293	40.6	293	0	293	13
Portugal	218	2.3	218	6.4	218	21.1	218	30.3	218	0	218	15.1
Spain	169	3	169	3	169	39.6	169	53.3	169	0	169	20.7
Sweden	74	0	74	0	74	4.1	74	1.4	74	0	74	0
Total (10 MSs)	**1,734**	**3.8**	**1,734**	**8.7**	**1,734**	**36.6**	**1,734**	**45.4**	**1,734**	**0**	**1,734**	**24.7**
Norway	263	0	263	0.8	263	1.5	263	1.9	263	0	263	0.4
Switzerland	190	5.3	190	5.8	190	41.1	190	40	190	0	190	15.8
2014												
Netherlands	292	3.8	292	5.8	292	28.1	292	44.5	292	0	292	22.3

All *E. coli* isolates tested were susceptible to meropenem. MS: Member States; N: number of isolates tested; % Res: percentage of resistant isolates.
(a): The reported occurrence of colistin resistance is unlikely to equate to the occurrence of *mcr-1/mcr-2* genes.
(b): ECOFF applied 1 mg/L.

Figure 60: Spatial distribution of ciprofloxacin resistance among indicator *E. coli* from calves under one year of age in reporting countries in 2015, using harmonised ECOFF
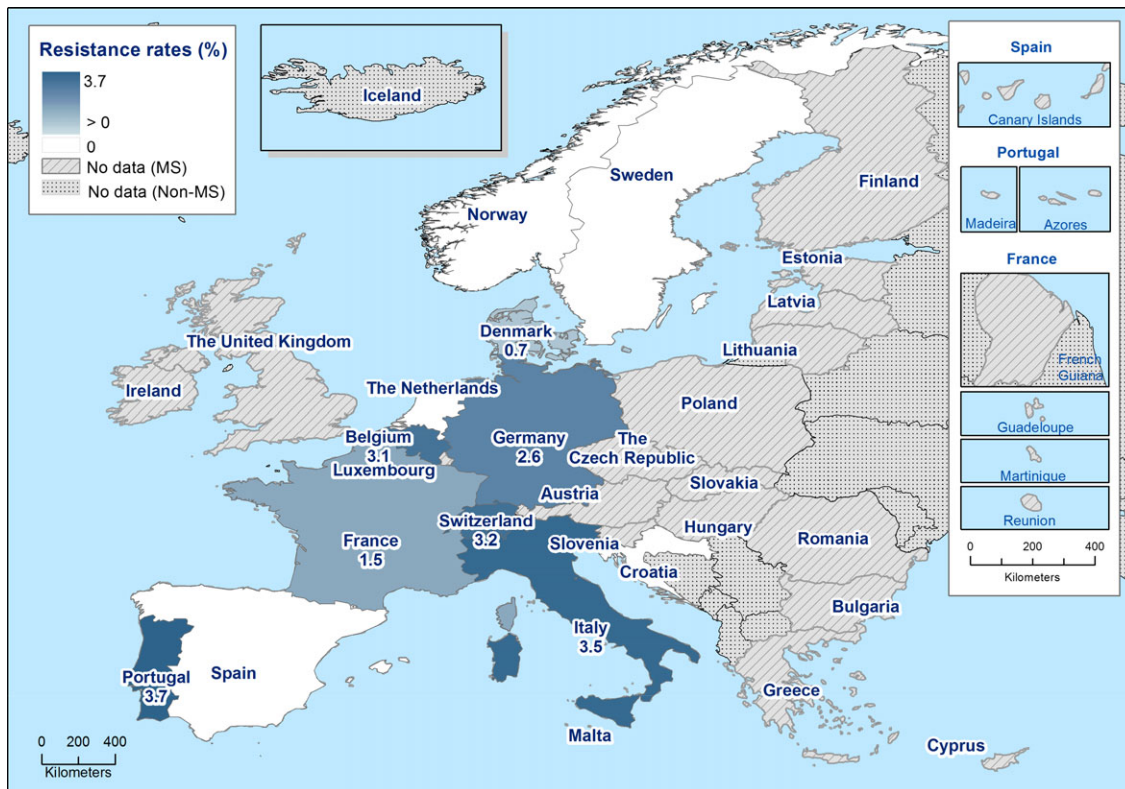
Figure 61: Spatial distribution of cefotaxime resistance among indicator *E. coli* from calves under one year of age in reporting countries in 2015, using harmonised ECOFF

Co-resistance to cefotaxime and ciprofloxacin in indicator E. coli *from calves under one year of age*

Very few isolates exhibited co-resistance to cefotaxime and ciprofloxacin using either ECOFFs or CBPs as interpretive criteria (Table COMESCHECALV). At the reporting country level, 0.8% (18/2,187) of all indicator *E. coli* isolates (originating from Belgium, France, Germany, Italy Portugal and Switzerland) showed co-resistance using microbiological cut-offs, whereas 0.4% (8/2,187) were resistant when clinical breakpoints were applied (Table COMESCHECALV). The clinical breakpoints for cefotaxime ($>$ 2 mg/L) and ciprofloxacin ($>$ 1 mg/L) are higher than the ECOFFS ($>$ 0.25 mg/L, $>$ 0.064 mg/L, respectively) accounting for this difference.

Temporal trends in resistance among indicator E. coli *from calves under one year of age*

There were not enough data to present the trends in resistance to selected antimicrobials in indicator *E. coli* from calves of less than one year from 2009 to 2015, and therefore, cattle data were used instead (Figure 62). Different production types of cattle to provide data for the years prior to 2015 may have been monitored in the countries considered and this introduces a source of variation into those results; trends should therefore be interpreted with caution.

Figure 62: Trends in ampicillin (AMP), cefotaxime (CTX), ciprofloxacin (CIP), nalidixic acid (NAL) and tetracyclines (TET) resistance in indicator *Escherichia coli* from cattle in reporting countries, 2009–2015, using harmonised ECOFFs
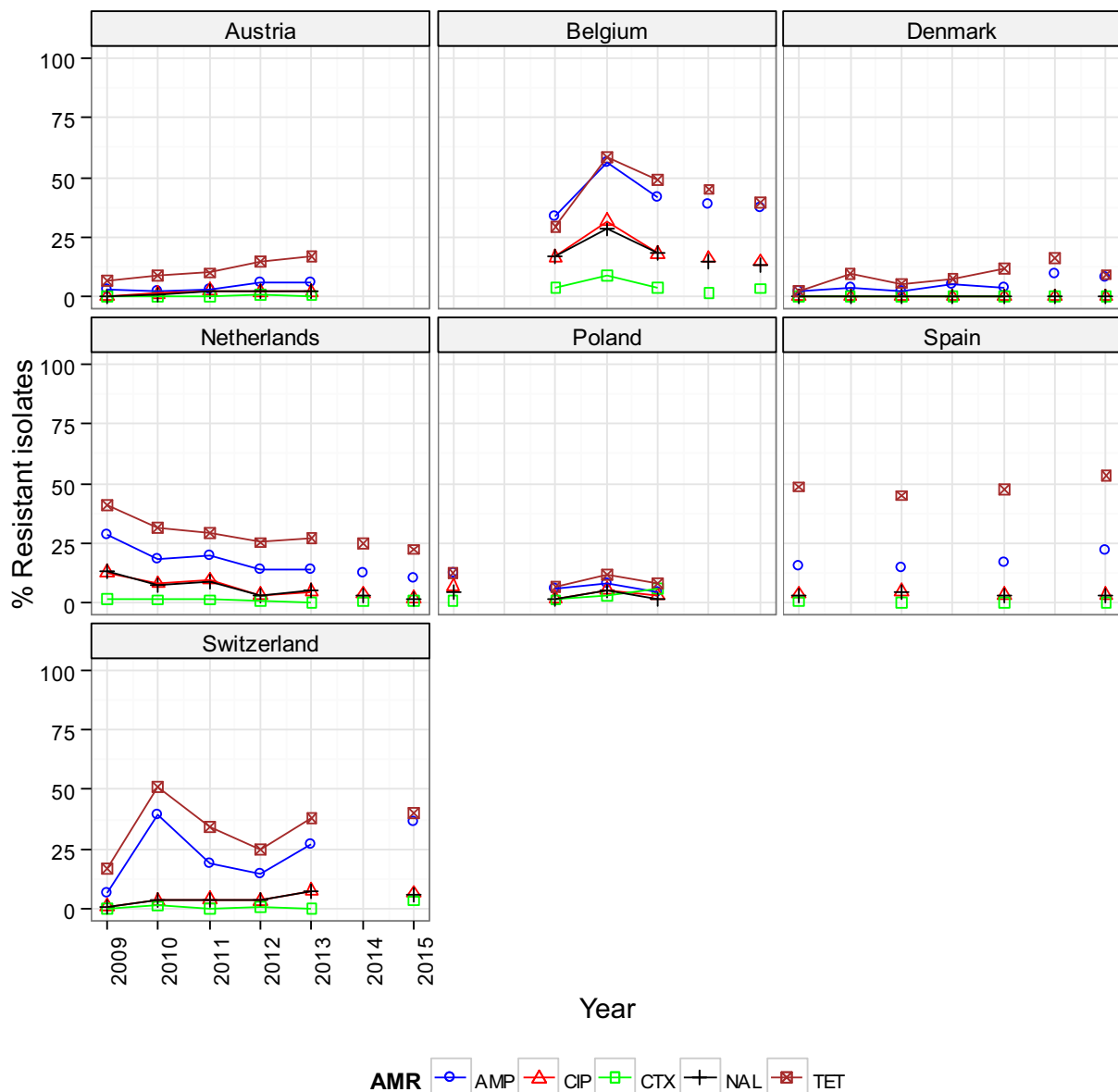
Statistically significant decreasing trends over four/five or more years, as tested by a logistic regression model (p ≤ 05), Statistically significant ***increasing*** trends over five or more years were observed for **ampicillin** and **tetracycline** in Austria (↑) and Denmark (↑), for **ampicillin, ciprofloxacin**, **nalidixic acid** and **cefotaxime** in Switzerland (↑) and for **cefotaxime** in Poland (↑). Statistically significant ***decreasing*** trends were observed for **ampicillin**, **ciprofloxacin**, **cefotaxime**, **nalidixic acid** and **tetracycline** in Belgium (↓) and the Netherlands (↓), and for **ampicillin** in Poland (↓).

Multiple resistance among indicator Escherichia coli *isolates from calves*

Twelve countries reported isolate-based data from calves. Considering all reporting countries, 55.1% of the isolates tested were fully susceptible (applying microbiological cut-offs) to the panel of antimicrobials tested. In Sweden, 95.9% of the isolates were fully susceptible. Levels of MDR (i.e. reduced susceptibility to three or more antimicrobial classes) ranged from very low to very high in reporting countries (Table COMESCHECALV). The frequency distributions (Figure 63) showed that, with the exception of Norway and Sweden, all reporting countries detected MDR to at least six antimicrobial classes.
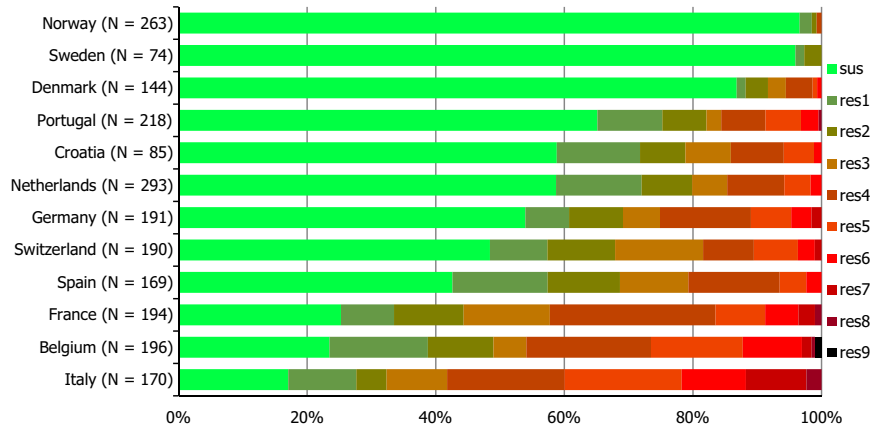
N: total number of isolates tested for susceptibility against the whole harmonised set of antimicrobials for *Escherichia coli*; sus: susceptible to all antimicrobial classes of the harmonised set for *Escherichia coli*; res1-res9: resistance to one up to eleven antimicrobial classes of the harmonised set for *Escherichia coli*.

Figure 63: Frequency distribution of *E. coli* isolates completely susceptible and resistant to 1–11 classes of antimicrobials in calves under one year of age in reporting countries, 2015

Spatial distribution of full susceptibility among indicator E. coli *from calves under one year of age*

The spatial distribution of full susceptibility to the panel of antimicrobials tested in *E. coli* from calves under one year of age is shown in Figure 64. The susceptibility to each individual antimicrobial was determined using epidemiological cut-off values; all isolates were tested against the same panel of antimicrobials. The highest levels of full susceptibility were shown by isolates from the Nordic countries Denmark, Norway and Sweden.
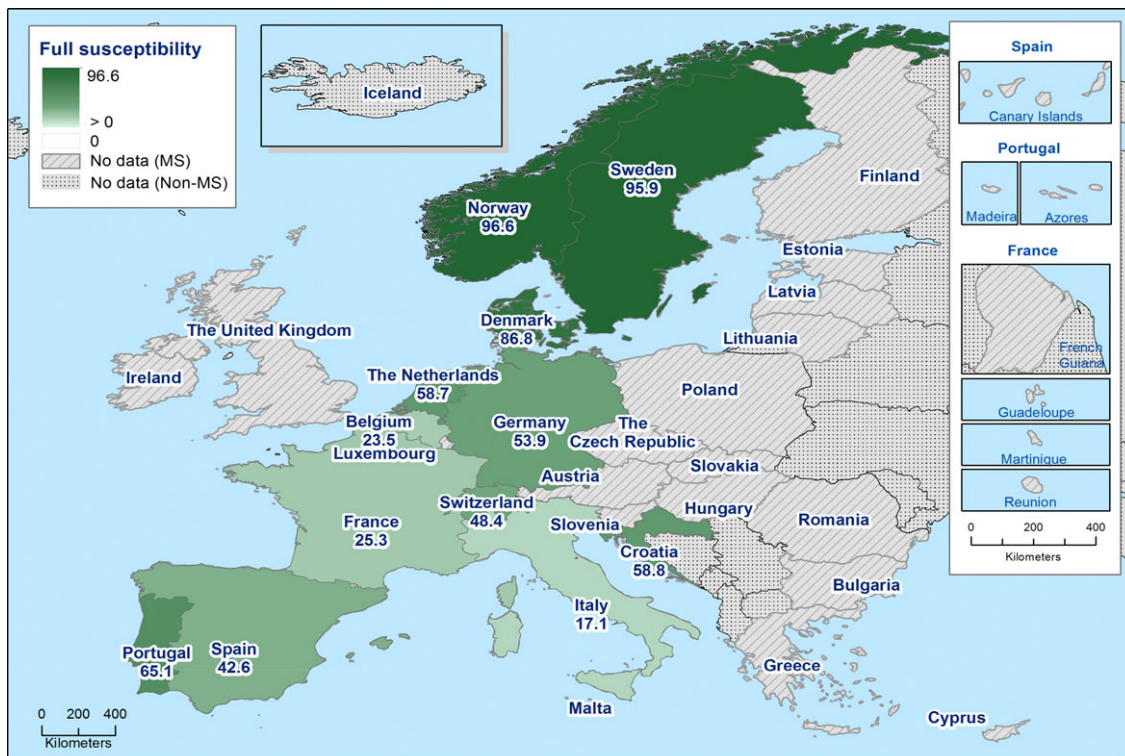
Figure 64: Spatial distribution of full susceptibility to the mandatory panel of antimicrobials tested among indicator *E. coli* from calves under one year of age in reporting countries in 2015, using harmonised ECOFFs

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Multi/co-resistance patterns among indicator E. coli *from calves under one year of age*

Indicator *E. coli* isolates resistant to cefotaxime and ciprofloxacin using CBPs were observed in low numbers from Belgium, France, Italy and Portugal, and ampicillin, sulfamethoxazole and tetracycline resistance was present in more than 94% of the co-resistant isolates tested (Table 34 and Table MULTIESCHECALV). These additional resistances (together with trimethoprim resistance in some cases) were noted in *E. coli* isolates showing high-level ciprofloxacin resistance (Table CIPESCHECATT).

Table 34: Co-resistance to fluoroquinolones and third-generation cephalosporins in indicator *E. coli* from calves under one year of age in reporting MSs, 2015

Country	N	Multidrug Resistance patterns of isolates resistant to both CIP and CTX (number of isolates)	Resistant to both CIP and CTX, applying ECOFFs		Resistant to both CIP and CTX, applying CBPs	
			N	% Res	N	% Res
Belgium	196	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	4	2.0	2	1.0
		CTX-CAZ-CIP-AMP-NAL-SMX-TET(1)				
		GEN-CHL-CTX-CAZ-CIP-AMP-COL-NAL-SMX-TET-TMP(2)				
France	194	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	3	1.5	2	1.0
		CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)				
		GEN-CHL-CTX-CAZ-CIP-AMP-COL-NAL-SMX-TET(1)				
Germany	191	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	2	1.0	0	0
		CTX-CAZ-CIP-AMP-SMX-TET-TMP(1)				
Italy	170	CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)	5	2.9	3	1.8
		CHL-CTX-CIP-AMP-NAL-SMX-TET-TMP(1)				
		CTX-CAZ-CIP-AMP-SMX-TET(1)				
		CTX-CAZ-CIP-AMP-SMX-TET-TMP(1)				
		GEN-CTX-CIP-AMP-NAL-TET(1)				
Portugal	218	CTX-CAZ-CIP-AMP-SMX-TET-TMP(2)	3	1.4	1	0.5
		GEN-CHL-CTX-CAZ-CIP-AMP-NAL-SMX-TET-TMP(1)				
Total (5 MSs)	**969**		**17**	**1.8**	**8**	**0.8**
Switzerland	190	GEN-CTX-CAZ-CIP-AMP-SMX-TET(1)	1	0.5	0	0

N: number of isolates tested; CIP: ciprofloxacin; CTX: cefotaxime; ECOFFs: epidemiological cut-off values; % Res: percentage of resistant isolates; CBPs: clinical breakpoints; CAZ: ceftazidime; NAL: nalidixic acid; AMP: ampicillin; TET: tetracycline; GEN: gentamicin; CHL: chloramphenicol; COL: colistin; SMX: sulfamethoxazole; TMP: trimethoprim; MSs: Member States.

3.3.2. Multiple drug resistance patterns in indicator *Escherichia coli* isolates

The MDR patterns in indicator *E. coli* from fattening pigs and calves under one year of age are shown in Tables MULTIESCHEPIG and MULTIESCHECALV.

3.3.2.1. Multiple drug resistance in *Escherichia coli* isolates from fattening pigs

Considering all reporting countries, then 1,799/4,720 (38.1%) of *E. coli* isolates from fattening pigs displayed MDR. A large number of different MDR patterns in indicator *E. coli* isolates from fattening pigs were evident (98 different patterns displayed by 1,799 isolates), reflecting the diverse nature of the *E. coli* strains tested (Table MULTIESCHEPIG). Resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim was observed as a core pattern in 52.8% of all MDR *E. coli* isolates from fattening pigs and was the predominant MDR pattern (20.0%). Patterns which occurred at a higher frequency (> 1%) did not include resistance to cefotaxime/ceftazidime; cefotaxime/ceftazidime resistance occurred as a component of infrequent MDR patterns in 3.1% of the isolates showing MDR. Sulfamethoxazole and tetracycline resistance frequently occurred as a component of MDR in *E. coli* from fattening pigs and was a component of 56 of the 98 MDR patterns detected (57.1%) and was observed in 81.0% of MDR isolates (1,457 out of 1,799).

3.3.2.2. Multiple drug resistance in *Escherichia coli* isolates from calves

Considering all reporting countries, then 626/2,187 (28.6%) of *E. coli* isolates from calves were MDR. A large number of different resistance patterns evident (63 different patterns displayed by 626 isolates), again reflecting the diverse nature of the *E. coli* strains which have been tested (Table MULTIESCHECALV). Resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim was observed as a core pattern in 55.6% of all MDR *E. coli* isolates from calves and was the predominant MDR pattern (21.6%). In calves, *E. coli* with three MDR patterns (including a common core pattern of resistance to ampicillin, sulfamethoxazole and tetracyclines) accounted for approximately 40.0% of the total number of multiresistant *E. coli* isolates for which data were available. Considering those resistance patterns occurring at a frequency greater than 1% of all indicators *E. coli* from calves of less than one year, these did not include resistance to cefotaxime/ceftazidime; however, cefotaxime/ceftazidime resistance occurred as a component of infrequent resistance patterns in 5.3% of MDR isolates. Sulfamethoxazole and tetracycline resistance occurred more frequently than in fattening pigs as a component of MDR in calves, occurring in 45 of the 63 (71.4%) resistance patterns observed and was present in 92.8% of calf MDR *E. coli* isolates (581 out of 626).

Resistance to colistin in *E. coli* from fattening pigs and calves

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 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 0.9% and 7.4% of the *E. coli* isolated from broilers and turkeys, respectively, were resistant to this antimicrobial.

Where colistin resistance is conferred by chromosomal alterations, then isolates with such alterations which have arisen by mutation, can increase in prevalence through clonal expansion. In plasmid-mediated colistin resistance, depending on the transmissibility and promiscuity of the plasmid and any other resistance genes which are carried by the plasmid, then a different progression in the development of resistance might be expected. In the case of promiscuous plasmids, this might involve rapid and extensive dissemination to a wide range of different *E. coli* strains.

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, poultry and food thereof since 2010 (Falgenhauer et al., 2016; Irrgang et al., 2016a). 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 of less than one year of age is shown in Figure 65. Co-resistance between colistin and cefotaxime/ceftazidime was shown by 1/4,270 (0.02%) of indicator *E. coli* isolates from fattening pigs (Portugal) whereas 6/4,270 (0.14%, Portugal, Romania, Spain) were co-resistant to colistin and ciprofloxacin, applying microbiological ECOFFS. 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), while 13/2,113 (0.6%) indicator *E. coli* isolates were co-resistant to colistin and ciprofloxacin (several MSs). 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*

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in calves under the Decision 2013/652/EU has 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, including resistance to ciprofloxacin.
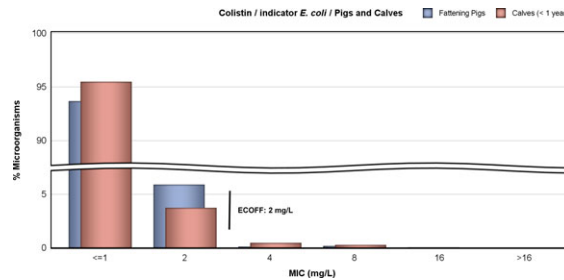
Figure 65: Distribution of MICs of colistin in indicator *E. coli* from fattening pigs and calves under one year of age, 2015

3.3.3. Discussion

Studying the antimicrobial resistance of indicator commensal *E. coli* from animals and food provides information on the reservoir of resistance genes occurring in those bacteria that could be transferred to bacteria that are pathogenic for humans and/or animals. It therefore has relevance to both public and animal health. The occurrence of resistance to antimicrobials in indicator *E. coli* is likely to depend on a number of factors including the selective pressure exerted by use of antimicrobials in various food-producing animal populations; clonal spread of resistant organisms; dissemination of particular genetic elements, such as resistance plasmids; and the effects of co-selection in multiresistant organisms. Indicator *E. coli* are cultured from a healthy, representative population of animals using non-selective culture media (containing no antimicrobials), and therefore, the most common clones of *E. coli* occurring in those animals are expected to be those most represented. When isolates are selected at random from non-selective culture plates, occasionally the minor components of the *E. coli* flora may be sampled.

A total of 27 MSs and two non-MSs provided quantitative *E. coli* MIC data in 2015 for at least one of the livestock species. Reported antimicrobial resistance data in *E. coli* isolates from food-producing animals, derived mainly from active and representative monitoring programmes, were chiefly based on randomised sampling performed at slaughterhouses. At the reporting MS group level, a high level of 'microbiological' resistance was observed to several antimicrobials among food-producing animals, with some countries reporting a very or extremely high occurrence of such resistance. As resistance levels tend to vary substantially between countries, the variation in resistance in pigs and cattle observed between 2009 and 2015, at the overall MS group level, may partly result from different MSs contributing to data as well as different production types of livestock being sampled. The sampling of different production types of animals over the years 2009 and 2015, especially in relation to cattle, may have also influence on the resistance trends observed at MS level. This was the fifth year that resistance data were reported separately for different production types of pigs and cattle and it was the first year that mandatory AMR monitoring in indicator *E. coli* for these animal categories was in place.

Considering all reporting MSs, resistance levels were higher by 8–11% in *E. coli* isolates from fattening pigs compared to isolates from calves of less than one year of age for those antimicrobials which have been used in veterinary medicine for many years, namely ampicillin, sulfamethoxazole, tetracyclines and trimethoprim. For all other antimicrobials and considering all MSs, levels of resistance were similar between fattening pigs and calves of less than one year of age. The differences in the occurrence of resistance to ampicillin, sulfamethoxazole tetracyclines and trimethoprim may reflect differences in the levels of historical and recent usage of these antimicrobials or differences in husbandry practices (for example, the ease with which all in-all out husbandry may be practised). The genes conferring resistance to these compounds are also frequently present on mobile genetic elements, such as class 1 integrons, which may carry multiple resistance genes. All MSs detected resistance to these compounds at moderate or higher prevalence levels (i.e. > 10%) in fattening pigs, although there was considerable variation between MSs in the range of values reported. The position was similar in calves of less than one year of age, except for the Nordic countries where a prevalence of resistance under 10% to these compounds

was generally reported. The widespread occurrence of resistance to these four compounds also extended to the MDR patterns, where they commonly featured in MDR isolates in both fattening pigs and calves. Considering all reporting MSs, resistance to gentamicin was similar in fattening pigs (3.4%) and in calves under one year of age (3.8%). Gentamicin is an interesting antimicrobial because there are differences in the degree of usage in different MSs of this and other antimicrobials to which cross-resistance may occur (e.g. apramycin). There was a large degree of variation between MSs in the prevalence of resistance to chloramphenicol in both fattening pigs and calves under one year of age; the picture in relation to chloramphenicol is complex, because chloramphenicol is no longer permitted for use in animals, but the compound florfenicol belonging to the same antimicrobial class is currently used in animals. Cross-resistance between chloramphenicol and florfenicol occurs with some mechanisms of resistance.

'Microbiological' resistance to fluoroquinolones (ciprofloxacin) – highest priority critically important class of antimicrobials for human medicine (Collignon et al., 2016; WHO, 2016) – was found at similar levels in *E. coli* isolates from fattening pigs and calves of less than one year, when considering all reporting MSs. However, at the individual MS level, there were large differences in the occurrence of resistance between different MSs and MSs detecting high levels of resistance in either fattening pigs or calves did not necessarily detect a high prevalence of resistance in both types of animals. The occurrence of resistance to nalidixic acid was usually similar to that for ciprofloxacin, suggesting that mutation was responsible for resistance. In a number of MSs, the occurrence of resistance to ciprofloxacin was slightly higher than that obtained for nalidixic acid, in both fattening pigs and calves of less than one year. In these cases, mechanisms such as transferable (plasmid-mediated) fluoroquinolone resistance conferred by i.e. *qnr* genes may have been responsible as they confer this phenotypic pattern of resistance. In Italy, a marked difference was observed between ciprofloxacin resistance in calves under one year of age (35.9%) and nalidixic acid resistance (19.4%); large differences (> 5%) were also observed in fattening pigs between ciprofloxacin and nalidixic acid resistance in Bulgaria, Cyprus, Italy, Poland, Portugal, Romania and Spain.

'Microbiological' resistance to third-generation cephalosporins (cefotaxime and ceftazidime) – another class categorised as highest priority critically important for human medicine (Collignon et al., 2016; WHO, 2016)– was infrequently detected in 2015 in *E. coli* from fattening pigs and calves less than one year where levels were < 5.5% in each reporting MSs. A number of reporting MSs recorded no resistance to cefotaxime or ceftazidime in *E. coli* from fattening pigs or calves less than one year.

The levels of MDR[19] in most reporting countries were relatively high in indicator *E. coli* isolates from both fattening pigs (10.0–98.2%) and calves under one year of age (0.8–67.6%); they were also high considering all reporting countries (38.1% in fattening pigs and 28.6% in calves under one year of age). As expected, the numbers of fully susceptible isolates showed the inverse pattern. This year is the first year in which maps have been included in the report providing (as a percentage) the proportion of fully susceptible isolates. In general, the Nordic countries showed higher levels of full susceptibility than other MSs; thus, in fattening pigs, Finland, Sweden and Norway were the only reporting countries with > 65% full susceptibility, while, in calves under one year of age, Denmark, Norway and Sweden were the only reporting countries with > 85% full susceptibility. Considering clinical resistance, co-resistance to cefotaxime and ciprofloxacin was detected at very to low levels in fattening pigs in seven MSs and in four MSs in calves under one year of age in 2015. These *E. coli* isolates were randomly chosen from non-selective culture plates and they may have limited direct relevance to human medicine; however, they provide an indication of the extent to which this combination of resistance is occurring in the *E. coli* flora of animals in the different reporting countries.

For 2015, the MDR patterns shown by indicator *E. coli* from fattening pigs and calves under one year of age from MSs reporting isolate-based data have been included in this report. Resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim was common, being observed as the core resistance pattern (with or without additional resistance) in 20.0% of all *E. coli* isolates from fattening pigs and was also in its own right the predominant MDR pattern. The same MDR pattern was predominant in calves under one year of age, occurring at a frequency of 21.6% amongst the MDR patterns obtained. As previously discussed, the common occurrence of resistance to these compounds is likely to reflect their widespread previous and current usage for treatment of animal disease and the frequent occurrence of genes conferring resistance to them in mobile genetic elements. There were other MDR patterns which accounted for more than 9.0% of the total MDR isolates in calves under one year of age. The occurrence of these particular patterns might reflect spread of particular clones of bacteria which exhibit that pattern of resistance or dissemination of plasmids carrying those

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[19] Proportions of isolates showing reduced susceptibility to at least three antimicrobial classes according to epidemiological cut-off values.

resistances and possibly being transmitted between different strains of *E. coli*. Strain typing of selected *E. coli* isolates and detailed examination of *E. coli* plasmids would assist in differentiating between clonal expansion of MDR *E. coli* strains and the spread of promiscuous MDR plasmids between different *E. coli* strains by bacterial conjugation. In fattening pigs, tetra-resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim occurred in 7.6% of all *E. coli* isolates and was the predominant MDR pattern; the same situation occurred in calves of less than one year where this pattern occurred in 7.2% of *E. coli* isolates. In fattening pigs and also in calves under one year of age, ciprofloxacin resistance was particularly noted in MDR patterns, and as discussed previously resistance to this compound can be mediated through chromosomal mutations or through transferable mechanisms of resistance. Ciprofloxacin resistance was observed in 8.9% of MDR *E. coli* isolates from fattening pigs (419/4,720) and in 8.8% of MDR *E. coli* isolates from calves less than one year (192/ 2,187). Considering the total number of different MDR patterns observed in fattening pigs 51/98 (52.0%) included ciprofloxacin resistance, while in calves under one year of age 32/63 (50.8%) included ciprofloxacin resistance. Considering the resistance patterns occurring at a higher frequency in fattening pigs and calves under one year of age, these did not generally include resistance to cefotaxime; however, cefotaxime resistance did occur as a component of infrequent resistance patterns. The figures for fattening pigs and calves of less than one year are much lower than those observed in 2014 for broilers and fattening turkeys, where ciprofloxacin resistance was particularly evident in MDR patterns. In 2014, ciprofloxacin resistance was observed in 84.7% of MDR *E. coli* isolates from broilers (2,386 out of 2,818) and in 74.4% (728 out of 979) of MDR *E. coli* isolates in turkeys.

Tigecycline resistance was infrequently detected in *E. coli* isolates from fattening pigs and calves under one year of age, with the exception of Cyprus, where 14.5% of isolates from fattening pigs showed resistance. Marked differences were evident between the results obtained for indicator *E. coli* (where resistance was rare) and *Salmonella* where resistance with MIC values very close to the ECOFF occurred more frequently, although the difference may be partly explained by a reduction of the EUCAST ECOFF value for *E. coli* not accounted for in this analysis.

The most common pattern of multiple resistance in *E. coli* isolates from fattening pigs that were co-resistant to ciprofloxacin and cefotaxime was resistance to chloramphenicol, ciprofloxacin, nalidixic acid, cefotaxime, ceftazidime, ampicillin, sulfamethoxazole, tetracyclines and trimethoprim. This occurred in 0.5% of the total number of *E. coli* isolates from fattening pigs and was detected in six out of nine MSs which reported co-resistant to ciprofloxacin and cefotaxime. Use of these antimicrobials or antimicrobial classes is likely to select isolates with this resistance pattern; clonal spread of this MDR strain is a further possibility which could be investigated through strain typing of these *E. coli* isolates. Co-resistance to ciprofloxacin and cefotaxime applying microbiological cut-offs was less common in fattening pigs (1.4% of *E. coli* isolates) than in calves under one year of age (1.8% of *E. coli*). Three *E. coli* isolates from calves of less than one year were detected which were resistant to cefotaxime/ ceftazidime, colistin and ciprofloxacin, constituting an extremely low proportion of the total number. The ability to identify co-resistance to those antimicrobials of most public health importance is an important attribute of the monitoring system.

Integrons can be associated with particular antimicrobial resistance genes and class 1 integrons classically carry the resistance gene *sul1*. The widespread occurrence of integrons and their associated antimicrobial resistance genes in indicator *E. coli* from animals is likely to account for some of the resistance patterns (or associations between resistances) which are evident in the MDR tables. The common core patterns of resistance to ampicillin, sulfamethoxazole, tetracyclines and trimethoprim (and combinations thereof) frequently observed in the monitoring of *E. coli* isolates are probably therefore related to the presence of integrons. Further analysis of selected indicator *E. coli* described in this report could include genetic characterisation.

Full resistance to all of the antimicrobials in the test panel was not observed in any isolates from fattening pigs and calves under one year of age. Although no *E. coli* isolates from fattening pigs and calves under one year of age were resistant to meropenem, further testing with the supplementary panel of cephalosporins and carbapenems revealed that a single isolate from calves of less than one year was resistant to ertapenem. The phenotypic resistance pattern of this isolate was suggestive of permeability change to the bacterial cell wall (loss of porins) acting in association with AmpC or ESBL enzymes and is discussed further in Section 3.5 on cephalosporin resistance.

3.4. Meticillin-resistant *Staphylococcus aureus*

A principal recommendation (EFSA, 2009a,c, 2012b) is that monitoring of food-producing animals, in particular intensively reared animals, is carried out periodically in conjunction with systematic surveillance of MRSA in humans, so that trends in the diffusion and evolution of zoonotically acquired MRSA in humans can be identified. Isolates representative of various animal and food origins should be analysed for determination of lineage, antimicrobial susceptibility and virulence-associated traits.

Meticillin-resistant *Staphylococcus aureus* (MRSA)

MRSA has been recognised as an important cause of infections in humans for decades. Strains of MRSA causing infections in humans can be divided into three broad categories, healthcare-associated (HA-), community-associated (CA-) and livestock-associated (LA-) MRSA. LA-MRSA has been detected in pigs and poultry, as well as other farm animal species in many countries worldwide. HA-MRSA and CA-MRSA include strains which predominantly affect humans, and these generally do not involve food-producing animals. LA-MRSA may also be harboured by humans, especially where there is occupational contact with affected livestock and carcases derived thereof. LA-MRSA may cause illness in humans, although transmissibility between humans has been shown to be very limited, even in healthcare facilities.

The EFSA's assessment of the public health significance of MRSA in animals and food (EFSA, 2009c) and the Joint Scientific Report of ECDC, EFSA and the European Medicines Agency (EMA) on MRSA in livestock, companion animals and food (EFSA, 2009a) provide more background information and recommendations on MRSA. These issues were also reviewed in the EFSA Scientific Report proposing technical specifications to improve the harmonisation of the monitoring and reporting of the prevalence, genetic diversity and multiresistance profile of MRSA in food-producing animals and food thereof (EFSA, 2012b).

Antimicrobial susceptibility in European invasive *Staphylococcus aureus* isolates is reported by the MSs to the European Antimicrobial Resistance Surveillance Network (EARS-Net) hosted by ECDC. Molecular typing data are not reported and thus, where there may be possible links to the animal reservoir of LA-MRSA, these cannot be detected easily with current monitoring procedures, at least at the European level. The EU/EEA population-weighted mean MRSA percentage (i.e. the percentage of invasive *S. aureus* isolates with resistance to meticillin) was 16.8% in 2015, which is a significant decrease from 18.8% in 2012. Large inter-country variation in the MRSA percentages could be noted, with generally lower percentages in Northern Europe and higher in Southern and South-Eastern parts.

Recent developments underline the usefulness of such monitoring, such as the detection of *mecC*-MRSA in pigs reported in Denmark (Angen et al., 2016). Angen et al. identified *mecC*-MRSA in domesticated pigs (a species in which it had not previously been reported) and presented evidence pointing to the transmission of *mecC*-MRSA between humans and pigs. In a further development, novel LA-MRSA (*mecA*) strains have been detected both in the urban human population in Denmark and in poultry meat, raising the possibility of food-borne transmission of LA-MRSA (Larsen et al., 2016).

Monitoring of MRSA in animals and food is currently performed by MSs voluntarily and the findings presented in this report underline the value of such monitoring.

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mecA* and *mecC*-Meticillin-resistant *Staphylococcus aureus

A variant of the meticillin resistance gene *mecA*, termed *mecC*, was identified in 2011 in MRSA from humans and cattle in Europe (García-Álvarez et al., 2011) and has subsequently been detected in ruminants, companion and wild animals (Paterson et al., 2014). *mecC*-MRSA accounted for approximately 2% of MRSA isolates from humans in Denmark in 2010 and 2011 (Petersen et al., 2013). A recent Danish study (Angen et al., 2016) demonstrated *mecC*-MRSA (mainly belonging to *spa*-type t843) in pigs and farm workers on a single farm which were closely related, suggesting transmission between humans and pigs on the farm. Whole genome sequencing and phylogenetic analysis showed clustering of multiple isolates on the farm from the farmer, suggesting that the farmer may possibly have been the source of introduction to the herd. Other human isolates from the same locality also clustered with the isolate from the farmer. This appears to be the first report of *mecC*-MRSA from domestic pigs. The farm was a mixed farm on which cattle were also present, although *mecC*-MRSA was not detected in the cattle on the farm.

3.4.1. Meticillin-resistant *Staphylococcus aureus* in food and animals

LA-MRSA isolates are the principal focus of this section, which summarises the MRSA prevalence and resistance results in various foodstuffs and food-producing animal species/populations reported by seven MSs and two non-MSs to EFSA in 2015 (Table MRSAOVERVIEW). Data on AMR of MRSA isolates from food-producing animals were reported by only eight countries in 2015; four of these countries also reported molecular typing data. This section also includes occurrence data reported on companion animals. To date, methods for the isolation of MRSA from food and animals have not been harmonised at the EU level, and therefore, the methods used by individual reporting MSs may differ in sensitivity. Similarly, the sampling strategies used by reporting MSs are not harmonised at the EU level and these may also influence the results obtained.

3.4.1.1. Meticillin-resistant *Staphylococcus aureus* in food

In 2015, Germany, Finland Slovakia and Spain, as well as Switzerland reported information on the occurrence of MRSA in various categories of food (Table 35). Finland investigated 303 batches of fresh pig meat, among which 3.0% tested positive for MRSA. Slovakia examined a range of food products for MRSA, and no positive isolates were obtained. Spain investigated fresh meat from rabbits and five positive samples were detected (8.3%). Switzerland investigated 301 batches of pig meat, among which 0.7% tested positive for MRSA. The corresponding *spa*-typing data were not available from some reporting MSs, as positive isolates were reported without specifying *spa*-type; Finland and Switzerland did report the corresponding *spa*-typing for the positive results. *Spa*-type t034 (a common *spa*-type associated with CC398) was reported from Switzerland and Finland. Finland also reported *spa*-type t2741 in meat from pigs and this *spa*-type is also associated with CC398. Generally, meat from several different animal species proved positive for MRSA, including meat from bovine, rabbits and pigs, at various levels of prevalence.

Table 35: Meticillin-resistant *Staphylococcus aureus* in food, 2015

Food categories / Country	Description	Sample unit	Number	
			Units tested	(%) positive for MRSA
Bakery products				
Slovakia	Catering, surveillance	Single	4	0
Cheeses/dairy products				
Slovakia	Catering/processing plant/retail, surveillance/monitoring	Single	112	0
	Processing plant/retail, surveillance/monitoring	Batch	17	0
Confectionery products and pastes				
Slovakia	Processing plant/retail, surveillance/monitoring	Single	268	0
		Batch	9	0
Foodstuffs intended for special nutritional uses				
Slovakia	Dried dietary foods for special medical purposes intended for infants below 6 months, retail, surveillance	Batch	1	0
Infant formula				
Slovakia	Dried/liquid/ready-to-eat, retail/hospital or medical care facility, monitoring/surveillance	Single	43	0
		Batch	84	0
Meat from bovine animals				
Spain	Meat products/minced meat, surveillance	Single	8	0
Slovakia	Meat preparation, meat products, catering, surveillance/monitoring		51	0
	Meat products, catering, surveillance	Batch	10	0
Switzerland	Retail, monitoring	Batch	298	0
Meat from deer (venison)				
Slovakia	Meat preparation, catering, monitoring	Single	1	0

Food categories / Country	Description	Sample unit	Number	
			Units tested	(%) positive for MRSA
Meat from pigs				
Finland	Fresh, retail, survey	Batch	303	9[a] (3.0%)
Germany	Carcase, slaughterhouse, monitoring – active	Batch	342	69 (20.2%)
	Fresh, retail, monitoring – active	Single	457	60 (13.1%)
Slovakia	Minced meat, meat preparation, meat products, catering, surveillance/monitoring	Single	118	0
	Meat preparation, catering, monitoring	Batch	5	0
Switzerland	Retail, monitoring	Batch	301	2[b] (0.7%)
Meat from poultry, unspecified				
Slovakia	Fresh, meat preparation, meat products, catering, surveillance/monitoring	Single	82	0
	Meat preparation, catering, monitoring	Batch	15	0
Meat from rabbit				
Slovakia	Meat preparation, catering, monitoring	Single	5	0
Spain	Fresh, retail, surveillance	Single	60	5 (8.3%)
Meat, red meat (meat from bovines, pigs, goats, sheep, horses, donkeys, bison and water buffalos)				
Slovakia	Meat preparation, minced meat, catering, surveillance	Single	7	0
Milk				
Slovakia	Raw milk, retail, survey	Single	5	0
		Batch	2	0
Other processed food products and prepared dishes				
Slovakia	Ices/noodles/sushi/sandwiches/ready-to-eat salads, catering/processing plant, monitoring/surveillance	Single	976	0
		Batch	208	0
Vegetables				
Slovakia	Precut, catering/hospital, monitoring/surveillance	Single	12	0
		Batch	62	0

(a): Isolates belonged to the *spa*-type t034 (6), t2741 (3).
(b): Isolates belonged to the *spa*-type t034 (2).

3.4.1.2. Meticillin-resistant *Staphylococcus aureus* in animals

Monitoring meticillin-resistant Staphylococcus aureus in food-producing animals

For 2015, Belgium, Germany and Spain, as well as Norway and Switzerland, reported data on the prevalence of MRSA in food-producing animals and/or their environment (Table 36).

In pigs, MRSA prevalence in batches of slaughter animals was assessed at the high level of 91.4% in Spain, while, in Germany, the MRSA prevalence in herds of breeding sows (breeders' areas) and herds of fattening pigs (weaners to growers' areas) from the same farrow-to-finish pig holdings was recorded at 26.3% and 41.3%, respectively. Switzerland reported a MRSA prevalence of 25.7% in slaughter pigs monitored at the slaughterhouse.

In cattle, Belgium reported moderate MRSA prevalence in both herds of dairy cows (10.4%) and herds of meat production animals (15.4%), whereas, in herds of calves of less than one year of age, a very high prevalence of 78.9% was recorded. At the animal level, a prevalence of 6.5% was registered in calves of less than one year in Switzerland.

Norway tested large numbers of pig herds (N = 821) and cattle herds (N = 179) in 2015, as part of a surveillance and eradication programme for LA-MRSA.[20] MRSA was detected in four pig herds and one cattle herd as a result of this surveillance, resulting in 0.5% and 0.6% prevalence, respectively. Norway has consistently demonstrated a very low/zero prevalence of MRSA-positive pig herds in

[20] Outlined at: http://www.vetinst.no/eng/Surveillance-programmes/Swine-MRSA

surveillance performed since 2008. This situation is likely to be favourable to achieving the goal of eradicating and then maintaining freedom from LA-MRSA. National eradication programmes for LA-MRSA have not been attempted in any other European country. The eradication programme involves slaughter and depopulation of affected herds, followed by thorough cleaning and disinfection and then restocking with pigs free from LA-MRSA. Further information and details on the Norwegian eradication programme are available in the specific text box below.

A number of different *spa*-types were reported (Table 36). The majority of isolates from pigs in Switzerland were *spa*-type t034, with lower numbers of t011; both of these *spa*-types are associated with MRSA CC398. The other *spa*-types detected in pigs in this country were single isolates of t899, which can be associated with either ST9 or CC398, as it consists of a CC398 chromosomal backbone having acquired the CC9 region containing the staphylococcal protein A gene (Guardabassi et al., 2009; Larsen et al., 2016), t032, t571, t4475, t1250 and t1145. The majority of MRSA isolates recovered from bovine animals in Belgium were *spa*-types t011, which is also associated with CC398, with lower numbers of t1580 and t1985. Although the vast majority of the *spa*-types detected were associated with CC398, there were some exceptions, such as, t037 and t044 detected in calves under one year of age in Belgium, which are *spa*-types associated with ST239 and ST80, respectively. Switzerland reported t008 in calves under one year of age and t032 from pigs; these *spa*-types are, respectively, associated with ST8 and CC22.

Surveillance and control of LA-MRSA in the Norwegian pig population

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Norwegian authorities have adopted a national surveillance and control strategy of livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) in the pig population. During the last decade, LA-MRSA has emerged in livestock in most European countries (Verkade and Kluytmans, 2014), and this emergence has raised public health concerns (Cuny et al., 2010). *S. aureus* is an important cause of nosocomial and community-acquired human disease, and MRSA is associated with increased morbidity, mortality and costs (Köck et al., 2010). Public health concerns were also the rationale behind the decision made by the Norwegian authorities in 2013 to impose measures to eradicate LA-MRSA from the pig population. This 'search and destroy' strategy aims to prevent pig holdings becoming a persistent domestic reservoir of MRSA with the potential of zoonotic transmission. To the authors' knowledge, Norway is the only country having implemented such a strategy.

In Norway, the 2008 EU Baseline study investigating 252 farms (EFSA, 2009b), and two national surveys conducted during 2011 and 2012 indicated a very low prevalence of LA-MRSA in the Norwegian pig population before 2013. The Norwegian pig population consists of approx. 1,250 sow farms and 800 finishing pig farms with an annual production of 1.6 million slaughtered pigs. Import of live pigs to Norway from other countries is negligible, and this is considered an important epidemiological and biosecurity feature of the Norwegian commercial pig population.

The LA-MRSA surveillance and control strategy includes annual pig population screenings, restrictions on trade of live animals upon suspicion, depopulation of pigs in LA-MRSA positive pig holdings, and thorough cleaning and disinfection of premises before restocking with pigs from MRSA negative holdings (Grøntvedt et al., 2016). After restocking, samples are collected from animals and the environment to assess the effectiveness of the MRSA eradication. Results from follow-up testing after restocking demonstrate that LA-MRSA eradication has been successful in the first attempt in more than 90% of the pig farms, and that only a few farms need to go through more than one eradication process. From the first traceable findings of LA-MRSA in 2013 and until the end of December 2015, LA-MRSA has been detected in six separate outbreaks including a total of 60 herds in Norway. This includes all farms identified through active surveillance or outbreak investigations. The primary introductions to each outbreak have likely been humans (Grøntvedt et al., 2016). This is in contrast to the 2010 EFSA report, identifying trade of live pigs as a major risk factor for transboundary spread of LA-MRSA (EFSA, 2012b).

Population surveillance, outbreak investigations and measure to eradicate LA-MRSA from pig farms is both a costly and labour intensive strategy. However, the imposed strategy has probably contributed substantially to preventing further dissemination of LA-MRSA, and in preventing an increased prevalence of LA-MRSA among pig farms and humans in Norway (Grøntvedt et al., 2016). The strategy is therefore considered relevant under Norwegian conditions, presently characterised by: a low overall prevalence of MRSA (including LA-MRSA) in humans, few primary introductions of LA-MRSA to the pig population, effective eradication of MRSA from positive pig farms which thereby prevented further transmission among pig farms, and an essentially closed pig population. Changes in these conditions may influence the authorities' choice of strategy regarding LA-MRSA in the future.

Table 36: Meticillin-resistant *Staphylococcus aureus* in food-producing animals (excluding clinical investigations), 2015

| Animal species | Production type/Description | Sample unit | Number | |
Country			Units tested	(%) Positive for MRSA
Cattle (bovine animals)				
Belgium	Calves (under one year of age), farm, monitoring – active	Holding	147	116[a] (78.9%)
	Dairy cows, farm, monitoring – active	Holding	96	10[b] (10.4%)
	Meat production animals, farm, monitoring – active	Holding	104	16[c] (15.4%)
Norway	Farm, control and eradication programmes	Herd	179	1[d] (0.6%)
Switzerland	Calves (under one year of age), slaughterhouse, monitoring	Animal	292	19[e] (6.5%)
Pigs				
Germany	Breeding animals, farm, monitoring – active	Herd	342	90 (26.3%)
	Fattening pigs, farm, monitoring – active	Herd	332	137 (41.3%)
Norway	Farm, control and eradication programmes	Herd	821	4[f] (0.5%)
Spain	Fattening pigs, slaughterhouse, monitoring – EFSA spec.	Batch	383	350 (91.4%)
Switzerland	Fattening pigs, slaughterhouse, monitoring	Animal	300	77[g] (25.7%)

(a): *spa*-types: t1985 (8 isolates), t3423 (5), t034 (15), t1451 (3), t044 (3), t1580 (7), t037 (8), t011 (64) and untypable (1).
(b): *spa*-types: t011 (4 isolates), t2383 (1), t034 (1), t1580 (1), t1985 (2) and unspecified (1).
(c): *spa*-types: t011 (9 isolates), t034 (2), t1580 (2), t2287 (1), t3423 (1), t1451 (1).
(d): *spa*-type: t011.
(e): *spa*-types: t011 (11 isolates), t034 (6) and t008 (2). The t008 isolates were PVL positive.
(f): *spa*-type: t011.
(g): *spa*-types: t034 (48 isolates), t011 (23), t032 (1), t899 (1), t571 (1), t4475 (1), t1250 (1), and t1145 (1).

Clinical investigations for meticillin-resistant Staphylococcus aureus *in food-producing animals*

Typically, clinical investigations differ from monitoring data in food-producing animals, as selective culture methods may not be used, the number of units tested may be low and the sample may involve a biased sample population. Although these data do not allow inferring prevalence and cannot be extrapolated at the population level, it is still considered relevant to report the range of animal species/populations which can be affected. In 2015, Ireland, the Netherlands and Slovakia reported data on clinical investigations for MRSA in different kinds of food-producing animals (Table 37).

Table 37: Meticillin-resistant *Staphylococcus aureus* in food-producing animals, clinical investigations, 2015

| Animal species | Production type/description | Sample unit | Number | |
Country			Units tested	(%) positive for MRSA
Cattle (bovine animals)				
Ireland	Dairy cows, farm	Animal	2,784	1 (0.04%)
Netherlands	Dairy cows, farm	Animal	1,344	4 (0.3%)
Slovakia	Adult cattle over 2 years/calves (under one year of age), farm	Animal	7	0
	Dairy cows, farm	Animal	366	44 (12.0%)
Goats				
Slovakia	Farm	Animal	18	5 (27.8%)
	Animals under one year of age, farm	Animal	3	2 (66.7%)
Pheasants				
Hungary	Meat production flocks, farm	Animal	1	1 (100%)
Pigs				
Slovakia	Fattening pigs, farm	Animal	2	0

Animal species	Production type/description	Sample unit	Number	
			Units tested	(%) positive for MRSA
Country				
Rabbits				
Slovakia	Veterinary clinics	Animal	1	0
Sheep				
Slovakia	Animals under one year of age (lambs or meat production, farm	Animal	5	0
	Milk ewes, farm	Animal	39	14 (35.9%)

Clinical investigations for meticillin-resistant Staphylococcus aureus *in companion animals*

The Netherlands and Slovakia reported data on MRSA in companion animals in 2015 (Table 38). The corresponding *spa*-typing data were not available. Denominator data (units tested) equalled samples positive for MRSA in data reported from the Netherlands.

Table 38: Meticillin-resistant *Staphylococcus aureus* in companion animals, clinical investigations, 2015

Animal species	Production type	Sample unit	Number	
Country			Units tested	(%) Positive for MRSA
Cats				
Netherlands	Pet animals	Animal	53	53 (100.0%)
Slovakia	Pet animals	Animal	108	18 (16.7%)
Dogs				
Netherlands	Pet animals	Animal	50	50 (100.0%)
Slovakia	Pet animals	Animal	308	64 (20.8%)
Solipeds, domestic				
Netherlands	Horses	Animal	56	56 (100.0%)
Slovakia	Horses	Animal	1	0

Temporal trends in the occurrence of meticillin-resistant Staphylococcus aureus

Spain reported data for 2012 and 2015; the prevalence increased from 84.1% in 2012 to 91.4% in 2015. Switzerland reported results on the yearly prevalence of MRSA in fattening pigs from 2009 to 2015 (Table 39).

Prevalence has increased annually, rising from 2.2% in 2009 to 26.5% in 2014, although, in 2015, it remained at almost the same level (25.7%) as in 2014. The marked increase is primarily the result of the diffusion within the Swiss population of fattening pigs of clones of *spa*-types t034 and t011, both belonging to the clonal complex CC398. Detailed longitudinal studies on pig farms recently performed in Switzerland have shown that individual animals are frequently intermittently colonised; colonisation of pigs may also occur in the lairage of abattoirs (Bangerter et al., 2016). Trends should therefore be evaluated taking account of these epidemiological results. The Swiss annual MRSA monitoring of pigs at slaughter, in which a single pig is examined from a herd, provides an estimate of MRSA prevalence which is subject to imprecision.

Table 39: Temporal occurrence of meticillin-resistant *Staphylococcus aureus* in animals

Country	Year	Production type/Description	Sample unit	Number	
				Units tested	(%) Positive for MRSA
Switzerland	2009	Fattening pigs, at slaughterhouse, nasal swabs	Animal	405	8 (2.2%)[a]
	2010	Fattening pigs, at slaughterhouse, nasal swabs	Animal	392	23 (5.9%)[b]
	2011	Fattening pigs, at slaughterhouse, nasal swabs, monitoring	Animal	392	22 (5.6%)[c]
	2012	Fattening pigs, at slaughterhouse, nasal swabs, monitoring	Animal	397	72 (18.1%)[d]
	2013	Fattening pigs, at slaughterhouse, nasal swabs, monitoring	Animal	351	73 (20.8%)[e]
	2014	Fattening pigs, at slaughterhouse, nasal swabs, monitoring	Animal	298	79 (26.5%)[f]
	2015	Fattening pigs, at slaughterhouse, nasal swabs, monitoring	Animal	300	77 (25.7%)[g]
Spain	2012	Fattening pigs, at slaughterhouse, caecum, monitoring	Batch	227	191 (84.1%)[h]
	2015	Fattening pigs, at slaughterhouse, caecum, monitoring	Batch	383	350 (91.4%)

(a): In 2009, isolates were reported as unspecified genotypes.
(b): In 2010, 17 isolates were of genotype ST398-t034-V, one was of genotype ST398-t011-V and five were of genotype ST49-t208-V.
(c): In 2011, 19 isolates were of genotype ST398-t034-V, one was of genotype ST398-t011-V, one was of genotype ST49-t208-V and one was of genotype ST1-t2279-IVc.
(d): In 2012, 61 isolates belonged to genotype CC398-t034, nine belonged to genotype CC398-t011 and two belonged to genotype ST49-t208.
(e): In 2013, 63 isolates belonged to genotype CC398-t034 and 10 belonged to genotype CC398-t011.
(f): In 2014, 57 isolates belonged to genotype CC398-t034, 19 belonged to genotype CC398-t011, and one was genotype ST49-t208, one was *spa*-type t2741 and one belonged to the *spa*-type t899.
(g): In 2015, 48 isolates belonged to genotype CC398-t034, 23 belonged to genotype CC398-t011, t1145(1), t1250(1), t032(1), t4475(1), t571(1), t899(1).
(h): In 2012, 97 isolates belonged CC398-t011, 8 belonged to genotype to genotype CC398-t034, *spa*-type t108(3), *spa*-type t1197(7), *spa*-type t1451(5), *spa*-type t2346(3), unspecified(68).

3.4.1.3. Susceptibility testing of meticillin-resistant *Staphylococcus aureus* isolates

In 2015, data on the antimicrobial susceptibility of MRSA isolates[21] were only reported by Belgium, Finland and Switzerland (Table 40). All countries used a broth dilution method and applied EUCAST ECOFFs to determine the susceptibility of isolates.

Tetracycline resistance was common in the MRSA isolates tested and, where *spa*-typing data were available, most isolates belonged to *spa*-types associated with CC398. This was expected, as livestock-associated MRSA isolates belonging to sequence type ST398 are usually tetracycline resistant (Crombé et al., 2013). Considering the susceptibility of MRSA isolates from meat from pigs, fattening pigs and cattle reported by Belgium, Finland and Switzerland, almost all the isolates were resistant to tetracyclines (Table 40).

Among of the MRSA isolates from calves under one year of age tested by Belgium and Switzerland, chloramphenicol resistance was observed in 8.6% and 5.3% of isolates, respectively.

The high proportion of MRSA isolates from the pig sector showing resistance to tiamulin and trimethoprim presumably reflects the relatively common usage of these compounds in pig medicine in many European countries.

Vancomycin is one of the antimicrobials of last resort for treating *S. aureus* infections in humans, and resistance to this antimicrobial is currently extremely rare. Both resistance to vancomycin and linezolid were not detected in MRSA from animals in 2015 (see also the footnote of Table 40).

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[21] All MRSA strains isolated were resistant to penicillin and to cefoxitin (data not shown).

Table 40: Occurrence of resistance to selected antimicrobials in MRSA from food and animals, 2015

Country	Chloramphenicol		Ciprofloxacin		Clindamycin		Erythromycin		Fusidic acid	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Cattle (bovine animals) calves (under one year of age)										
Belgium	116	8.6	116	55.2	116	99.1	116	98.3	116	1.7
Switzerland	19	5.3	19	15.8	19	73.7	19	73.7	19	5.3
Cattle (bovine animals) dairy cows										
Belgium	10	0	10	50.0	10	40.0	10	40.0	10	20.0
Cattle (bovine animals) meat production animals										
Belgium	16	0	16	56.3	16	56.3	16	43.8	16	12.5
Pigs fattening pigs										
Switzerland	2	0	2	50.0	2	100	2	100	2	50.0
Meat from pigs										
Finland	9	0	9	33.3	9	100	9	55.6	9	0
Switzerland	77	0	77	11.7	77	72.7	77	70.1	77	2.6

Country	Gentamicin		Kanamycin		Linezolid		Mupirocin		Quinupristin/ Dalfopristin	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Cattle (bovine animals) calves (under one year of age)										
Belgium	116	62.9	116	66.4	116	0	116	0	116	15.5
Switzerland	19	15.8	19	15.8	19	0	19	5.3	19	31.6
Cattle (bovine animals) dairy cows										
Belgium	10	50.0	10	50.0	10	0	10	0	10	20.0
Cattle (bovine animals) meat production animals										
Belgium	16	68.8	16	68.8	16	0	16	0	16	25.0
Pigs fattening pigs										
Switzerland	2	0	2	0	2	0	2	0	2	100
Meat from pig										
Finland	9	0	9	0	9	0	9	0	9	77.8
Switzerland	77	5.2	77	5.2	77	0	77	1.3	77	68.8

Country	Rifampicin		Streptomycin		Sulfamethoxazole		Tetracyclines		Tiamulin		Trimethoprim	
	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res	N	% Res
Cattle (bovine animals) calves (under one year of age)												
Belgium	116	1.7	116	26.7	116	9.5	116	99.1	116	8.6	116	93.1
Switzerland	19	5.3	19	42.1	19	0	19	100	19	31.6	19	36.8
Cattle (bovine animals) dairy cows												
Belgium	10	10.0	10	40.0	10	10.0	10	100	10	20.0	10	90.0
Cattle (bovine animals) meat production animals												
Belgium	16	0	16	25.0	16	25.0	16	93.8	16	25.0	16	81.3
Pigs fattening pigs												
Switzerland	2	0	2	100	2	0	2	100	2	100	2	100
Meat from pig												
Finland	9	0	9	44.4	9	0	9	100	9	88.9	9	66.7
Switzerland	77	2.6	77	54.5	77	5.2	77	98.7	77	70.1	77	71.4

N: number of isolates tested; % Res: percentage of resistant isolates; −: no data reported.
All MRSA isolates tested were resistant to cefoxitin and penicillin as expected, and susceptible to linezolid and vancomycin.

3.4.2. Discussion

Monitoring of MRSA in animals and food is currently voluntary and only a limited number of countries reported MRSA data to EFSA in 2015. A number of certain MRSA strains detected in animals and animal products has indicated that animals can acquire and disseminate other MRSA strains than those which might strictly be regarded as LA-MRSA (Battisti et al., 2010; Normanno et al., 2015).

Although food is not currently considered to be a relevant source of MRSA infection or colonisation of humans (EFSA, 2009c), the monitoring of MRSA in various food products performed in several MSs consistently indicates that MRSA can be detected, quite frequently, in different types of food. Such food included poultry meat, rabbit meat and pork in 2015. It should be underlined that the laboratory techniques used to detect MRSA employ selective bacterial culture and thus, very low levels of contamination can be detected. LA-MRSA is considered a poor coloniser of humans and occurs uncommonly in persons without direct or indirect contact with livestock or carcases derived thereof (Graveland et al., 2010). Only low numbers of samples of some food categories were tested, and therefore, interval estimation of prevalence is likely to be wide, as a result of small sample sizes. Cross-contamination between carcases on slaughterhouse lines or during production processes may result in a higher prevalence in meat produced from animals than in the animals themselves. A recent report has however suggested that some strains of LA-MRSA may be adapted to colonise and infect humans and implicate poultry meat as a possible source for humans (Larsen et al., 2016).

Meticillin-resistant _Staphylococcus aureus_ – possible food-borne transmission

Larsen et al., 2016 describe cases of sporadic colonisation or illness in people living in an urban environment in Denmark with a particular type of LA-MRSA, CC9/CC398, _spa_-type t899. The isolates all harboured the ΦSa3 phage which carried the immune evasion cluster genes _scn_ (encoding the staphylococcal complement protein inhibitor), _chp_ (chemotaxis inhibitor protein) and _sak_ (staphylokinase). Carriage of these genes is considered an adaptation to enable _S. aureus_ colonisation and infection of man and is not usually a feature of animal _S. aureus_ strains, including LA-MRSA (Cuny et al., 2015). Similar isolates to those detected in humans were detected in poultry and poultry meat and some of the isolates from humans and turkey meat also contained DNA sequences which have been suggested to indicate poultry adaptation. One of the human cases had occupational exposure to meat and another had a brother who was a poultry farmer. These urban LA-MRSA isolates were highly related genetically when epidemiological links between human cases were apparent, suggesting transmission between persons or exposure to a common source. The authors suggest that food-borne transmission was the most probable explanation, at least in some of their reported LA-MRSA t899 cases.

The authors conclude that their findings do not change the generally accepted tenet that food-borne transmission plays a minor role in the epidemiology of LA-MRSA; nevertheless, the study indicates the value of ongoing surveillance of LA-MRSA in animals and food and the benefit of detailed genetic characterisation.

Considering the three broad epidemiological classes of MRSA (LA-MRSA, HA-MRSA and CA-MRSA), whenever _spa_-typing data were available, only _spa_-types associated with CC398 were reported from meat in 2015. _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. Where _spa_-typing data were not available, the susceptibility of isolates can give some indication of the type of MRSA likely to have been detected, because LA-MRSA belonging to CC398 are usually resistant to tetracycline (Crombé et al., 2013), although this is not a definitive characteristic since tetracycline resistance may also occur in other strains of MRSA.

Although the majority of _spa_-types detected were all associated with CC398, there were some notable exceptions. In calves under one year of age in Belgium, t037 and t044, which are _spa_-types associated with ST239 and ST80, respectively, were detected. MRSA ST80 _spa_-type t044 constitutes a sequence type and associated _spa_-type observed in a widely disseminated European clone of community-associated MRSA (Larsen et al., 2008), although _spa_-type t044 has also been associated with sequence type ST9 in a report of a pig with pneumonia (Lulitanond et al., 2013). MRSA _spa_-type t044 has been previously reported from monitoring of nasal swabs in pigs at slaughter in Belgium, with two positive batches detected of 327 batches examined in 2013. MRSA ST239 (associated with _spa_-type t037) is a dominant sequence type of HA-MRSA; _spa_-type t037 ST239 was also recovered from Belgian poultry in 2011 (Butaye and Nemeghaire, 2012). CA-MRSA tend to possess the PVL and Belgium provided

additional typing data and confirmed that the isolates of *spa*-type t044 from calves were negative for PVL, but one of the two MRSA *spa*-type t044 from pigs reported previously in 2013 was PVL positive. It seems likely therefore that all three categories of MRSA have been detected in Belgium over the period 2013–2015. The detection of low numbers of isolates of HA-MRSA and CA-MRSA in animals might be the result of infrequent and possibly transient colonisation of livestock with human MRSA strains from animal attendants rather than persistent establishment of these strains in farm livestock.

Switzerland detected two isolates of t008 in calves under one year of age; this *spa*-type is associated with ST8. This *spa*-type and sequence type combination is seen in isolates of the globally significant CA-MRSA USA300 strain, which is PVL positive. Switzerland has confirmed that the t008 isolates are PVL-positive; further molecular typing is proceeding to determine whether these isolates are CA-MRSA USA300. The findings are potentially important, as the CA-MRSA USA300 strain can cause severe infections in humans and has a markedly different epidemiology from HA-MRSA strains (Tenover and Goering, 2009). Switzerland also reported t032 from pigs which is a *spa*-type associated with CC22, usually considered an HA-MRSA. The detection of MRSA strains exhibiting characteristics suggestive of CA-MRSA in calves in two countries is an interesting development. 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 (for example, persistent colonisation of the animal attendants with CA-MRSA or HA-MRSA) is not known.

Switzerland has performed annual surveillance for MRSA in pigs at slaughter since 2009 and it is noteworthy that those *spa*-types associated with CC398 have shown a steady increase in prevalence to 2014/2015 when the previously increasing prevalence appears to have stabilised. Data relating to colonisation by MRSA CC398 in humans in European countries show a similar recent, upward trend in some countries, for example, an increase in MRSA CC398 as a proportion of all MRSA detections in nasopharyngeal swabbing of patients at 39 hospitals from 14% in 2008 to 29% in 2012 was noted in north-western Germany (Köck et al., 2013). In the Netherlands, 15% of human carriers of MRSA CC398 do not report direct contact with pigs or veal calves; indirect transmission from animals or direct transmission from colonised humans are possible sources (Lekkerkerk et al., 2015). Although LA-MRSA CC398 is considered a poor coloniser of human (Graveland et al., 2010), it can cause serious, fatal infections in humans, especially in patients who are prone to acquire staphylococcal infections (Berning et al., 2015). Berning et al. reported case details of two fatal infections, both of which occurred in persons with direct links to pig farms or pig farming.

Considering trends in the occurrence of MRSA in food, the monitoring of MRSA in meat products was performed on a variety of different products and sometimes involved low numbers of samples. Switzerland and Finland reported the results of *spa*-typing of MRSA isolates from meat. Both countries reported the detection of s*pa*-type t034 in meat from pigs (a common *spa*-type associated with CC398); Finland also reported *spa*-type t2741 in pork. *Spa*-type t2741 has emerged as a new dominant clone in fattening pigs in Finland, where it was reported to occur on 15 of 18 MRSA positive fattening pig farms, while *spa*-type t034 occurred in 5/18 herds and in four of those herds, both *spa*-types t034 and t2741 were present (Heikinheimo et al., 2016). Two subclones of *spa*-type t2741 were identified in research in Finland – one possessing the *ermB* gene and showing erythromycin resistance and the other lacking the gene and susceptible to erythromycin. Erythromycin-resistant and susceptible isolates of *spa*-type t2741 were reported from meat from pigs by Finland in 2015. The importance of characterising MRSA isolates is underlined by the observation that this *spa*-type t2741 which has become dominant in fattening pigs in Finland accounted for 7% of recent CC398 human infections in Finland (Heikinheimo et al., 2016).

Lincosamide resistance and macrolide susceptibility is a phenotype which can be conferred by the genes *lnuA/B/C/D/F* in staphylococci (Lozano et al., 2012; Heikinheimo et al., 2016) and was also reported in the recent study of animal isolates from Finland, where *lnuB* was frequently detected (Heikinheimo et al., 2016). Considering the susceptibility of MRSA isolates from cattle, pigs and pork to clindamycin and erythromycin reported by Belgium, Switzerland and Finland, there was either an equal occurrence of resistance to both compounds, or clindamycin resistance exceeded erythromycin resistance, the latter phenotype suggesting the possible presence of *lnu* genes. Tetracycline resistance was present in the majority of MRSA isolates subjected to susceptibility testing. Tetracycline resistance, as well as lincosamide resistance with macrolide susceptibility, are both features which are or can be associated with livestock-associated MRSA (Lozano et al., 2012; Crombé et al., 2013).

In summary, the monitoring of MRSA in 2015 has provided extremely useful information on the occurrence of MRSA in livestock and food. The situation continues to develop and evolve and there is a clear requirement for continued monitoring and appropriate molecular characterisation of MRSA isolates recovered from livestock and food, as the situation, known by the monitoring data available, is constantly evolving.

3.5. Third-generation cephalosporin and carbapenem resistance in *Escherichia coli* and *Salmonella*

Resistance to third-generation cephalosporins: the importance of extended-spectrum beta-lactamases (ESBLs), AmpC-enzymes and carbapenemases

Occurrence of ESBLs and acquired AmpC (aAmpC) beta-lactamases is considered to be an important emerging issue in Gram-negative bacteria of public health significance. ESBLs and AmpC beta-lactamases are enzymes that hydrolyse ESBL antimicrobials. Bacteria which produce ESBL/aAmpC-enzymes are usually resistant to many or all third-generation cephalosporins, which are highest priority critically important antimicrobials (Collignon et al., 2016; WHO, 2016) for the treatment of systemic or invasive Gram-negative bacterial infections in humans. Apart from their widespread use to treat *E. coli* infections, these drugs play a critical role in the treatment of certain invasive *Salmonella* infections, particularly in children and immunosuppressed patients.

Enterobacteria may become resistant to third-generation cephalosporins by several different mechanisms. The most common is the production of beta-lactamases. These enzymes are encoded by genes which can be located on either plasmids (small covalently closed circles of DNA), which can be transferred between bacteria during bacterial conjugation, or which are located on the bacterial chromosome. There are a number of different types of beta-lactamase which can confer resistance to third-generation cephalosporins. Based on structural similarities (amino acid content) they are subdivided into four classes, designated A to D in the Ambler classification: ESBL enzymes of the TEM, SHV and CTX-M families belong to class A, ESBL enzymes of the OXA-family are included in Class D, while class C includes the AmpC beta-lactamases. The beta-lactamase encoding genes can be chromosomal and intrinsic i.e. present naturally in the bacterial species (often referred as chromosomal, 'c'), or acquired ('a'), gained by transfer between bacteria.

The occurrence of beta-lactamases in *Salmonella* and *E. coli* (both pathogens and commensals) is mostly due to the acquisition of genes usually from other Enterobacteriaceae by conjugation and to a lesser extent, transduction. The clonal spread of ESBL- or AmpC- carrier bacteria is also important, as exemplified by the worldwide occurrence of the pandemic clone of *E. coli* sequence type 131, carrying the ESBL enzyme CTX-M-15, primarily occurring in humans and causing significant mortality and morbidity (Rogers et al., 2011). Wild-type *Salmonella* do not possess endogenous beta-lactamase encoding genes. Although all four different types of beta-lactamase classes have been found in *Salmonella*, within the EU, the most important mechanism of resistance to third-generation cephalosporins in *Salmonella* is the production of ESBLs followed by the production of aAmpCs. *E. coli* also possesses endogenous AmpC beta-lactamase encoding genes, that in some circumstances can be activated (i.e. through mutations in the promotor regions), and also confer resistance to third-generation cephalosporins. As for *Salmonella*, the most frequent mechanism of resistance to third-generation cephalosporins in *E. coli* is primarily the production of ESBLs, followed by that of aAmpC, although fluctuations in the level of occurrence or differences between countries and sectors may be expected. Commensal bacteria, such as indicator *E. coli*, may contribute to the dissemination of ESBLs/aAmpC, as these resistance mechanisms are usually transferable.

The emergence during the last years of resistance to carbapenems, last line antimicrobials for human medicine is considered as an important public health concern. Carbapenems are used for the treatment of highly resistant infections in humans, including, for example, the treatment of infections with Gram-negative bacteria producing ESBLs. Resistance to carbapenems in Gram-negative bacteria is mainly related to the production of carbapenemases (beta-lactamases) and the acquisition of carbapenemase-encoding genes, although other mechanisms (i.e. related to cell permeability) also exist. The most frequent beta-lactamases with carbapenemase activity can be found in the class A (KPC), class D (OXA-type carbapenemases) and Class B (metallo beta-lactamases like NDM, VIM and IMI) of Ambler's classification. Although carbapenem antimicrobials are not used in food-producing animals in the EU, resistance has occasionally been detected in bacteria carried by animals (EFSA BIOHAZ Panel, 2013; Woodford et al., 2013; Guerra et al., 2014), and dissemination from humans to animals directly or through environmental routes is suspected.

Considering the public health relevance of resistance to third-/fourth-generation cephalosporins, and carbapenem compounds, the new legislation on harmonised monitoring of antimicrobial resistance in food-producing animals and food (Commission implementing Decision 2013/652/EU) has laid down the mandatory monitoring of resistance to representative substances of these antimicrobial classes in *Salmonella* and indicator *E. coli* from 2014 onwards. All *Salmonella* and indicator *E. coli* isolates exhibiting microbiological resistance to cefotaxime, ceftazidime or meropenem are subsequently subjected to further testing using a supplementary panel of substances to obtain more detailed phenotypic characterisation of any resistance detected to third-generation cephalosporins and/or the carbapenem compound meropenem.

> **Rationale for the choice of certain substances included in the supplementary panel**
>
> - Cefotaxime and ceftazidime have been included in the supplementary panel because, although most ESBL confer resistance to both compounds, some ESBL enzymes primarily confer resistance to one or the other compound.
> - Confirmatory synergy testing has been also foreseen so that an ESBL phenotype may be identified.
> - Cefoxitin has been also included so that an AmpC phenotype may be identified.
> - Meropenem, imipenem and ertapenem have been included so that putative carbapenemase producers may be identified.
> - Temocillin (6-α-methoxy-ticarcillin) efficacy is unaffected by most ESBL and AmpC-enzymes and this substance may be particularly useful in human medicine to treat urinary tract infections caused by ESBL-producing Gram-negative organisms (Livermore and Tulkens, 2009). Susceptibility to temocillin enables further phenotypic characterisation of carbapenemases.

From the results of such further testing, it has thus been possible to infer the presumptive class of beta-lactamase enzyme which was responsible for conferring the phenotypic profile of resistance to third-generation cephalosporins or meropenem detected, providing additional epidemiological information. The monitoring of indicator *E. coli* and *Salmonella* spp. did not utilise selective primary isolation media containing cephalosporins so the results generally relate to organisms selected at random from primary culture media.

In 2015, the 'specific' monitoring of ESBL-/AmpC-/Carbapenemase-producing *E. coli* (by using selective media containing cephalosporins) was also performed on a mandatory basis by majority of MSs and Norway and Switzerland. The corresponding results have also been presented below, and the results of the 'routine' and 'specific' monitoring are available for comparison, where this is possible. Italy did not perform the supplementary testing (panel 2) but provided results from molecular analyses. Ten MSs also reported results of a 'specific' monitoring of carbapenemase-producing microorganisms (by using selective media containing carbapenems), performed voluntarily.

> **Identification of presumptive ESBL-, AmpC- and/or carbapenemase producers (also see material and methods section)**
>
> To infer the class of beta-lactamase enzyme responsible for conferring the phenotypic profile of resistance to third-generation cephalosporins or meropenem detected, the EUCAST guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance (EUCAST, 2013) were applied. A screening breakpoint for cefotaxime and/or ceftazidime (> 1 mg/L) was applied to screen for ESBL and AmpC-producers, as these isolates typically (with only a few exceptions) show MICs for cefotaxime and/or ceftazidime > 1 mg/L, whereas different resistance mechanisms are expected in the microbiologically resistant isolates (MIC > ECOFFs) exhibiting MICs lower than the screening breakpoint. Some of the countries also voluntarily reported results from the detection of ESBL-/AmpC-resistance genes in the third-generation cephalosporin resistant isolates. These data were included with the classifications made on the basis of resistance phenotype. For the occurrence and prevalence tables shown in this section, presumptive ESBL-producers were considered as those exhibiting an ESBL- and/or ESBL-/AmpC-phenotype, and presumptive AmpC-producers, those with an AmpC and AmpC-/ESBL-phenotype.

3.5.1. Third-generation cephalosporin and carbapenem resistance in *Salmonella* isolates from humans (voluntary testing and reporting)

3.5.1.1. Distribution of ESBL- and AmpC-phenotypes in *Salmonella* by country

In 2015, 64 of the 10,225 *Salmonella* isolates from humans (0.6%, 18 MSs and Norway), tested for both cefotaxime and ceftazidime, were 'microbiologically' resistant to both antimicrobials. Eight MSs and one non-MS (of 11 MSs and Norway reporting resistant isolates), further tested all or some of their suspected isolates for presence of ESBL- and/or AmpC. ESBL-producing *Salmonella* were identified in 0.5% of the tested isolates in the EU MSs with the highest occurrence in Italy (5.6%), Cyprus (2.9%) and France (1.1%) (Table 41). AmpC was less frequent, identified in 0.1% of tested isolates. Only one isolate was reported to be AmpC + ESBL. No isolates were reported resistant to carbapenems, although it should be noted that meropenem resistance was interpreted with clinical breakpoints in seven of the 19 countries.

Table 41: ESBL- and AmpC-phenotypes in *Salmonella* spp. isolates from humans by country, 2015

Country	Total *Salmonella* tested for CTX & CAZ	Res to CTX & CAZ	Phenotype								Serovars
			ESBL		AmpC		AmpC + ESBL		Atypical phenotype		
	N	N	N	%	N	%	N	%	N	%	
Austria	1,556	6	5	0.3	1	0.1					Group B, Infantis (2), Typhimurium (2), Virchow
Cyprus	35	1	1	2.9							Saintpaul
France	560	10	6	1.1	4	0.7					Chester (2), Haifa, Heidelberg (2), Kentucky (2), monophasic Typhimurium, Newport, Stanley
Italy	71	4	4	5.6							Infantis (4)
Netherlands	787	9	6	0.8					3	0.4	Enteritidis, monophasic Typhimurium (3), Typhimurium (5)
Romania	169	1					1	0.6			Enteritidis
Slovenia	390	3	2	0.5	1	0.3					Group B, Infantis, Stanley
Spain	1,999	10	4	0.2	1	0.1					Infantis, monophasic Typhimurium (3), Thompson. (5 isolates not further typed)
Total (8 MSs)	**5,567**	**44**	**28**	**0.5**	**7**	**0.1**	**1**	**0.0**	**3**	**0.1**	
Norway	349	3	3	0.9							Choleraesuis, Infantis, Poona

ESBL: extended-spectrum beta-lactamase; N = isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

3.5.1.2. Distribution of ESBL- and AmpC-phenotypes in *Salmonella* by serovars

When assessing the same data by serotype, ESBL was most commonly found in *S.* Choleraesuis, *S.* Haifa and *S.* Heidelberg; however, few isolates had been tested of these serovars (Table 42). ESBL was detected in 5.8% of *S.* Infantis in four MSs and one non-MS with CTX-M-2 and CTX-M-9 as the reported genotypes, where available. Among monophasic *S.* Typhimurium 1,4,[5],12:i:-, seven isolates were ESBL and one AmpC however the proportions were low due to the high frequency of this serovar in human cases.

Table 42: ESBL- and AmpC-phenotypes and genotypes in *Salmonella* spp. isolates from humans by serovar, 2015 (8 MSs and Norway)

Serovar	Tested for CTX & CAZ	Res to CTX & CAZ	Phenotype								Genotype
			ESBL		AmpC		AmpC + ESBL		Atypical phenotype		
	N	N	N	%	N	%	N	%	N	%	
Chester	104	2		0.0	2	1.9					DHA-1
Choleraesuis	5	1	1	20.0							
Enteritidis	1,727	3	1	0.1			1	0.1			
Group B	45	2	1	2.2	1	2.2					TEM
Haifa	4	1	1	25.0							SHV-12
Heidelberg	7	2	1	14.3	1	14.3					CTX-M-15; CMY-2
Infantis	155	11	9	5.8							CTX-M-2 & CTX-M-9 (2); CTX-M-9 (1)
Kentucky	145	2	2	1.4							TEM-15; CTX-M-14
Monophasic Typhimurium 1,4,[5],12:i:-	1,043	8	6	0.6	1	0.1					SHV-12; CTX-M-9 (2); CMY-2

Serovar	Tested for CTX & CAZ	Res to CTX & CAZ	Phenotype									Genotype
			ESBL		AmpC		AmpC + ESBL		Atypical phenotype			
	N	N	N	%	N	%	N	%	N	%		
Newport	51	1	1	2.0								CTX-M-15
Poona	13	1	1	7.7								
Saintpaul	16	1	1	6.3								
Stanley	248	2	1	0.4	1	0.4						CMY-2
Thompson	39	1	1	2.6								CTX-M-65
Typhimurium	862	2	3	0.3	1	0.1			3	0.3		TEM & CTX-M-1
Virchow	40	1	1	2.5								SHV

ESBL: extended-spectrum beta-lactamase; N: isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

3.5.2. Third-generation cephalosporin and carbapenem resistance in *Salmonella* isolates from food and animals (routine monitoring)

In 2015, third-generation cephalosporin resistance was identified in a range of *Salmonella* serovars when isolates were tested with the Panel 1 of antimicrobials (Table 6). Occurrence data in *Salmonella* spp. are presented in Table 43 below and further results at the serovar level are also tabulated in the appendices. Resistant isolates were also tested using the supplementary panel for susceptibility to beta-lactams (Panel 2 of antimicrobials, Table 8).

3.5.2.1. Third-generation cephalosporin and carbapenem resistance in *Salmonella* from food

Resistance to carbapenems in Salmonella from meat from pigs and meat from bovine animals

None of the *Salmonella* isolates from meat from pigs subjected to supplementary testing (7 isolates resistant to cephalosporins, see below) were microbiologically resistant to meropenem, ertapenem or imipenem. Similarly, none of the isolates from meat from bovine animals were microbiologically resistant to meropenem or subjected to supplementary testing, and thus no data on ertapenem or imipenem susceptibility were reported for these isolates.

Resistance to cefotaxime and ceftazidime in Salmonella from pig meat

In the 17 reporting MSs, resistance to cefotaxime and/or ceftazidime in *Salmonella* spp. isolates from pig meat tested with Panel 1 of antimicrobials was either not detected or reported at low levels (Table SALMPIGMEATD) in Belgium (two isolates resistant to cefotaxime and ceftazidime, 1.1% of the isolates tested) in the Czech Republic (one isolate resistant to both antimicrobials, 4.3%), Germany (two isolates resistant to both antimicrobials, 3.9%), Portugal (two isolates resistant to both antimicrobials, 4.2%) and in Spain (one isolate resistant to cefotaxime, 0.8%).

The resistant isolates notably belonged to serovars *S.* Typhimurium (Table TYPHIPIGMEATD), *S.* Derby (Table DERBYPIGMEATD), *S.* Bredeney, and *S.* Infantis. Resistance to cefotaxime or ceftazidime was not detected in monophasic *S.* Typhimurium and *S.* Rissen isolates from meat from pigs (Tables MOTYPHIPIGMEATD, RISSENPIGMEATD).

Resistance to cefotaxime and ceftazidime in Salmonella from meat from bovine animals

In the seven reporting MSs, no *Salmonella* isolates from bovine meat were resistant to cefotaxime or ceftazidime in 2015 (Table SALMBOVMEATD), and therefore, no supplementary beta-lactam susceptibility testing was performed on isolates.

3.5.2.2. Third-generation cephalosporin and carbapenem resistance in *Salmonella* from animals

Resistance to carbapenems in Salmonella from fattening pigs and calves under one year of age

The single *Salmonella* isolate from fattening pigs subjected to supplementary testing, was not microbiologically resistant to ertapenem, imipenem or meropenem. None of the isolates from calves

under one year of age were resistant to meropenem or subjected to supplementary testing, and thus no data on ertapenem or imipenem susceptibility were reported.

Resistance to cefotaxime and ceftazidime in Salmonella from fattening pigs

Very low occurrence of resistance to cefotaxime (0.7%) and ceftazidime (0.5%) was reported for *Salmonella* spp. isolates from the six reporting MSs, reflecting no resistance in all of the reporting countries, except Italy where low resistance was recorded (Table SALMFATPIGD).

Two out of the three *Salmonella* isolates resistant to cefotaxime and, respectively, one out of two *Salmonella* isolates resistant to ceftazidime from Italy were *S*. Typhimurium (Table TYPHIFATPIGD). One monophasic *S*. Typhimurium was resistant to both cefotaxime and ceftazidime (Table MOTYPHIFATPIGD).

Resistance to cefotaxime and ceftazidime in Salmonella from calves under one year of age

Out of the 45 *Salmonella* isolates from calves under one year of age reported by three countries, none were resistant to cefotaxime or/and ceftazidime.

Table 43: Occurrence of resistance to beta-lactam compounds in *Salmonella* spp. isolates from fattening pigs and meat from pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015

Country	Total number of *Salmonella* spp. tested	Number subjected to supplementary testing and number resistant[a]								
		Cefotaxime		Ceftazidime		Cefoxitin		Cefepime[b]		Temocillin[c]	
		N	n Res	N	n Res	N	n Res	N	n Res	N	n Res
Meat from pigs											
Belgium	183	1	1	1	1	1	0	1	1	1	0
Czech Republic	23	1	1	1	1	1	1	1	1	1	0
Germany	51	2	2	2	2	2	0	2	2	2	0
Poland	10	1	0	1	0	1	1	1	1	1	0
Portugal	48	2	2	2	2	2	2	2	2	2	0
Spain	128	1	1	1	0	1	0	1	1	1	0
Total (6 MSs)	**443**	**8**	**7**	**8**	**6**	**8**	**4**	**8**	**8**	**8**	**0**
Fattening pigs											
Italy	91	3	3	3	2	3	1	3	3	3	1

ECOFFs: epidemiological cut-off values; N: number of isolates tested; n Res: number of the isolates resistant; MSs: Member States.
(a): No resistance to carbapenems was reported.
(b): Interpretive cut-off applied for cefepime: > 0.125 mg/L.
(c): Interpretive cut-off applied for temocillin: > 32 mg/L.

3.5.2.3. Resistance phenotypes identified in *Salmonella* spp. from meat from pigs and fattening pigs

The ESBL- or AmpC-phenotype was particularly associated with certain serovars, suggesting possible clonal expansion of particular strains.

Salmonella spp. isolates with an ESBL phenotype (Table 44) were detected in meat from pigs in Germany (two *S*. Derby), Belgium (one *S*. unspecified serovar) and from fattening pigs in Italy (one *S*. Typhimurium and one monophasic *S*. Typhimurium).

Salmonella spp. isolates with an AmpC phenotype (Table 44) were detected in meat from pigs in Portugal (two *S*. Bredeney) 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 the Czech Republic (*S*. Infantis).

Table 44: Presumptive ESBL- and AmpC-producing *Salmonella* spp. isolates from meat from pigs and fattening pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015[a]

Country	Total number of *Salmonella* tested	Number of *Salmonella* with supplementary testing	ESBL[b]		ESBL with clavulanic-SYN only for CTX[c]		ESBL with clavulanic-SYN only for CAZ[d]		AmpC[e]		AmpC + ESBL[f]	
			N	%[g]	N	%[g]	n	%[g]	n	%[g]	n	%[g]
Meat from Pigs												
Belgium	183	1	1	0.5	–	–	–	–	–	–	–	–
Czech Republic	23	1	1	–	–	–	–	–	1	–	1	4.3[h]
Germany	51	2	2	3.9	–	–	–	–	–	–	–	–
Poland	10	1	–	–	–	–	–	–	–	–	–	–
Portugal	48	2	–	–	–	–	–	–	2	4.2	–	–
Spain[i]	128	1	–	–	–	–	–	–	–	–	–	–
Total (6 MSs)	**443**	**8**	**4**	**0.9**	**–**	**–**	**–**	**–**	**3**	**0.7**	**1**	**0.2**
Fattening Pigs												
Italy[j]	91	3	2	2.2	–	–	–	–	1	1.1	–	–

ESBL: extended-spectrum beta-lactamase; n: isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see Chapter 1.2.5).

(b): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(c): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(d): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(e): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(f): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate.These isolates are also included in the ESBL and AmpC columns.

(g): Percentage of the total number of *Salmonella* isolates tested (with panel 1).

(h): Cefoxitin MIC = 16 mg/L.

(i): Ceftazidime and cefotaxime MIC ≤ 1 mg/L.

(j): Molecular data were reported by Italy: two isolates were positive for SHV-12. For the isolate with AmpC-phenotype (cefoxitin MIC > 64 mg/L and no synergy) no gene was reported.

3.5.3. Third-generation cephalosporin and carbapenem resistance in indicator *Escherichia coli* isolates from animals (routine monitoring)

In 2015, third-generation cephalosporin resistance was identified in indicator *E. coli* isolates from fattening pigs tested with the panel 1 of antimicrobials (Table 6). Resistant isolates were also subjected to supplementary beta-lactams susceptibility testing (Panel 2, Table 8). Cefotaxime and ceftazidime resistance in indicator *E. coli* isolates from fattening pigs was detected in 18 out of the 29 reporting countries, whereas in indicator *E. coli* from calves under one year of age, resistance to these antimicrobials was reported by seven out of the 12 countries. Overall, resistance to third-generation cephalosporins was either not detected or was reported at low levels (Tables ESCHEPIGD and ESCHECALVD).

3.5.3.1. Third-generation cephalosporin resistance in indicator *E. coli* from fattening pigs

Resistance to cefotaxime, ceftazidime and carbapenem compounds

Resistance to cefotaxime in indicator *E. coli* isolates from fattening pigs was reported by 27 reporting MSs and 2 non-MSs (Norway and Switzerland) (Table ESCHEPIGD). The levels of resistance recorded were very low and low, whereas, in 10 MSs, resistance to cefotaxime and ceftazidime was not detected in isolates from fattening pigs (Table 45). Overall, resistance levels in reporting countries were low at 1.4% for cefotaxime and 1.3% for ceftazidime.

Meropenem-resistant indicator *E. coli* isolates from fattening pigs were not reported by any of 29 reporting countries. None of the isolates subjected to supplementary testing (16 countries) were microbiologically resistant to ertapenem, and only one isolate from Cyprus was reported resistant to imipenem without showing resistance to other carbapenems, suggesting the presence of other resistance mechanisms rather than carbapenemases (Table ESCHEPIGD2).

Presumptive ESBL- and AmpC-producers identified

Presumptive ESBL-producing Indicator *E. coli* isolates were detected in fattening pigs from 12 MSs and Norway. Significant numbers of isolates showed synergy with only one of the two indicator cephalosporins (cefotaxime and ceftazidime) used in combination with clavulanate to detect synergy. The proportion of all *E. coli* isolates from fattening pigs with an ESBL-phenotype was low or very low in all countries. Eight MSs and Norway reported presumptive AmpC-producing isolates, although the proportion of total *E. coli* with this phenotype was very low and low in all MSs (Table 46). Cyprus reported one isolate with an 'ESBL + AmpC' phenotype.

A presumptive carbapenemase-producing *E. coli* from meat from pigs in Belgium

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

3.5.3.2. Third-generation cephalosporin resistance in indicator *E. coli* from calves under one year of age

Resistance to cefotaxime, ceftazidime and carbapenem compounds

Data on resistance in indicator *E. coli* isolates from calves under one year of age were reported by 10 MSs and two non-MSs (Norway and Switzerland). The levels of resistance recorded for third-generation cephalosporins were low and very low; Croatia, the Netherlands, Spain, Sweden and Norway did not detect any resistance. Overall, resistance levels in reporting countries were higher in calves less than one year of age than in those from fattening pigs, at 1.7% for cefotaxime and 1.4% for ceftazidime (Table ESCHECALVD).

None of the isolates reported were microbiologically resistant to meropenem. From the isolates subjected to supplementary testing (from five MS and Switzerland) no imipenem-resistant was reported. Only one ertapenem-resistant indicator *E. coli* isolate was reported by Denmark (Table 47); however, the genotype was not confirmed. Loss of porins in conjunction with AmpC-enzyme production may account for resistance to ertapenem in the absence of resistance to the other carbapenems tested.

Presumptive ESBL- and AmpC-producers identified

Indicator *E. coli* isolates with an ESBL-phenotype were detected in calves under one year of age in five MSs and one non-MS. Significant numbers of isolates showed synergy with cefotaxime only. The proportion of all *E. coli* isolates from calves under one year of age with an ESBL-phenotype was low or very low in all countries. Germany reported one *E. coli* isolate with a presumptive AmpC phenotype in calves under one year of age. Belgium reported one isolate with a presumptive 'ESBL+AmpC' phenotype (Table 48).

Table 45: Occurrence of resistance to beta-lactam and carbapenem compounds in indicator *E. coli* isolates from fattening pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015

Country	Total number of *E. coli* tested	Cefotaxime		Ceftazidime		Cefoxitin		Cefepime		Ertapenem		Temocillin	
		N	n Res	N	n Res	N	n Res	N	n Res	N	n Res	N	n Res
Austria	163	4	3	4	3	4	0	4	3	4	0	4	0
Belgium	186	2	2	2	2	2	1	2	1	2	0	2	0
Cyprus	55	4	3	4	3	4	1	4	3	4	0	4	0
Czech Republic	187	5	5	5	4	5	3	5	2	5	0	5	0
Estonia	85	1	1	1	1	1	1	1	0	1	0	1	0
France	200	1	1	1	1	1	0	1	1	1	0	1	0
Germany	212	8	7	8	6	8	2	8	5	8	0	8	0
Greece	116	6	6	6	6	6	0	6	6	6	0	6	0
Hungary	170	2	2	2	2	2	0	2	2	2	0	2	0
Ireland	147	1	1	1	1	1	1	1	0	1	0	1	0
Netherlands	298	1	1	1	1	1	1	1	0	1	0	1	0
Poland	170	9	7	9	6	9	0	9	6	9	0	9	0
Portugal	198	10	10	10	10	10	0	10	10	10	0	10	0
Romania	399	6	6	6	6	6	2	6	5	6	0	6	0
Spain	170	1	1	1	1	1	0	1	1	1	0	1	0
Sweden	200	2	0	2	0	2	0	2	0	2	0	2	0
Total (MSs 16)	**2,956**	**63**	**56**	**63**	**53**	**63**	**12**	**63**	**45**	**63**	**0**	**63**	**0**
Norway	270	2	2	2	2	2	1	2	1	2	0	2	0
Switzerland	182	4	0	4	0	4	0	4	0	4	0	4	0

No *E. coli* isolates from fattening pigs were resistant to meropenem. Cyprus reported the presence of one isolate resistant to imipenem.
Interpretive cut-off applied for temocillin: > 32 mg/L.
ECOFFs: epidemiological cut-off values; N: number of the isolates tested; n Res: number of the isolates resistant; MSs: Member States.

Table 46: Presumptive ESBL- and AmpC producing indicator *E. coli* isolates from fattening pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015[a]

Country	Total number of *E. coli* tested	Number of *E. coli* with supplementary testing[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
			n	%[h]	n	%[h]	n	%[h]	N	%[h]	n	%[h]
Austria	163	4	3	1.8	–	–	–	–	–	–	–	–
Belgium	186	2	1	0.5	1	0.5	–	–	1	0.5	–	–
Cyprus	55	4	3	5.5	1	1.8	1	1.8	1	1.8	1	1.8
Czech Republic	187	5	2	1.1	2	1.1	–	–	3	1.6	–	–
Estonia	85	1	–	–	–	–	–	–	1	1.2	–	–
France	200	1	1	0.5	–	–	–	–	–	–	–	–
Germany	212	8	5	2.4	1	0.5	–	–	2	0.9	–	–
Greece	116	6	6	5.2	1	0.9	–	–	–	–	–	–
Hungary	170	2	2	1.2	–	–	–	–	–	–	–	–
Ireland	147	1	–	–	–	–	–	–	1	0.7	–	–
Netherlands	298	1	–	–	–	–	–	–	1	0.3	–	–
Poland	170	9	7	4.1	3	1.8	–	–	–	–	–	–
Portugal	198	10	10	5.1	1	0.5	–	–	–	–	–	–
Romania	399	6	3	0.8	2	0.5	–	–	2	0.5	–	–
Spain	170	1	1	0.6	–	–	–	–	–	–	–	–
Sweden	200	2	–	–	–	–	–	–	–	–	–	–
Total (16 MSs)	**2,956**	**63**	**44**	**1.5**	**12**	**0.4**	**1**	**0.03**	**12**	**0.4**	**1**	**0.03**
Norway	270	2	1	0.4	1	0.4	–	–	1	0.4	–	–
Switzerland	182	4	–	–	–	–	–	–	–	–	–	–

ESBL: extended-spectrum beta-lactamase; n= isolates with this phenotype; %: percentage of isolates from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States; no genes were reported for these isolates by MSs.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see Chapter 1.2.5).

(b): For some MSs, it include isolates microbiologically resistant to cefotaxime and/or ceftazidime but with MIC ≤ 1 mg/L for both antimicrobials, suggesting the presence of other mechanisms (as stated above, were not further classified).

(c): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(d): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(e): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(f): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(g): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are included in the ESBL and AmpC columns.

(h): Percentage of the total number of *E. coli* isolates tested (with panel 1).

Table 47: Occurrence of resistance to beta-lactam and carbapenem compounds in indicator *E. coli* isolates from calves under one year of age collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015

Country	Total number of *E. coli* tested	Number subjected to supplementary testing and number resistant											
		Cefotaxime		Ceftazidime		Cefoxitin		Cefepime		Ertapenem		Temocillin	
		N	n Res	N	n Res	N	n Res	N	n Res	N	n Res	N	n Res
Belgium	196	6	6	6	6	6	1	6	6	6	0	6	0
Denmark	144	1	1	1	0	1	1	1	1	1	1[(a)]	1	0
France	194	4	3	4	4	4	0	4	3	4	0	4	0
Germany	191	5	5	5	4	5	1	5	4	5	0	5	0
Italy	170	6	6	6	3	6	0	6	6	6	0	6	0
Portugal	218	8	8	8	7	8	0	8	8	8	0	8	0
Total (6 MSs)	**1,113**	**30**	**29**	**30**	**24**	**30**	**3**	**30**	**28**	**30**	**1**	**30**	**0**
Switzerland	190	8	4	8	4	8	0	8	4	8	0	8	0

No *E. coli* isolates from calves under one year of age were resistant to imipenem or meropenem.

Interpretive cut-off applied for temocillin: > 32 mg/L.

ECOFFs: epidemiological cut-off value; MSs: Member States.

(a): The genotype of the ertapenem-resistant isolate from Denmark was not confirmed. Loss of porins in conjunction with AmpC-enzyme production may account for resistance to ertapenem in the absence of resistance to the other carbapenems tested.

Table 48: Presumptive ESBL- and AmpC-producing indicator *E. coli* isolates from calves under one year of age collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015[a]

Country	Total number of *E. coli* tested	Number of indicator *E. coli* with supplementary testing[b]	ESBL[c]		ESBL with clavulanic- SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
			N	%[h]	n	%[h]	n	%[h]	n	%[h]	n	%[h]
Belgium	196	6	5	2.5	1	0.5	–	–	1	0.5	1	0.5
Denmark	144	1	–	–	–	–	–	–	–	–	–	–
France	194	4	3	1.5	–	–	–	–	–	–	–	–
Germany	191	5	3	1.6	–	–	–	–	1	0.5	–	–
Italy[i]	170	6	6	3.5	3	1.8	–	–	–	–	–	–
Portugal	218	8	8	3.7	1	0.5	1	0.5	–	–	–	–
Total (6 MSs)	**1,113**	**30**	**25**	**2.2**	**5**	**0.4**	**1**	**0.1**	**2**	**0.2**	**1**	**0.1**
Switzerland	190	8	4	2.1	1	0.5	1	0.5	–	–	–	–

ESBL.: extended-spectrum beta-lactamase; n= isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): For some MSs, it include isolates microbiologically resistant to cefotaxime and ceftazidime but with MIC ≤ 1 mg/L for both antimicrobials, suggesting the presence of other mechanisms (as stated above, were not further classified).

(c): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(d): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(e): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(f): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(g): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are included in the ESBL and AmpC columns.

(h): Percentage of the total number of *E. coli* isolates tested (with panel 1).

(i): Molecular data were reported by Italy, and the isolates were positive for CTX-M- (5 isolates) and SHV-12 (1) ESBL-encoding genes.

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

In certain types of monitoring, selective media containing cephalosporins may be used to investigate the presence of cephalosporin-resistant organisms in a particular sample, even when they are present at low levels. This type of monitoring (which is referred to as 'specific monitoring' in this report) provides a different type of result from that which would be obtained from non-selective culture. The selective media used (containing cefotaxime at 1 mg/L) in specific monitoring provides a greater sensitivity for detecting resistant organisms in a sample.

For 2015, the specific ESBL-/AmpC-/carbapenemase-producing monitoring was performed on a mandatory basis on meat from pigs (fresh meat at retail) by 23 MSs and 2 non-MSs (Tables ESCHEPIGMEATESBL, ESCHEPIGMEATESBL2), on meat from bovine animals (fresh meat at retail) by 24 MSs and 2 non-MSs (Tables ESCHEBOVMEATESBL, ESCHEBOVMEATESBL2), of fattening pigs by 28 MSs and 2 non-MSs (Tables ESCHEPIGESBL, ESCHEPIGDESBL2) and on calves under one year of age by 10 MSs and 2 non-MSs (Tables ESCHECALVESBL, ESCHECALVESBL2).

Italy collected the samples according to the Legislation, but instead of reporting results from the supplementary testing, only results from molecular analyses were reported. Occurrence data from ESBL- and AmpC-phenotypes have not been included in the following Tables, but are presented in the text of the respective subsections and in the maps.

3.5.4.1. Specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in meat from pigs

Data on specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in pig meat were reported by 23 MSs and 2 non-MSs (Norway and Switzerland) (Tables ESCHEPIGMEATESBL, ESCHEPIGMEATESBL2). Italy reported only results from molecular analyses (Table 49).

Considering meat from pigs, 22 MSs tested 5,350 retail meat samples and following culture on selective media, 7.0% yielded presumptive ESBL-producing *E. coli*, while 2.3% yielded presumptive AmpC-producing *E. coli* and 0.4% yielded *E. coli* with an ESBL + AmpC phenotype (Table 50).

Italy tested 279 samples. Among the 25 isolates recovered from these samples, 22 tested positive for ESBL-encoding genes (all isolates positive for different CTX-M-genes, mainly encoding for CTX-M-1) and 3 tested positive for CMY-2 AmpC-genes. The total prevalence found was 7.9% of *E. coli* isolates with an ESBL-phenotype, and 1.1% with an AmpC-phenotype.

In most but not all countries, the detection of ESBL-producing *E. coli* exceeded that of AmpC-producing *E. coli*, with the exception of Cyprus, Finland and Norway. All ESBL-producing *E. coli* were categorised as presumptive cefotaximase-producers. South-eastern, south central and southern-western MSs tended to report higher prevalence of ESBL-/AmpC-producing *E. coli* than the Nordic countries and, to a lesser extent, than MSs from Western Europe (Figure 66).

Table 49: Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from pigs collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

Country	Total number of *E. coli* tested[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
		N	%[h]	N	%[h]	N	%[h]	n	%[h]	n	%[h]
Austria	20	19	95.0	6	30.0	–	–	1	5.0	–	–
Belgium[i,j]	16	14	87.5	6	37.5	–	–	2	12.5	–	–
Bulgaria	12	10	83.3	5	41.7	–	–	3	25.0	1	8.3
Croatia	4	2	50.0	1	25.0	–	–	2	50.0	–	–
Cyprus	7	2	28.6	2	28.6	–	–	6	85.7	1	14.3
Czech Republic[j]	46	28	60.9	18	39.1	–	–	20	43.5	2	4.3
Denmark	5	3	60.0	1	20.0	–	–	2	40.0	–	–
Estonia	5	4	80.0	1	20.0	–	–	2	40.0	1	20.0
Finland	1	–	–	–	–	–	–	1	100	–	–
France	4	4	100	2	50.0	–	–	–	–	–	–
Germany	22	21	95.5	6	27.3	–	–	2	9.1	2	9.1
Greece	9	9	100.0	–	–	–	–	–	–	–	–
Hungary	26	23	88.5	15	57.7	–	–	4	15.4	2	7.7
Latvia	11	9	81.8	5	45.5	–	–	2	18.2	–	–
Lithuania[j]	16	13	81.3	7	43.8	–	–	3	18.8	–	–
Portugal[j]	39	32	82.1	9	23.1	–	–	8	20.5	1	2.6
Romania	20	14	70.0	8	40.0	–	–	7	35.0	1	5.0
Slovakia	5	3	60.0	–	–	–	–	2	40.0	–	–
Slovenia	8	7	87.5	–	–	–	–	1	12.5	–	–
Spain[j]	36	29	80.6	9	25.0	–	–	10	27.8	3	8.3
Sweden[i]	1	1	100	–	–	–	–	–	–	–	–
United Kingdom	6	5	83.3	2	33.3	–	–	1	16.7	–	–
Total (22 MSs)	**319**	**252**	**78.9**	**103**	**32.4**	**–**	**–**	**79**	**24.8**	**14**	**4.4**

Country	Total number of *E. coli* tested[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
		N	%[h]	N	%[h]	N	%[h]	n	%[h]	n	%[h]
Norway	2	–	–	–	–	–	–	2	100	–	–
Switzerland	2	2	100	–	–	–	–	–	–	–	–

ESBL: extended-spectrum beta-lactamase; n= isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member Stats.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): For some MSs, it include isolates microbiologically resistant to cefotaxime and/or ceftazidime but with MIC ≤ 1 mg/L for both antimicrobials, suggesting the presence of other mechanisms (as stated above, were not further classified).

(c): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(d): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(e): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(f): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(g): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also in the ESBL and AmpC columns.

(h): Percentage of the total number of *E. coli* isolates tested (with panel 2).

(i): Molecular data were reported by Belgium for six isolates which were positive for CTX-M- (5 isolates) and SHV- (1) ESBL-encoding genes, and Sweden, one isolate with CTX-M-55.

(j): Some of these isolates were reported as microbiologically resistant to carbapenems (Belgium, 1 isolate resistant to meropenem, ertapenem and imipenem but not confirmed as carbapenemase-producer; Czech Republic, Lithuania and Spain, with 1, 1, and 3 isolates resistant to ertapenem, and 1 isolate from Portugal resistant to imipenem).

Table 50: Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from pigs collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

Country	Total number of samples tested	ESBL[b] %Prev	ESBL[b] %95CI	ESBL with clavulanic-SYN only for CTX[c] %Prev	ESBL CTX[c] %95CI	ESBL with clavulanic-SYN only for CAZ[d] %Prev	ESBL CAZ[d] %95CI	AmpC[e] %Prev	AmpC[e] %95CI	AmpC + ESBL[f] %Prev	AmpC + ESBL[f] %95CI
Austria	224	9.3	5.2–12.9	2.9	1–5.7	0.0	0–1.6	0.5	0–2.5	0.0	0–1.6
Belgium	119	11.8	6.6–19	5.0	1.9–10.7	0.0	0–3.1	1.7	0.2–5.9	0.0	0–3.1
Bulgaria	461	20.8	–	10.4	–	0.0	0–0.8	6.2	–	2.1	–
Croatia	148	1.4	0.2–4.8	0.7	0–3.7	0.0	0–2.5	1.4	0.2–4.8	0.0	0–2.5
Cyprus	121	1.7	0.2–5.8	1.7	0.2–5.8	0.0	0–3	5.0	1.8–10.5	0.8	0–4.5
Czech Republic	302	9.3	6.2–13.1	6.0	3.6–9.3	0.0	0–1.2	6.6	4.1–10	0.7	0.1–2.4
Denmark	289	1.2	0.2–3	0.4	0–1.9	0.0	0–1.3	0.8	0.1–2.5	0.0	0–1.3
Estonia	150	2.7	0.7–6.7	0.7	0–3.7	0.0	0–2.4	1.3	0.2–4.7	0.7	0–3.7
Finland	303	0.0	0–1.2	0.0	0–1.2	0.0	0–1.2	0.3	0–1.8	0.0	0–1.2
France	275	1.5	0.4–3.7	0.7	0.1–2.6	0.0	0–1.3	0.0	0–1.3	0.0	0–1.3
Germany	454	5.5	2.9–7	1.6	0.5–2.9	0.0	0–0.8	0.5	0.1–1.6	0.5	0.1–1.6
Greece	156	5.8	2.7–10.7	0.0	0–2.3	0.0	0–2.3	0.0	0–2.3	0.0	0–2.3
Hungary	300	7.7	4.9–11.3	5.0	2.8–8.1	0.0	0–1.2	1.3	0.4–3.4	0.7	0.1–2.4
Latvia	150	6.5	2.8–11.1	3.6	1.1–7.6	0.0	0–2.4	1.5	0.2–4.7	0.0	0–2.4
Lithuania	150	8.7	4.7–14.4	4.7	1.9–9.4	0.0	0–2.4	2.0	0.4–5.7	0.0	0–2.4
Portugal	150	21.3	15.1–28.8	6.0	2.8–11.1	0.0	0–2.4	5.3	2.3–10.2	0.7	0–3.7
Romania	399	11.1	–	6.3	–	0.0	0–0.9	5.5	–	0.8	–
Slovakia	150	2.0	0.4–5.7	0.0	0–2.4	0.0	0–2.4	1.3	0.2–4.7	0.0	0–2.4
Slovenia	150	4.7	1.9–9.4	0.0	0–2.4	0.0	0–2.4	0.7	0–3.7	0.0	0–2.4
Spain	301	9.6	6.5–13.5	3.0	1.4–5.6	0.0	0–1.2	3.3	1.6–6	1.0	0.2–2.9
Sweden	286	0.3	0–1.9	0.0	0–1.3	0.0	0–1.3	0.0	0–1.3	0.0	0–1.3
United Kingdom	312	2.1	0.5–3.7	0.9	0.1–2.3	0.0	0–1.2	0.4	0–1.8	0.0	0–1.2
Total (22 MSs)	**5,350**	**7.0**	**6.3–7.7**	**2.9**	**2.5–3.4**	**0.0**	**0–0.1**	**2.3**	**1.9–2.7**	**0.4**	**0.24–0.6**
Norway	243	0.0	0–1.5	0.0	0–1.5	0.0	0–1.5	0.8	0.1–2.9	0.0	0–1.5

Country	Total number of samples tested	ESBL[b]		ESBL with clavulanic-SYN only for CTX[c]		ESBL with clavulanic-SYN only for CAZ[d]		AmpC[e]		AmpC + ESBL[f]	
		%Prev	%95CI	%Prev	%95CI	%Prev	%95CI	%Prev	%95CI	%Prev	%95CI
Switzerland	301	1.0	0.1 2.4	0.0	0.0 1.2	0.0	0.0 1.2	0.0	0.0 1.2	0.0	0.0 1.2

ESBL: extended-spectrum beta-lactamase; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): All isolates showing clavulanate synergy with cefotaxime or ceftazidime or synergy with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(c): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(d): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(e): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(f): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns.

(a)

(b)

Figure 66: Prevalence of presumptive ESBL- (a) and AmpC- (b) producing *E. coli* isolates from meat from pigs collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing or molecular typing confirmation in 2015

3.5.4.2. Specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in meat from bovine animals

In the case of meat from bovine animals, 24 MSs and 2 two non-MSs (Norway and Switzerland) reported data on specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in meat from bovine animals. Tables ESCHEBOVMEATESBL, ESCHEBOVMEATESBL2). Italy reported only results from molecular analyses (Table 51).

Twenty-three MSs tested 5,329 retail meat samples and following culture on selective media, 5.0% yielded presumptive ESBL-producing *E. coli*, while 1.8% yielded presumptive AmpC-producing *E. coli* and 0.3% yielded *E. coli* with an ESBL+AmpC phenotype (Table 52).

Italy tested 304 samples. Among the 5 isolates recovered from these samples 13 were positive for ESBL-encoding genes (different CTX-M-genes, mainly encoding for CTX-M-1) and two for CMY-2 AmpC-genes. The total prevalence found was 4.3% of *E. coli* isolates with an ESBL-phenotype and 0.7% with an AmpC-phenotype.

In most but not all countries, the detection of ESBL *E. coli* exceeded that of AmpC *E. coli* – Cyprus, Estonia, Greece and Slovakia – and the figures for all reporting countries were remarkably similar to those obtained for meat from pigs. South-eastern, south central and southern-western MSs tended to report higher prevalence of ESBL-/AmpC-producing *E. coli* than the Nordic countries and, to a lesser extent, than MSs from western Europe (Figure 67).

Table 51: Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from bovine animals collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

Country	Total number of *E. coli* tested[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
		N	%[h]	N	%[h]	n	%[h]	n	%[h]	N	%[h]
Austria	7	7	100	1	14.3	0	0	0	0	0	0
Belgium[i]	9	7	77.8	4	44.4	0	0	2	22.2	0	0
Bulgaria	13	9	69.2	4	30.8	0	0	6	46.2	2	15.4
Croatia	4	4	100	3	75.0	0	0	0	0	0	0
Cyprus[j]	10	3	30.0	0	0	0	0	8	80.0	1	10.0
Czech Republic[j]	40	27	67.5	15	37.5	0	0	14	35.0	1	2.5
Denmark	8	8	100	3	37.5	0	0	0	0	0	0
Estonia	3	1	33.3	0	0	0	0	2	66.7	0	0
Finland[k]	0	–	–	–	–	–	–	–	–	–	–
France	1	1	100	1	100	0	0	0	0	0	0
Germany[j]	15	14	93.3	5	33.3	0	0	2	13.3	1	6.7
Greece	3	1	33.3	0	0	0	0	2	66.7	0	0
Hungary	24	23	95.8	9	37.5	0	0	2	8.3	1	4.2
Latvia	9	7	77.8	3	33.3	0	0	2	22.2	0	0
Lithuania	11	10	90.9	6	54.5	0	0	1	9.1	0	0
Netherlands	1	0	0	0	0	0	0	1	100	0	0
Portugal	12	11	91.7	6	50.0	0	0	1	8.3	0	0
Romania	4	4	100	2	50.0	0	0	1	25.0	1	25
Slovakia	5	0	0	0	0	0	0	3	60.0	0	0
Slovenia	2	1	50.0	0	0	0	0	1	50.0	0	0
Spain	26	20	76.9	5	19.2	0	0	8	30.8	2	7.7
Sweden[k]	0	–	–	–	–	–	–	–	–	–	–
United Kingdom	2	1	50	1	50.0	0	0	1	50.0	0	0
Total (23 MSs)	**209**	**159**	**76.1**	**68**	**32.7**	**0**	**0**	**57**	**27.3**	**9**	**4.3**

Country	Total number of E. coli tested[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
		N	%[h]	N	%[h]	n	%[h]	n	%[h]	N	%[h]
Norway	3	2	66.7	1	33.3	0	0	1	33.3	0	0
Switzerland	1	0	0	0	0	0	0	0	0	0	0

ESBL.: extended-spectrum beta-lactamase; n= isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): For some MSs, it includes isolates microbiologically resistant to cefotaxime and ceftazidime but with MIC ≤ 1 mg/L for both antimicrobials, suggesting the presence of other mechanisms (as stated above, were not further classified).

(c): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(d): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(e): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(f): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(g): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns.
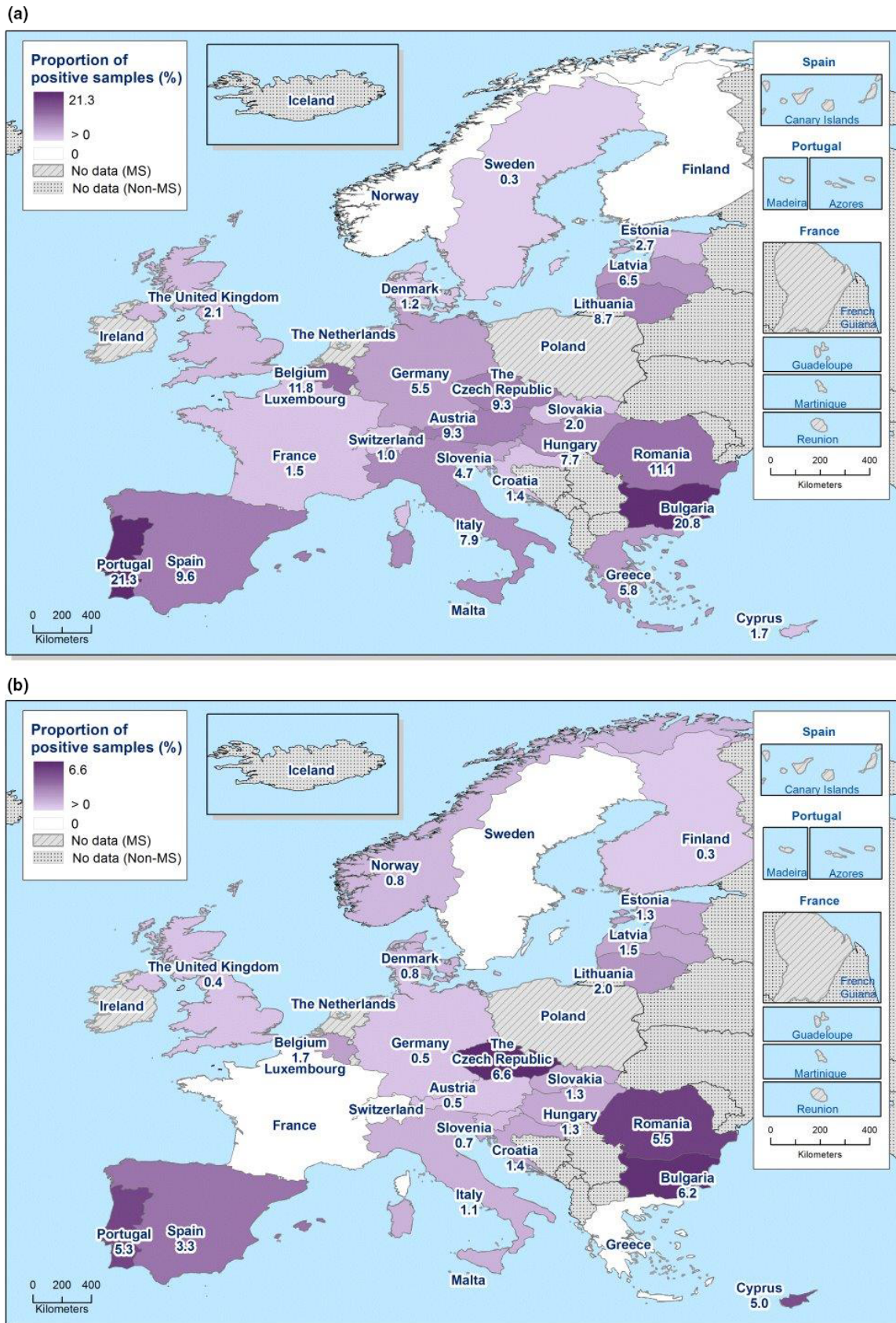
(h): Percentage of the total number of E. coli isolates tested with panel 2.

(i): Molecular data were reported by Belgium. At least two isolates were confirmed as positive for CTX-M-1 ESBL-encoding genes.

(j): Some of these isolates were reported as microbiologically resistant to carbapenems (Belgium, 1 isolate resistant to meropenem, ertapenem and imipenem but not confirmed as carbapenemase-producer; Czech Republic, Lithuania and Spain, with 1, 1, and 3 isolates resistant to ertapenem, and 1 isolate from Portugal resistant to imipenem).

(k): Finland and Sweden investigated 300 and 289 samples, respectively. None tested positive.

Table 52: Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from bovine animals collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

In the table below, each category shows its %Prev(g) and its 95% confidence interval (%95CI) as a lower–upper range.

Country	Total number of samples tested	ESBL[b] %Prev(g)	ESBL[b] %95CI	ESBL with clavulanic-SYN only for CTX[c] %Prev(g)	CTX[c] %95CI	ESBL with clavulanic-SYN only for CAZ[d] %Prev(g)	CAZ[d] %95CI	AmpC[e] %Prev(g)	AmpC[e] %95CI	AmpC + ESBL[f] %Prev(g)	AmpC + ESBL[f] %95CI
Austria	234	3	1.2–6.1	0.4	0–2.4	0	0–1.6	0	0–1.6	0	0–1.6
Belgium	91	11.1	3.1–15.2	6.3	1.2–10.9	0	0–4	3.2	0.3–7.7	0	0–4
Bulgaria	461	17.3	0.9–3.7	7.7	0.2–2.2	0	0–0.8	11.5	0.5–2.8	3.8	0.1–1.6
Croatia	150	2.7	0.7–6.7	2	0.4–5.7	0	0–2.4	0	0–2.4	0	0–2.4
Cyprus	122	2.5	0.5–7	0	0–3	0	0–3	6.6	2.9–12.5	0.8	0–4.5
Czech Republic	290	9.3	6.2–13.3	5.2	2.9–8.4	0	0–1.3	4.8	2.7–8	0.3	0–1.9
Denmark	315	2.5	1.1–4.9	1	0.2–2.8	0	0–1.2	0	0–1.2	0	0–1.2
Estonia	150	0.7	0–3.7	0	0–2.4	0	0–2.4	1.3	0.2–4.7	0	0–2.4
Finland[h]	300	–	0–1.2	–	0–1.2	–	0–1.2	–	0–1.2	–	0–1.2
France	264	0.4	0–2.1	0.4	0–2.1	0	0–1.4	0	0–1.4	0	0–1.4
Germany	452	3.7	1.7–5.1	1.3	0.4–2.6	0	0–0.8	0.5	0.1–1.6	0.3	0–1.2
Greece	69	1.4	0–7.8	0	0–5.2	0	0–5.2	2.9	0.4–10.1	0	0–5.2
Hungary	268	8.6	5.5–12.6	3.4	1.5–6.3	0	0–1.4	0.7	0.1–2.7	0.4	0–2.1
Latvia	150	6.2	1.9–9.4	2.7	0.4–5.7	0	0–2.4	1.8	0.2–4.7	0	0–2.4
Lithuania	150	7.3	3.2–11.9	4.4	1.5–8.5	0	0–2.4	0.7	0–3.7	0	0–2.4
Netherlands	289	0	0–1.3	0	0–1.3	0	0–1.3	1	0–1.9	0	0–1.3
Portugal	150	7.3	3.7–12.7	4	1.5–8.5	0	0–2.4	0.7	0–3.7	0	0–2.4
Romania	224	12.5	0.5–4.5	6.3	0.1–3.2	0	0–1.6	3.1	0–2.5	3.1	0–2.5
Slovakia	150	0	0–2.4	0	0–2.4	0	0–2.4	2	0.4–5.7	0	0–2.4
Slovenia	150	0.7	0–3.7	0	0–2.4	0	0–2.4	0.7	0–3.7	0	0–2.4
Spain	299	6.9	4.1–10.1	1.7	0.5–3.9	0	0–1.2	2.8	1.2–5.2	0.7	0.1–2.4
Sweden[h]	289	–	0–1.3	–	0–1.3	–	0–1.3	–	0–1.3	–	0–1.3
United Kingdom	312	1	0–1.8	1	0–1.8	0	0–1.2	1	0–1.8	0	0–1.2
Total (23 MSs)	**5,329**	**5.0**	**4.4–5.6**	**2.1**	**1.7–2.5**	**0**	**0–0.1**	**1.8**	**1.5–2.2**	**0.3**	**0.17–0.49**
Norway	244	0.8	0.1–2.9	0.4	0–2.3	0	0–1.5	0.4	0–2.3	0	0–1.5

Country	Total number of samples tested	ESBL[b]		ESBL with clavulanic-SYN only for CTX[c]		ESBL with clavulanic-SYN only for CAZ[d]		AmpC[e]		AmpC + ESBL[f]	
		%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI
Switzerland	298	0	0 1.2	0	0 1.2	0	0 1.2	0	0 1.2	0	0 1.2

ESBL.: extended-spectrum beta-lactamase; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.
(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).
(b): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).
(c): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.
(d): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.
(e): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).
(f): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns.
(g): Percentage of the total number of *E. coli* isolates tested (with panel 2).
(h): Finland and Sweden investigated 300 and 289 samples, respectively. None tested positive.

(a)

(b)
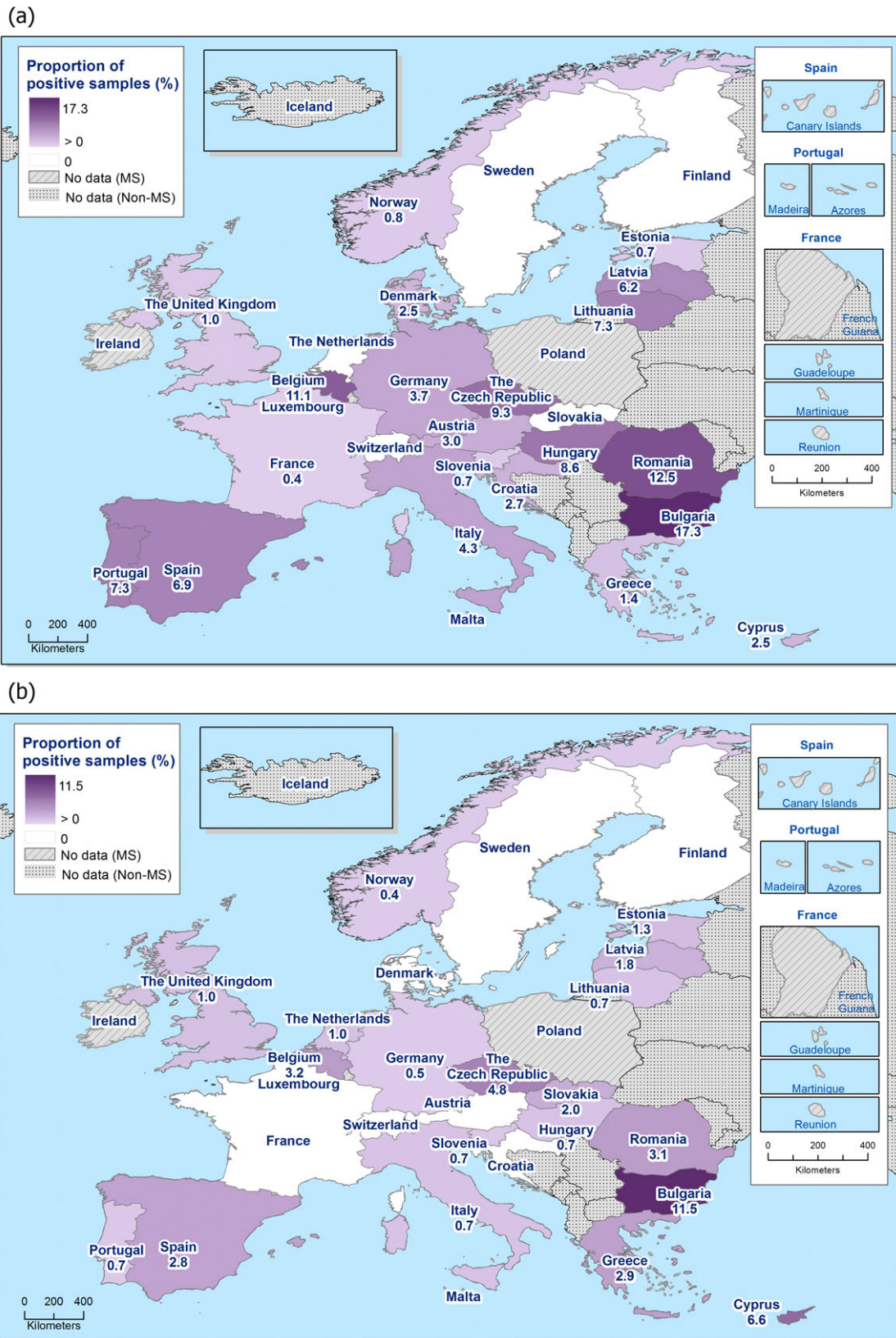
Figure 67: Prevalence of presumptive ESBL- (a)/AmpC- (b) producing *E. coli* isolates from meat from bovine animals collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing in 2015

3.5.4.3. Specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in fattening pigs

Data on specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in fattening pigs were reported by 28 MSs two non-MSs (Norway and Switzerland). (Tables ESCHEPIGESBL, ESCHEPIGDESBL2) Italy reported only results from molecular analyses (Table 53).

In fattening pigs, 6,167 caecal samples were tested by the 27 MSs and following selective culture, 31.9% of samples yielded presumptive ESBL-producing *E. coli* while 9.7% yielded presumptive AmpC-producing *E. coli* and 1.5% yielded *E. coli* with an ESBL + AmpC phenotype (Table 54). The prevalence of presumptive ESBL-producing *E. coli* varied widely between reporting countries, occurring on from 1% to 81.5% of pig caecal samples examined. Presumptive ceftazidimase-producing *E. coli* were much less prevalent than the presumptive cefotaximase-producing *E. coli*, being detected at low levels in less than one-third of the reporting MSs.

Italy tested 306 samples. Among the 214 isolates recovered from these samples 195 tested positive for ESBL-encoding genes (189 isolates were positive for different CTX-M, mainly CTX-M-1 and 6 for SHV-12 encoding genes), 17 for CMY-2 AmpC-genes, and one isolate with both a CTX-M and an ACC- AmpC-genes. The total prevalence found was 64% of *E. coli* isolates with an ESBL-phenotype, and 5.9% with an AmpC-phenotype.

ESBL phenotype *E. coli* exceeded AmpC phenotype *E. coli* in all reporting countries except for Denmark, Finland, Ireland, Slovakia and Sweden. Southern MSs tended to report higher prevalence of ESBL-producing *E. coli* than those from Northern Europe and, to a lesser extent, than MSs from Central and Western Europe. The distribution of the prevalence of AmpC-producing *E. coli* in fattening pigs is less contrasted than that of ESBL-producing *E. coli* and countries from Northern Europe recorded some of the highest prevalence observed (Figure 68).

A carbapenemase-producing *E. coli* isolated from fattening pigs in Germany

One isolate reported by Germany showed a carbapenemase-producer phenotype (meropenem resistance, but also ertapenem and imipenem). The presence of carbapenemase-encoding genes in this isolate was confirmed by the MS and reported to EFSA.

Table 53: Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from fattening pigs collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

Country	Total number of *E. coli* tested[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
		n	%[h]	n	%[h]	n	%[h]	n	%[h]	n	%[h]
Austria	134	124	92.5	63	47	0	0	12	9	2	1.5
Belgium[i]	174	164	94.3	66	37.9	1	0.6	11	6.3	1	0.6
Bulgaria	72	61	84.7	0	0	0	0	13	18.1	2	2.8
Croatia[i]	34	16	47.1	7	20.6	1	2.9	16	47.1	0	0
Cyprus	14	10	71.4	5	35.7	0	0	3	21.4	3	21.4
Czech Republic[i]	93	65	69.9	44	47.3	0	0	34	36.6	6	6.5
Denmark	78	19	24.4	13	16.7	0	0	58	74.4	0	0
Estonia	33	26	78.8	0	0	0	0	7	21.2	1	3
Finland	9	1	11.1	0	0	0	0	8	88.9	0	0
France[i]	107	97	90.7	27	25.2	0	0	10	9.3	0	0
Germany[i]	155	132	85.2	43	27.7	2	1.3	29	18.7	6	3.9
Greece	38	38	100	7	18.4	0	0	0	0	0	0
Hungary	177	134	75.7	64	36.2	3	1.7	56	31.6	13	7.3
Ireland[i]	44	15	34.1	6	13.6	0	0	28	63.6	1	2.3
Latvia	73	60	82.2	20	27.4	0	0	16	21.9	3	4.1
Lithuania	27	27	100	13	48.1	0	0	0	0	0	0
Luxembourg	22	18	81.8	7	31.8	0	0	4	18.2	0	0
Malta	68	0	–	0	–	0	–	0	–	0	–
Netherlands	56	31	55.4	12	21.4	0	0	25	44.6	0	0
Poland[i]	112	78	69.6	26	23.2	1	0.9	32	28.6	3	2.7
Portugal[i]	197	180	91.4	57	28.9	0	0	36	18.3	19	9.6
Romania[i]	223	186	83.4	72	32.3	6	2.7	46	20.6	10	4.5
Slovakia[i]	59	12	20.3	5	8.5	0	0	48	81.4	2	3.4
Slovenia	44	43	97.7	20	45.5	0	0	2	4.5	1	2.3
Spain[i]	281	264	94	87	31	1	0.4	27	9.6	10	3.6
Sweden[i]	35	3	8.6	0	0	0	0	27	77.1	0	0
United Kingdom[i]	82	65	79.3	32	39	1	1.2	21	25.6	4	4.9

Country	Total number of E. coli tested[b]	ESBL[c]		ESBL with clavulanic-SYN only for CTX[d]		ESBL with clavulanic-SYN only for CAZ[e]		AmpC[f]		AmpC + ESBL[g]	
		n	%[h]	n	%[h]	n	%[h]	n	%[h]	n	%[h]
Total (27 MSs)	**2,441**	**1,869**	**76.6**	**696**	**28.5**	**16**	**0.66**	**569**	**23.3**	**87**	**3.6**
Norway[i]	29	1	3.4	0	0	0	0	29	100	1	3.4
Switzerland	77	51	66.2	20	26	2	2.6	19	24.7	1	1.3

ESBL: extended-spectrum beta-lactamase; n= isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): For some MSs, it includes isolates microbiologically resistant to cefotaxime and ceftazidime but with MIC ≤ 1 mg/L for both antimicrobials, suggesting the presence of other mechanisms (not further classified).

(c): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(d): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(e): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(f): Isolates with microbiological resistance to cefoxitin (MIC ≥ 8 mg/L), suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(g): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns.

(h): Percentage of the total number of E. coli isolates tested (with panel 2).

(i): Some of these isolates were reported as microbiologically resistant to carbapenems (resistance to ertapenem: 1 Croatia, 2 Czech Republic, 1 France, 2 Ireland, 2 Poland, 1 Portugal, 4 Romania, 4 Slovakia, 6 Spain, 2 United Kingdom; Belgium, 5 isolate resistant to ertapenem and 1 to imipenem; Norway, 2 resistant to ertapenem and 1 resistant to imipenem; Germany, 1 isolate resistant o meropenem, ertapenem and imipenem and confirmed as carbapenemase-producer by this MSs).

(j): Molecular data were reported by Sweden. Four of the isolates were positive for CTX-M-55 (2 isolates) or CTX-M-15 (UOE-1, 1 isolate) ESBL-encoding genes, or CMY-2 AmpC-encoding genes (only found in one isolate the ones with AmpC-phenotype).

Table 54: Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from fattening pigs collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

Country	Total number of samples tested	ESBL[b]		ESBL with clavulanic-SYN only for CTX[c]		ESBL with clavulanic-SYN only for CAZ[d]		AmpC[e]		AmpC + ESBL[f]	
		%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI
Austria	257	48.2	42–54.5	24.5	19.4–30.2	0	0–1.4	4.7	2.4–8	0.8	0.1–2.8
Belgium	300	54.7	48.8–60.4	22	17.4–27.1	0.3	0–1.8	3.7	1.8–6.5	0.3	0–1.8
Bulgaria	160	38.1	30.6–46.1	0	0–2.3	0	0–2.3	10.6	4.4–13.5	1.6	0.2–4.4
Croatia	91	17.6	10.4–27	7.7	3.1–15.2	1.1	0–6	17.6	10.4–27	0	0–4
Cyprus	147	6.8	3.3–12.2	3.4	1.1–7.8	0	0–2.5	2.0	0.4–5.8	2.0	0.4–5.8
Czech Republic	302	21.5	17.0–26.6	14.6	10.8–19.1	0	0–1.2	11.3	7.9–15.4	2.0	0.7–4.3
Denmark	273	7	4.2–10.7	4.8	2.6–8	0	0–1.3	21.3	16.5–26.6	0	0–1.3
Estonia	87	29.9	20.5–40.6	0	0–4.2	0	0–4.2	8	3.3–15.9	1.1	0–6.2
Finland	306	0.3	0–1.8	0	0–1.2	0	0–1.2	2.6	1.1–5.1	0	0–1.2
France	298	34.7	27.3–38.2	9.6	6.1–12.9	0	0–1.2	3.6	1.6–6.1	0	0–1.2
Germany	352	39.5	32.4–42.8	12.8	9–16.1	0.6	0.1–2	8.7	5.6–11.6	1.8	0.6–3.7
Greece	116	32.8	24.3–42.1	6	2.5–12	0	0–3.1	0	0–3.1	0	0–3.1
Hungary	300	44.7	39–50.5	21.4	16.8–26.4	1	0.2–2.9	18.6	14.4–23.5	4.3	2.3–7.3
Ireland	145	10.3	5.9–16.5	4.1	1.5–8.8	0	0–2.5	19.3	13.2–26.7	0.7	0–3.8
Latvia	150	40	32.1–48.3	13.3	8.3–19.8	0	0–2.4	10.7	6.2–16.7	2	0.4–5.7
Lithuania	151	17.9	12.1–24.9	8.6	4.7–14.3	0	0–2.4	0	0–2.4	0	0–2.4
Luxembourg	161	11.9	6.8–17.1	4.3	1.8–8.8	0	0–2.3	2.5	0.7–6.2	0	0–2.3
Malta	68	–	0–5.3	–	0–5.3	–	0–5.3	–	0–5.3	–	0–5.3
Netherlands	300	10.3	7.1–14.3	4	2.1–6.9	0	0–1.2	8.3	5.5–12.1	0	0–1.2
Poland	299	26.8	21.2–31.5	8.9	5.8–12.5	0.3	0–1.8	10.7	7.4–14.8	1.0	0.2–2.9
Portugal	296	65.2	55–66.4	20.6	14.9–24.2	0	0–1.2	13	8.7–16.4	6.8	3.9–9.8
Romania	399	46.6	41.6–51.6	18.1	14.4–22.2	1.5	0.6–3.2	11.5	8.6–15.1	2.5	1.2–4.6
Slovakia	131	9.1	4.8–15.5	3.8	1.3–8.7	0	0–2.8	36.7	28.4–45.5	1.5	0.2–5.4
Slovenia	151	28.5	21.4–36.4	13.3	8.3–19.7	0	0–2.4	1.3	0.2–4.7	0.7	0–3.6
Spain	324	81.5	76.8–85.6	26.9	22.1–32	0.3	0–1.7	8.3	5.6–11.9	3.1	1.5–5.6
Sweden	303	1	0.2–2.9	0	0–1.2	0	0–1.2	8.9	6–12.7	0	0–1.2

Country	Total number of samples tested	ESBL[b] %Prev[g]	ESBL[b] %95CI	ESBL with clavulanic-SYN only for CTX[c] %Prev[g]	ESBL with clavulanic-SYN only for CTX[c] %95CI	ESBL with clavulanic-SYN only for CAZ[d] %Prev[g]	ESBL with clavulanic-SYN only for CAZ[d] %95CI	AmpC[e] %Prev[g]	AmpC[e] %95CI	AmpC + ESBL[f] %Prev[g]	AmpC + ESBL[f] %95CI
United Kingdom	300	21.7	17.1 – 26.8	10.7	7.4 – 14.7	0.3	0 – 1.8	7	4.4 – 10.5	1.3	0.4 – 3.4
Total (27 MSs)	**6,167**	**31.9**	**29.2 – 33.1**	**11.9**	**10.5 – 12.1**	**0.3**	**0.1 – 0.4**	**9.7**	**8.5 – 10**	**1.5**	**1.1 – 1.7**
Norway	258	0.4	0 – 2.1	0	0 – 1.4	0	0 – 1.4	11.2	7.7 – 15.7	0.4	0 – 2.1
Switzerland	300	17	12.9 – 21.7	6.7	4.1 – 10.1	0.7	0.1 – 2.4	6.3	3.9 – 9.7	0.3	0 – 1.8

ESBL.: extended-spectrum beta-lactamase; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).
(b): All isolates showing clavulanate synergy with cefotaxime or ceftazidime or ceftazidime or synergy with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).
(c): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.
(d): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.
(e): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).
(f): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns
(g): Percentage of the total number of *E. coli* isolates tested (with panel 2).

Figure 68: Prevalence of presumptive ESBL- (a) and AmpC- (b) producing *E. coli* isolates from fattening pigs collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing in 2015

3.5.4.4. Specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in calves under one year of age

Data on specific ESBL-/AmpC-/carbapenemase-producing *E. coli* monitoring in calves under one year of age were reported by 10 MSs and 2 non-MSs (Norway and Switzerland) (Tables ESCHECALVESBL, ESCHECALVESBL2). Italy reported only results from molecular analyses. Only MSs with a substantial production of veal calves should mandatorily perform the specific monitoring of ESBL-/AmpC-/carbapenemase-producing *E. coli* in this animal population (Table 55).

In calves of less than one year of age, nine MSs tested 2,343 caecal samples and following selective culture, 36.8% of samples yielded presumptive ESBL-producing *E. coli*, while 4.8% yielded presumptive AmpC-producing *E. coli* and 2.0% yielded *E. coli* with an ESBL + AmpC phenotype. ESBL *E. coli* exceeded AmpC *E. coli* in all reporting countries except for Denmark, Norway and Sweden. The prevalence of presumptive ESBL-producing *E. coli* varied widely between reporting countries, occurring on from 0% to 60% of bovine caecal samples examined. Only one reporting country detected presumptive ceftazidimase-producing *E. coli* at low level (Table 56).

Italy tested 223 samples. All 179 isolates recovered from these samples tested positive for ESBL-encoding genes (173 isolates were positive for different CTX-M, mainly CTX-M-1 and CTX-M-15, and 6 for SHV-12 encoding genes), 17 tested positive for CMY-2 AmpC-genes, and one isolate with both a CTX-M and an ACC- AmpC-genes. The total prevalence found was 64% of *E. coli* isolates with an ESBL-phenotype, and 5.9% with an AmpC-phenotype.

Northern countries and, to a lesser extent, the Netherlands recorded lower prevalence of ESBL-producing *E. coli* than the other reporting countries. The range of variation of the prevalence of AmpC-producing *E. coli* observed is less important but a similar geographical pattern is observed (Figure 69).

Table 55: Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from calves of less than one year of age collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[(a)]

Country	Total number of *E. coli* tested[(b)]	ESBL[(c)]		ESBL with clavulanic-SYN only for CTX[(d)]		ESBL with clavulanic-SYN only for CAZ[(e)]		AmpC[(f)]		AmpC + ESBL[(g)]	
		N	%[(h)]	n	%[(h)]	n	%[(h)]	n	%[(h)]	n	%[(h)]
Belgium	188	180	95.7	46	24.5	2	1.1	17	9	10	5.3
Croatia	11	7	63.6	4	36.4	0	0	4	36.4	0	0
Denmark	14	6	42.9	3	21.4	0	0	7	50	0	0
France[(i)]	147	135	91.8	51	34.7	0	0	24	16.3	12	8.2
Germany[(i)]	210	199	94.8	31	14.8	0	0	19	9	8	3.8
Netherlands[(i)]	43	41	95.3	12	27.9	0	0	6	14	4	9.3
Portugal	132	122	92.4	16	12.1	0	0	17	12.9	7	5.3
Spain[(i)]	148	140	94.6	33	22.3	0	0	13	8.8	5	3.4
Sweden	2	0	0	0	0	0	0	1	50	0	0
Total (9 MSs)	**895**	**830**	**92.7**	**196**	**21.9**	**2**	**0.223**	**108**	**12.1**	**46**	**5.14**
Norway	1	0	0	0	0	0	0	1	100	0	0
Switzerland	112	76	67.9	19	17	1	0.9	37	33	4	3.6

ESBL: extended-spectrum beta-lactamase; n= isolates with this phenotype; %: percentage of isolates with this phenotype from the total tested; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): For some MSs, it include isolates microbiologically resistant to cefotaxime and ceftazidime but with MIC ≤ 1 mg/L for both antimicrobials, suggesting the presence of other mechanisms (as stated above, were not further classified).

(c): All isolates showing clavulanate synergy with cefotaxime, ceftazidime or both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(d): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(e): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(f): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(g): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns.

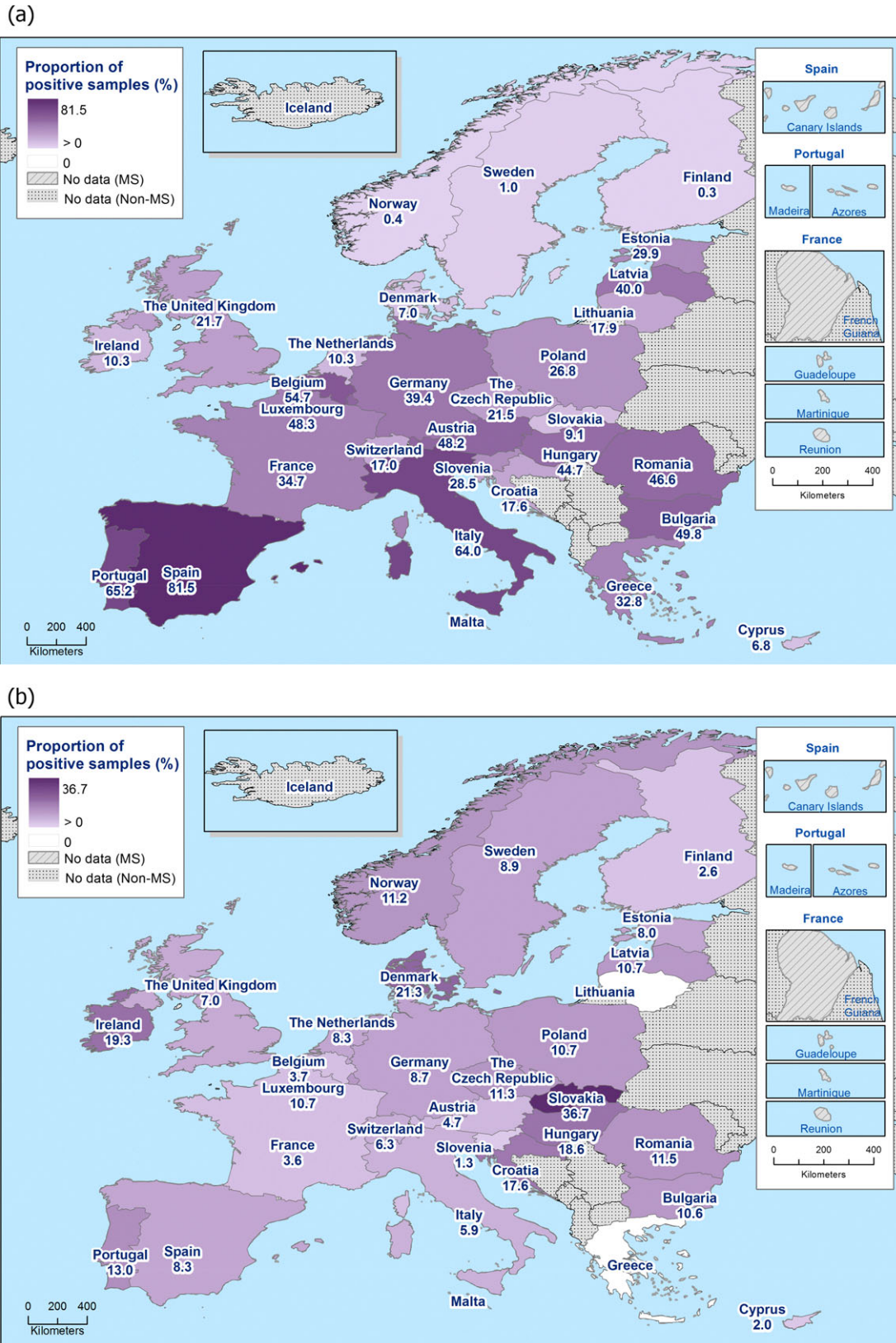(h): Percentage of the total number of *E. coli* isolates tested (with panel 2).

(i): Some of these isolates were reported as microbiologically resistant to carbapenems (ertapenem resistance: 4 France, 5 Germany; imipenem resistance: 1 the Netherlands; Spain, 4 ertapenem- and 1 imipenem-resistant isolates).

Table 56: Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from calves of less than one year of age collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015[a]

Country	Total number of samples tested	ESBL[b]		ESBL with clavulanic-SYN only for CTX[c]		ESBL with clavulanic-SYN only for CAZ[d]		AmpC[e]		AmpC + ESBL[f]	
		%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI	%Prev[g]	%95CI
Belgium	300	60	54.2 65.6	15.4	11.4 19.9	0.7	0.1 2.4	5.6	3.3 8.9	3.3	1.6 6
Croatia	89	7.9	3.2 15.5	4.5	1.2 11.1	0	0 4.1	4.5	1.2 11.1	0	0 4.1
Denmark	299	3	0.7 4.3	1.5	0.2 2.9	0	0 1.2	3.5	0.9 4.8	0	0 1.2
France	306	46.2	38.5 49.9	17.5	12.7 21.3	0	0 1.2	8.2	5.1 11.4	4.1	2 6.7
Germany	363	57.5	49.5 60	9	5.9 11.9	0	0 1	5.5	3.2 8.1	2.3	1 4.3
Netherlands	300	13.7	10 18.1	4	2.1 6.9	0	0 1.2	2	0.7 4.3	1.3	0.4 3.4
Portugal	292	43.7	36.1 47.7	5.7	3.2 8.7	0	0 1.3	6.1	3.4 9.2	2.5	1 4.9
Spain	318	45.2	38.5 49.7	10.7	7.3 14.3	0	0 1.2	4.2	2.2 6.9	1.6	0.5 3.6
Sweden	76	0	0 4.7	0	0 4.7	0	0 4.7	1.3	0 7.1	0	0 4.7
Total (9 MSs)	**2,343**	**36.8**	**33.5 37.4**	**8.7**	**7.3 9.6**	**0.1**	**0 0.3**	**4.8**	**3.8 5.5**	**2.0**	**1.4 2.6**
Norway	264	0	0 1.4	0	0 1.4	0	0 1.4	0.4	0 2.1	0	0 1.4
Switzerland	298	25.5	20.7 30.8	6.4	3.9 9.8	0.3	0 1.9	12.4	8.9 16.7	1.4	0.4 3.4

ESBL.: extended-spectrum beta-lactamase; SYN: synergy; CTX: cefotaxime; CAZ: ceftazidime; MSs: Member States.

(a): According to EUCAST Guidelines (EUCAST, 2013), only isolates showing an MIC > 1 mg/L for cefotaxime and/or ceftazidime (screening breakpoint) were considered (see chapter 1.2.5).

(b): All isolates showing clavulanate synergy with cefotaxime or ceftazidime or synergy with both compounds, suggesting the presence of an ESBL (independently of the presence of other mechanisms).

(c): Isolates showing synergy with cefotaxime only, suggesting the presence of an ESBL with cefotaximase activity.

(d): Isolates showing synergy with ceftazidime only, suggesting the presence of an ESBL with ceftazidimase activity.

(e): Isolates with microbiological resistance to cefoxitin, suggesting the presence of an AmpC-enzyme (independently of the presence of other mechanisms).

(f): Isolates showing synergy with cefotaxime or ceftazidime and with microbiological resistance to cefoxitin, suggesting the presence of ESBL and AmpC-enzymes in the same isolate. These isolates are also included in the ESBL and AmpC columns

(g): Percentage of the total number of *E. coli* isolates tested (with panel 2).
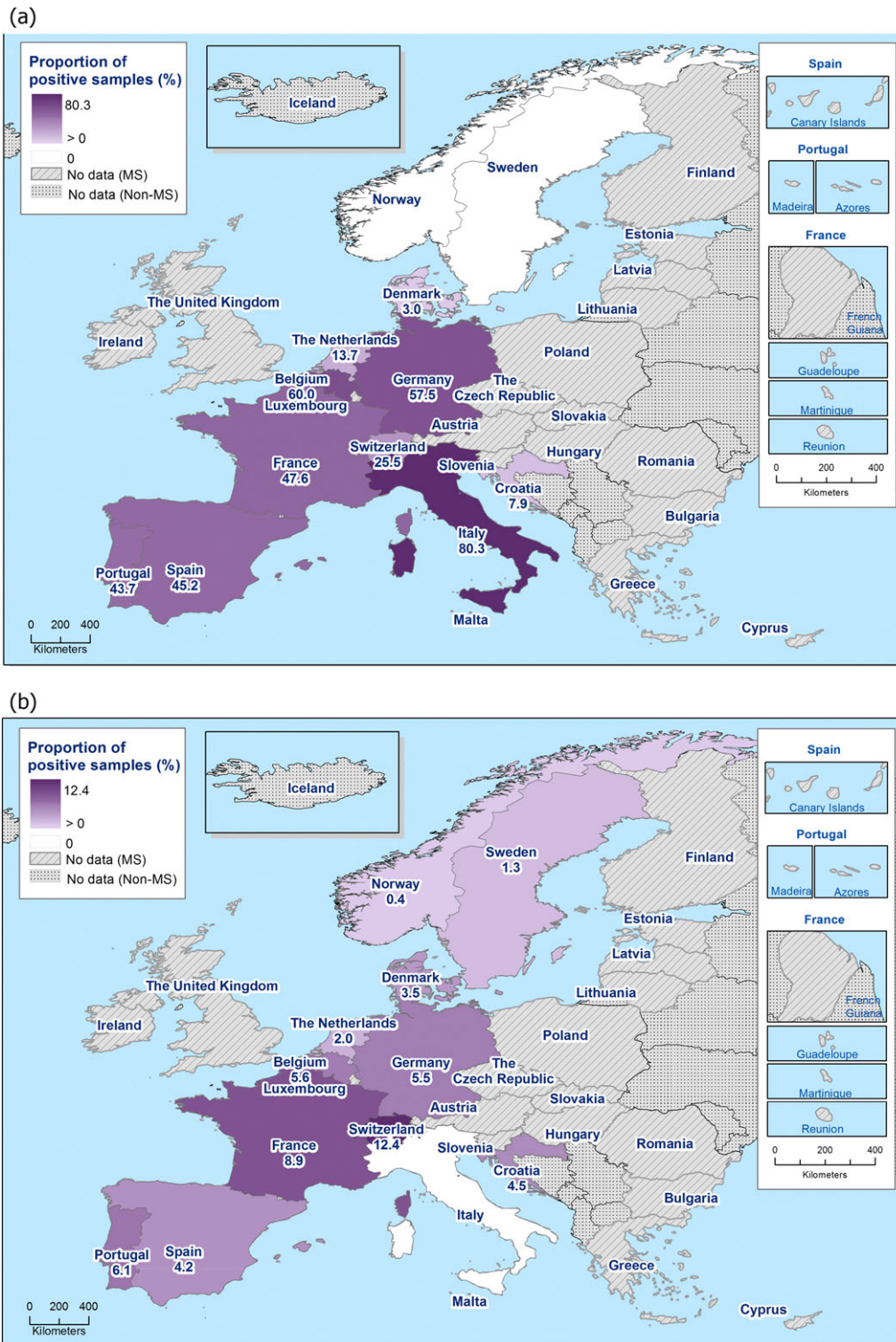
(a)

(b)

Figure 69: Prevalence of presumptive ESBL- (a) and AmpC- (b) producing *E. coli* isolates from calves of less than one year of age collected within the specific ESBL-/AmpC-/carbapenemase-producing monitoring and subjected to supplementary testing or molecular typing confirmation in 2015

3.5.5. Specific monitoring of carbapenemase-producing *E. coli* in 2015

The specific monitoring of carbapenemase-producing microorganisms was performed and reported by a number of MSs on a voluntary basis in 2015, in accordance with the Commission Implementing Decision 2013/652/EU (Table 57). All these MSs focused on the isolation of *E. coli.* Eight MSs (Table 57) reported results from the investigation of the presence of carbapenemase-producing *E. coli* in meat from pigs (1,833 samples analysed) and fattening pigs (2,584 samples). These MSs also investigated meat from bovine animals (1,818 samples), yielding the same result. Only three countries reported data on the specific monitoring of bovine animals (682 samples) and two countries reported data on the specific monitoring of calves under one year of age (516 samples). None carbapenemase-producing *E. coli* isolate was identified among these samples.

Table 57: Prevalence of carbapenemase-producing *E. coli* from fattening pigs and calves under one year of age and meat thereof collected within the specific carbapenemase-producing monitoring in 2015

Country	Number of samples tested on selective culture media	Number of samples tested positive for carbapenemase-producing *E. coli*	Prevalence (95%CI)		
Meat from pigs – fresh					
Austria	216	0	0.0	0	1.7
Czech Republic	302	0	0.0	0	1.2
Estonia	150	0	0.0	0	2.4
Finland	303	0	0.0	0	1.2
France	275	0	0.0	0	1.3
Portugal	151	0	0.0	0	2.4
Slovenia	150	0	0.0	0	2.4
Sweden	286	0	0.0	0	1.3
Total (8 MSs)	**1,833**	**0**	**0.0**	**0**	**0.2**
Meat from bovine animals – fresh					
Austria	226	0	0.0	0	1.6
Czech Republic	290	0	0.0	0	1.3
Estonia	150	0	0.0	0	2.4
Finland	300	0	0.0	0	1.2
France	264	0	0.0	0	1.4
Portugal	149	0	0.0	0	2.4
Slovenia	150	0	0.0	0	2.4
Sweden	289	0	0.0	0	1.3
Total (8 MSs)	**1,818**	**0**	**0.0**	**0**	**0.2**
Pigs – fattening pigs					
Austria	247	0	0.0	0	1.5
Czech Republic	302	0	0.0	0	1.2
Estonia	87	0	0.0	0	4.5
Finland	306	0	0.0	0	1.2
Netherlands	300	0	0.0	0	1.2
France	298	0	0.0	0	1.2
Portugal	296	0	0.0	0	1.2
Slovenia	151	0	0.0	0	2.4
Sweden	303	0	0.0	0	1.2
United Kingdom	294	0	0.0	0	1.2
Total (10 MSs)	**2,584**	**0**	**0.0**	**0**	**0.2**
Cattle (bovine animals)					
France	306	0	0.0	0	1.2
Netherlands	300	0	0.0	0	1.2
Sweden	76	0	0.0	0	4.7

Country	Number of samples tested on selective culture media	Number of samples tested positive for carbapenemase-producing *E. coli*	Prevalence (95%CI)		
Total (3 MSs)	**682**	**0**	**0.0**	**0**	**1.0**
Cattle (bovine animals) calves (under 1 year)					
Netherlands	300	0	0.0	0	1.2
Portugal	216	0	0.0	0	1.7
Total (2 MSs)	**516**	**0**	**0.0**	**0**	**1.0**

3.5.6. Discussion

Third-generation cephalosporins are antimicrobials of particular importance because they are frequently used as the first-line treatment in invasive Gram-negative infections, for example infections caused by *E. coli* or *Salmonella*. In 2015, as in the previous years, resistance to third-generation cephalosporins was generally detected at low levels in *Salmonella* and indicator *E. coli* isolates recovered from fattening pigs and calves under one year of age and meat thereof.

3.5.6.1. Third-generation cephalosporin and carbapenem resistance in *Salmonella* from humans (voluntary testing and reporting)

For the first time in this report, data on ESBL- and AmpC-producing *Salmonella* in humans are presented. Monitoring of these enzymes is voluntary for the public health reference laboratories, although ECDC recommends screening following a phenotypical testing algorithm based on the 'EUCAST guidelines for detection of resistance mechanisms and specific resistances of clinical and/or epidemiological importance' (EUCAST, 2013; ECDC, 2016). The 19 countries reporting microbiological resistance to both of the 3rd-generation cephalosporins included in the panel were therefore asked to provide results of additional testing, including synergy tests, if available. Of these, eight MSs had performed testing for presence of ESBL and AmpC. ESBL-producing *Salmonella* were identified in 0.5% of the isolates and in seven of eight MSs and encompassed 12 different serovars. *S.* Infantis with ESBL was detected in half of the MSs. ESBL-carrying monophasic *S.* Typhimurium 1,4,[5],12:i:- was identified in three of the eight MSs but their proportion was small in comparison to the total number of monophasic *S.* Typhimurium isolates. Two MSs reported a few ESBL-producing and one AmpC-producing *S.* Typhimurium. AmpC-producing *Salmonella* were overall reported from six of eight MSs at a lower proportion than ESBL-producers. Considering some of the serovars identified with ESBL and/or AmpC in humans (e.g. Kentucky and Stanley), other sources in addition to pork, e.g. poultry (ECDC and EFSA, 2016a) as well as a number of other types of food, are probably also contributing to the presence of such bacteria in humans. Further agreements within the ECDC Food- and Waterborne Diseases and Zoonoses network (FWD-Net) are required to increase the monitoring, and facilitate the reporting of ESBL-/AmpC- and carbapenemase-producing *Salmonella* in human isolates.

3.5.6.2. Third-generation cephalosporin resistance in indicator *E. coli* from food and animals (routine monitoring)

The routine AMR monitoring in commensal indicator *E. coli* was performed based on examining the phenotypic expression of a single randomly selected *E. coli* isolate from non-selective culture plates. This approach enables the assessment of the occurrence of randomly selected *E. coli* being resistant to cephalosporins and their categorisation as presumptive ESBL-/AmpC-/carbapenemase-producers. Although routine monitoring provides a lower degree of sensitivity – particularly where ESBL-producing *E. coli* constitutes a small proportion of the total *E. coli* flora – than that of specific monitoring based on selective media, it is primarily useful for consumer risk assessment, as *E. coli* is presumably transferred along the food chain in a random fashion (EFSA, 2012a).

The phenotypic findings indicate that ESBL-producing *E. coli* are commoner in indicator *E. coli* from fattening pigs and calves of less than one year than AmpC-producing *E. coli*. The ESBL-producing *E. coli* are predominantly both cefotaximases and ceftazidimases or cefotaximases and ceftazidimase activity alone is uncommon. These observations are of course likely to reflect genetic differences in the ESBL enzyme carried by the *E. coli* isolates and are in accord with many recent national studies, which have shown the predominance of the CTX-M family of enzymes conferring ESBL resistance in *E. coli* in food-producing animals. These enzymes are predominantly cefotaximases or both cefotaximases and ceftazidimases (Bonnet, 2004).

3.5.6.3. Third-generation cephalosporin resistance in *Salmonella* from humans, food and animals

The analysis of *Salmonella* serovars with similar characteristics detected in food, man and food-producing animals can assist in source attribution and epidemiological investigations, as well as suggesting areas for investigation at the molecular level, which may confirm that isolates are closely related.

In the monitoring performed in 2015, **S. Infantis** resistant to cefotaxime or ceftazidime was detected in humans in Austria, Italy, Slovenia, Spain and Norway, and where data were available, the ESBL enzymes CTX-M-2 and CTX-M-9 were reported. Considering the monitoring in animals and meat, a single isolate of *S*. Infantis was reported by the Czech Republic in meat from pigs which had both an 'ESBL + AmpC' phenotype. In total, 17 MSs reported results for *Salmonella* from pig meat. Italy recently reported the detection of third-generation cephalosporin resistance in *S*. Infantis in broilers and broiler meat, linked to possession of the ESBL enzyme CTX-M-1 (Franco et al., 2015); broilers will be monitored under the framework of the EU monitoring in 2016. Human cases of infection with *S*. Infantis exhibiting third-generation cephalosporin resistance have also been previously reported in France and Belgium, linked to poultry, which possessed the ESBL enzyme TEM-52 (Cloeckaert et al., 2007). *S.* Infantis is a serovar which is emerging worldwide (Hendriksen et al., 2011). The monitoring presented in this report as well as the published literature, therefore suggest a complex picture, with the acquisition of different ESBL genes in different *S.* Infantis isolates and subsequent clonal expansion.

Monophasic *S*. Typhimurium is currently the third most frequent serovar causing human infections in Europe, with 5,770 cases in 2015 (Chapter 3.1). 1,437 human isolates were reported, with 1.2% resistant to third-generation cephalosporins. While resistance was not detected in monophasic *S*. Typhimurium isolates from pig (N = 187) or bovine (N = 14) carcases, or from calves under one year of age (N = 7), it was observed in those from fattening pigs (N = 130), with a single isolate from Italy resistant to third-generation cephalosporins. From the monitoring reported of human monophasic *S*. Typhimurium cases, 6/1,043 isolates for which data were available had an ESBL phenotype and 1/1,043 had an AmpC phenotype (Table 1), with the enzymes SHV-12, CTX-M-9 and CMY-2 detected; the isolate from fattening pigs in Italy also possessed SHV-12 (Table 4). Thus, in the case of monophasic *S*. Typhimurium, the monitoring highlights detection of ESBL-producing isolates with common characteristics (the production of SHV-12) and indicates where further more detailed comparison of isolates may be useful. A number of reasons may account for the differences between the types of beta-lactamase enzyme encountered in monophasic *S*. Typhimurium isolates recovered from humans and those animal and meat types monitored in 2015, not least that other animal species, other food sources or sources outside Europe are responsible.

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

For the specific ESBL/AmpC/carbapenemase monitoring, culture methods using a non-selective enrichment and a selective medium containing a third-generation cephalosporin for the detection of ESBL-/AmpC-/carbapenemase-producing *E. coli* were used, as recommended by the EURL-AR. The selective medium contains 1 mg/L of cefotaxime, the screening breakpoint recommended by EUCAST to maximise sensitivity and specificity of the detection of AmpC- and ESBL-producing *E. coli*. The specific monitoring therefore employs culture of samples on selective media, which is able to detect very low numbers of resistant isolates present within a sample. The method enables the determination of the proportion of the total number of samples tested containing ESBL-/AmpC-/carbapenemases-producing *E. coli* even when low numbers of such resistant *E. coli* are present. The sensitivity to detect the producer *E. coli* by this approach is higher than that obtained when performing the routine monitoring in which *E. coli* are randomly selected from the total *E. coli* population present, especially when investigating populations with a low prevalence of ESBL-producing *E. coli*. The absolute sensitivity of the method has not however been determined. If large numbers of AmpC-producing *E. coli* are present in samples, they may obscure the concurrent presence of ESBL-producing *E. coli* in the same samples, because only one confirmed *E. coli* is subjected to further testing per sample. The proportion of AmpC-producing *vs*. ESBL-producing *E. coli* present within a sample can therefore influence the culture result obtained. Within this monitoring, carbapenemase-producing isolates resistant to third-generation cephalosporins could also be identified, although the probability to identify them similarly depends on the number of ESBL-/AmpC-producers which may concurrently be present in the sample. In addition, 'ESBL + AmpC' phenotype *E. coli* tended to occur as a low proportion of

cefotaxime-resistant *E. coli* and it is possible that this proportion is below the threshold of detection in countries where the prevalence of cefotaxime resistance is low.

In 2015, specific monitoring of ESBL-/AmpC-/carbapenemase-producing *E. coli* was performed on caecal contents from fattening pigs, calves under one year of age and fresh meat (retail) from these animals. This specific ESBL-/AmpC-/carbapenemase-producer monitoring was performed on a mandatory basis – Italy reported only results from molecular analyses. The important number of countries and the large total numbers of samples tested by MSs remove the uncertainty inherently associated with small sample sizes. Overall and in most but not all countries, the detection of presumptive ESBL-producing *E. coli* exceeded that of AmpC-producing *E. coli* in fattening pigs, calves and meat derived thereof. The prevalence of presumptive ESBL-producing *E. coli* in the animals tested varied widely between reporting countries, occurring on from 1% to 81.5% of pig caecal samples examined – one of the isolates presented a carbapenemase-producer phenotype (see below) – and on from 0% to 60% of bovine caecal samples examined. Prevalence figures observed for the two kinds of meat studied were generally lower than those observed in animals and remarkably similar in all reporting countries.

In both fattening pigs and calves under one year of age, ESBL-producing *E. coli* isolates which showed clavulanate synergy with both cefotaxime and ceftazidime or with cefotaxime only, greatly exceeded the proportion of isolates which showed clavulanate synergy with ceftazidime only. This suggests that cefotaximases greatly exceed ceftazidimases among the ESBL-producing *E. coli* which were detected in the specific monitoring in both fattening pigs and calves under one year of age. This finding is in accordance with the findings for randomly selected *E. coli* – the findings for both the routine monitoring and specific monitoring are very similar in this regard. The similarity of the findings from the non-selective and selective media points against the selective medium employed – which contains the EUCAST screening breakpoint concentration of cefotaxime – as preferentially detecting cefotaximases.

It is also of note that the Nordic countries are over-represented among those countries reporting AmpC phenotype *E. coli* exceeding ESBL phenotype *E. coli* in animals and the reason for this is unknown. The countries in which presumptive ESBL *E. coli* exceeded AmpC *E. coli* were also not the same when the results of specific monitoring for meat and animals producing that meat are considered and this may reflect variation inherent with low numbers of resistant isolates frequently recovered from meat, although other factors might also be important (for example, imported food, cross-contamination).

Overall, the specific monitoring highlighted that the occurrence of presumptive 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 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 after slaughter with *E. coli* from the digestive tract of pigs and calves under one year of age.

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 humans 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.

3.5.6.5. Carbapenemase-producing *E. coli* in 2015

The emergence and spread of microorganisms with acquired carbapenemases is of public health concern. Although the reports on carbapenemase-producing microorganisms isolated from food-producing animals and foods are still scarce, the numbers tend to be gradually increasing (EFSA BIOHAZ Panel, 2013; Guerra et al., 2014; Rubin et al., 2014; Abdallah et al., 2015; Zurfluh et al., 2015; Fischer et al., 2016; Irrgang et al., 2016b; Mollenkopf et al., 2017). Carbapenemase-producing *E. coli* and/or *Salmonella* have been isolated from poultry and pig farms (Fischer et al., 2016; Irrgang et al., 2016b). Following the adoption of EU Legislation (Decision 2013/652/EU), MSs implemented the

surveillance of carbapenem-resistance in both *Salmonella* and *E. coli:* carbapenems were included in the antimicrobial susceptibility testing. Specific monitoring of ESBL-/AmpC-/carbapenemase-producing *E. coli* became mandatory from 2015 onwards, with the voluntary option to perform specific monitoring focusing only on carbapenemase-producing microorganisms – mainly *E. coli.*

To increase the probability of detecting carbapenem-resistant microorganisms, it was recommended to perform the specific monitoring of carbapenemase-producing microorganisms (mainly *E. coli*, but with the option to report other enterobacteria such as *Salmonella*). Culture methods using a non-selective enrichment and selective media containing carbapenems for the detection of producer *E. coli* (protocol recommended by the EURL-AR) were recommended to be used. In this monitoring, which was performed on a voluntary basis, bacteria producing carbapenemases that do not confer resistance to cephalosporins (i.e. OXA-48) could also be identified. Some MSs also performed this voluntary selective culture to investigate the presence of carbapenemase-producing organisms in meat from pigs (8 MSs; 1,833 samples analysed), meat from bovine animals (8 MSs, 1,818 samples), fattening pigs (10 MSs, 2,584 samples), cattle (3 MSs, 682) or bovines under one year of age (2 MSs, 516 samples).

Regarding carbapenem non-susceptibility and detection of putative carbapenemase-producers within indicator *E. coli* and/or *Salmonella*, after validation of data (retesting of antimicrobial susceptibility and species identification by several MSs), none of the data reported for the isolates collected within the monitoring suggested the presence of carbapenemase-producers among these isolates, with the exception of single *E. coli* isolates from Belgium (retail pig meat) and Germany (fattening pigs). Ertapenem and/or imipenem resistance was however observed in some isolates with an ESBL or/and an AmpC phenotype and this could be related to the presence of another resistance mechanism which confers a degree of resistance to the carbapenem compounds (i.e. ESBL or AmpC production in conjunction with loss of porins).

Detection of a single carbapenemase-producing *E. coli* from pig meat

The routine monitoring data on indicator *E. coli* in meat from pigs (retail), performed and reported by Belgium on a voluntary basis, revealed the presence of an isolate with a presumptive carbapenemase-producer phenotype. The presence of carbapenemase-, ESBL-, and AmpC-encoding genes in this isolate, confirmed by whole genome sequence analyses, was communicated to EFSA by this MS. This is the first occasion that the presence of carbapenemase-producing isolates recovered within the harmonised, (in this case voluntary), routine monitoring programme of meat had been reported to EFSA.

Belgium confirmed the detection of carbapenemase-producing *E. coli* from pig meat sampled at retail under the framework of voluntary routine monitoring of indicator *E. coli* on non-selective culture media. The presence of a carbapenem-resistance gene together with an ESBL and an AmpC encoding genes provided subsequent definitive confirmation. Belgian colleagues report that this finding will be the subject of a scientific publication in due course.

The published findings will provide further detailed information. The potential sources of carbapenemase-producing bacteria present on meat include the animals from which the meat was derived, the environment in which the meat was produced, cross-contamination with other items during production, as well as those persons involved in handling and preparing the meat.

Among the isolates collected within the ESBL/AmpC/carbapenemase monitoring of isolates from **fattening pigs**, Germany also reported the presence of an isolate showing a carbapenemase-producer-phenotype. The presence of carbapenemase-encoding genes in this isolate was confirmed by the MS. Although for this country there have been previous reports on the isolation of **VIM-1** producing *E. coli* and *Salmonella* in food-producing animals (EFSA BIOHAZ Panel, 2013; Guerra et al., 2014; Fischer et al., 2016), 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 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 such monitoring is capable of detecting carbapenemase-producing *E. coli*.

As stated above, several countries (Austria, Czech Republic, Estonia, Finland, France, Portugal, Slovenia, Sweden, UK) voluntarily reported data from 2015 on the specific monitoring for carbapenemase-producing microorganisms. All of these countries focused on indicator *E. coli*, and most of them analysed samples from pigs/meat thereof as well as from bovine origin. According to the

data reported, no other carbapenemase-producing indicator *E. coli* isolates were identified among the samples analysed (Table 57). While this initial data is reassuring and suggests an extremely low occurrence of carbapenemase-producing *E. coli* in those animal species and types of meat which were monitored, a comprehensive overview will be possible when this specific monitoring is more widely adopted by all MSs, including those MSs where carbapenemase-producing microorganisms isolated livestock and/or food thereof have been already identified.

3.5.6.6. Further assessment

This report has described principally the phenotypic monitoring, but where the type of beta-lactamase enzyme which is responsible for conferring the resistance detected to third-generation cephalosporins has been reported, details have also been included. Categorising isolates which are resistant to third-generation cephalosporins and/or carbapenems according to their ESBL-, AmpC- and or carbapenemase phenotype provides useful epidemiological information on the reservoirs of the different types of resistance present in *E. coli* in different food-producing animal populations and categories of foodstuffs; in future, further development is likely to include expansion of the numbers of MSs reporting genotyping data.

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Abbreviations

%	percentage of resistant isolates per category of susceptibility or multiple resistance
% f	percentage frequency of isolates tested
% Res	percentage of resistant isolates
–	no data reported
APHA	Animal and Plant Health Agency
AMR	antimicrobial resistance
AST	antimicrobial susceptibility testing
BIOHAZ	EFSA Panel on Biological Hazards
CA-SFM	French Society for Microbiology
CBP	clinical breakpoints
CC	clonal complex
CLSI	Clinical and Laboratory Standards Institute
CP	carbapenemase producer
CTX-M	cefotaximase
DD	disk diffusion method
DIN	Deutsches Institut für Normung
DL	dilution method
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECDC	European Centre for Disease Prevention and Control
ECOFF	epidemiological cut-off value
EEA	European Economic Area
ESBL	extended-spectrum beta-lactamase
ETEC	enterotoxigenic *E. coli*
EUCAST	European Committee on Antimicrobial Susceptibility Testing
EURL-AR	EU Reference Laboratory for Antimicrobial Resistance (www.crl-ar.eu)
FWD	food- and waterborne diseases and zoonoses
HACCP	hazard analysis and critical control point

HPA	Health Protection Agency (UK)
I	intermediate
IZD	inhibition zone diameter
JIACRA	Joint Interagency Antimicrobial Consumption and Resistance Analysis
MDR	multiple drug resistance
MIC	minimum inhibitory concentration
MRSA	meticillin-resistant *Staphylococcus aureus*
MS	Member State
MSSA	meticillin-susceptible *Staphylococcus aureus*
NA	not applicable
NCP	National Control Programme
NRL	National Reference Laboratory
PCU	population correction unit
PMQR	Plasmid mediated quinolone resistance
PVL	Panton–Valentine leucocidin
Q	quantitative
QRDR	quinolone resistance-determining regions
R	resistant
res1–res9	resistance to one antimicrobial substance/resistance to nine antimicrobial substances of the common set for *Salmonella*
S	susceptible
SIR	susceptible, intermediate, resistant
ST	sequence type
TESSy	The European Surveillance System
VTEC	vero(cyto)toxigenic *E. coli*
WGS	whole genome sequencing
WHO	World Health Organization

Antimicrobial substances

AMC	amoxicillin/clavulanate
AMP	ampicillin
AZM	azithromycin
CAZ	ceftazidime
CHL	chloramphenicol
CIP	ciprofloxacin
CLI	clindamycin
CST	colistin
CTX	cefotaxime
ERY	erythromycin
FUS	fusidic acid
GEN	gentamicin
KAN	kanamycin
LZD	linezolid
MER	meropenem
MUP	mupirocin
NAL	nalidixic acid
QD	quinupristin/dalfopristin
RIF	rifampicin
SUL	sulfonamides
STR	streptomycin
SXT	sulfamethoxazole
TGC	tigecycline
TIA	tiamulin
TET	tetracycline
TMP	trimethoprim

MSs of the EU and other reporting countries in 2015

Austria	AT
Belgium	BE
Bulgaria	BG
Croatia	HR
Cyprus	CY
Czech Republic	CZ
Denmark	DK
Estonia	EE
Finland	FI
France	FR
Germany	DE
Greece	GR
Hungary	HU
Ireland	IE
Italy	IT
Latvia	LV
Lithuania	LT
Luxembourg	LU
Malta	MT
Netherlands	NL
Poland	PL
Portugal	PT
Romania	RO
Slovakia	SK
Slovenia	SI
Spain	ES
Sweden	SE
United Kingdom	UK

Non-MSs reporting, 2015

Iceland	IS
Norway	NO
Switzerland	CH

Definitions

'Antimicrobial-resistant isolate'	In the case of quantitative data, an isolate was defined as 'resistant' to a selected antimicrobial when its minimum inhibitory concentration (MIC) value (in mg/L) was above the cut-off value or the disc diffusion diameter (in mm) was below the cut-off value. The cut-off values, used to interpret MIC distributions (mg/L) for bacteria from animals and food, are shown in Material and methods, Tables 5, 6 and 7
	In the case of qualitative data, an isolate was regarded as resistant when the country reported it as resistant using its own cut-off value or break point
'Level of antimicrobial resistance'	The percentage of resistant isolates among the tested isolates
'Reporting MS group'	MSs (MSs) that provided data and were included in the relevant table for antimicrobial resistance data for the bacteria–food/animal category–antimicrobial combination
Terms used to describe the antimicrobial resistance levels	Rare: < 0.1%
	Very low: 0.1–1.0%
	Low: > 1.0–10.0%
	Moderate: > 10.0–20.0%
	High: > 20.0–50.0%
	Very high: > 50.0–70.0%
	Extremely high: > 70.0%

Appendix A – Raw data only used for calculating the SIR

Table A.1: PCU-fattening pigs, in 27 MSs, 2015

Country	PCU pigs 2015
Austria	315,011.38
Belgium	782,490.72
Bulgaria	59,149.93
Croatia	52,767.11
Cyprus	37,559.60
Czech Republic	172,898.50
Denmark	1,537,994.91
Estonia	39,207.56
Finland	136,708.49
France	1,571,031.19
Germany	3,427,610.25
Hungary	264,951.26
Greece	97,369.18
Iceland	5,219.50
Ireland	243,059.33
Italy	686,523.41
Latvia	33,647.06
Lithuania	59,608.28
Luxembourg	9,677.93
Malta	4,114.18
Netherlands	1,408,114.84
Norway	104,305.50
Poland	1,216,781.64
Portugal	285,925.69
Romania	247,034.91
Slovakia	47,880.84
Slovenia	25,273.99
Spain	3,068,144.11
Sweden	166,349.07
Switzerland	178,894.84
United Kingdom	671,747.38

Appendix B – List of usable data

The numbering in the Appendix B corresponds to the section numbers

Summary (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_summary.zip

Table abbreviation	Table name
SUMTABL1	Summary of phenotypic characterisation of third generation cephalosporin resistance in *Salmonella* from humans, meat from pigs and fattening pigs in 2015
SUMTABL2	Summary of phenotypic characterisation of third-generation cephalosporin resistance in *E. coli* from fattening pigs and calves under 1 year of age in 2015 (routine monitoring)
SUMTABL3	Summary of phenotypic characterisation of third-generation cephalosporin resistance in ESBL-/AmpC-producing *E. coli* from fattening pigs, calves, meat from pigs and meat from bovine animals deriving from specific monitoring in 2015

B.2.   Matherial and methods (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_materials_methods.zip

Table abbreviation	Table name
MMTABL1	Antimicrobials reported, methods used, type of data reported and interpretive criteria applied by MSs for human *Salmonella* AST data in 2015
MMTABL2	Antimicrobials reported, method used, type of data reported and interpretive criteria applied by MSs for human *Campylobacter* AST data in 2015
MMTABL3	Panel of antimicrobial substances included in AMR monitoring, EUCAST ECOFFs and concentration ranges tested in *Salmonella* spp. and indicator commensal *E. coli* (first panel)
MMTABL4	Panel of antimicrobial substances included in AMR monitoring, EUCAST ECOFFs and concentration ranges tested in *C. jejuni* and *C. coli*
MMTABL5	Panel of antimicrobial substances, EUCAST ECOFFs and concentration ranges used for testing only *Salmonella* spp. and indicator commensal *E. coli* isolates resistant to cefotaxime, ceftazidime or meropenem (second panel)

B.3.1.   *Salmonella* (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_salmonella.zip

B.3.1.1.   Antimicrobial resistance in *Salmonella* isolates from humans

Table abbreviation	Table name
COMDERBYHUM	Complete susceptibility, MDR and co-resistance in *Salmonella* Derby from humans in 2015
COMMONTYPHIHUM	Complete susceptibility, MDR and co-resistance in monophasic *Salmonella* Typhimurium from humans in 2015
COMSALMHUM	Complete susceptibility, MDR and co-resistance in *Salmonella* spp. from humans in 2015
COMTYPHIHUM	Complete susceptibility, MDR and co-resistance in *Salmonella* Typhimurium from humans in 2015
DERBYHUM	Antimicrobial resistance in *Salmonella* Derby from humans per country in 2015
ENTERHUM	Antimicrobial resistance in *Salmonella* Enteritidis from humans per country in 2015
INFANHUM	Antimicrobial resistance in *Salmonella* Infantis from humans per country in 2015

Table abbreviation	Table name
KENTHUM	Antimicrobial resistance in *Salmonella* Kentucky from humans per country in 2015
MONTYPHIHUM	Antimicrobial resistance in monophasic *Salmonella* Typhimurium 1,4,[5],12:i:- from humans per country in 2015
NEWPORTHUM	Antimicrobial resistance in *Salmonella* Newport from humans per country in 2015
PARATYPHIBJAVAHUM	Antimicrobial resistance in *Salmonella* Paratyphi B var. L+ tartrate+ (Java) from humans per country in 2015
RISSENHUM	Antimicrobial resistance in *Salmonella* Rissen from humans per country in 2015
SALMHUM	Antimicrobial resistance in *Salmonella* spp. (all non-typhoidal serovars) from humans per country in 2015
SALMTRAVHUM	Proportion of tested *Salmonella* spp. isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country in 2015
STANLEYHUM	Antimicrobial resistance in *Salmonella* Stanley from humans per country in 2015
TYPHIHUM	Antimicrobial resistance in *Salmonella* Typhimurium from humans per country in 2015
VIRCHOWHUM	Antimicrobial resistance in *Salmonella* Virchow from humans per country in 2015

B.3.1.2. Antimicrobial resistance in *Salmonella* isolates from animals and food

Table abbreviation	Table name
SALMOVERVIEWD	Decision Overview of countries reporting antimicrobial resistance data using MICs on *Salmonella* spp. all serovars from humans and various animal and food categories in 2015
SERCALVESD	Frequency distribution of *Salmonella* serovars in calves (under 1 year), in 2015
SERFATPIGSD	Frequency distribution of *Salmonella* serovars in fattening pigs, in 2015
SERFATPIGSD2	Panel2: Frequency distribution of *Salmonella* serovars in fattening pigs, in 2015
SERBOVMEATD	Decision: Frequency distribution of *Salmonella* serovars in meat from bovine animals, in 2015
SERPIGMEATD	Decision: Frequency distribution of *Salmonella* serovars in meat from pigs, in 2015
SERPIGMEATD2	Decision Panel2: Frequency distribution of *Salmonella* serovars in meat from pigs, in 2015
SALMPIGMEATD	Occurrence of resistance for selected antimicrobials in *Salmonella* spp. isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
SALMPIGMEATD2	Decision Panel2: Occurrence of resistance for selected antimicrobials in *Salmonella* spp. isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
TYPHIPIGMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Typhimurium isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
TYPHIPIGMEATD2	Decision Panel2: Occurrence of resistance for selected antimicrobials in *Salmonella* Typhimurium isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
MOTYPHIPIGMEATD	Decision: Occurrence of resistance for selected antimicrobials in monophasic *Salmonella* Typhimurium isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
DERBYPIGMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Derby isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
DERBYPIGMEATD2	Decision Panel2: Occurrence of resistance for selected antimicrobials in *Salmonella* Derby isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
RISSENPIGMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Rissen isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values

Table abbreviation	Table name
INFANTISPIGMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Infantis isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
SALMBOVMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* spp. isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
TYPHIBOVMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Typhimurium isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
INFANTISBOVMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Infantis isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
ENTERBOVMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Enteritidis isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
DERBYBOVMEATD	Decision: Occurrence of resistance for selected antimicrobials in *Salmonella* Derby isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
MONOTYPHIBOVMEATD	Decision: Occurrence of resistance for selected antimicrobials in monophasic *Salmonella* Typhimurium isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
SALMFATPIGD	Occurrence of resistance for selected antimicrobials in *Salmonella* spp. isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
SALMFATPIGD2	Panel2: Occurrence of resistance for selected antimicrobials in *Salmonella* spp. isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
TYPHIFATPIGD	Occurrence of resistance for selected antimicrobials in *Salmonella* Typhimurium isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
TYPHIFATPIGD2	Panel2: Occurrence of resistance for selected antimicrobials in *Salmonella* Typhimurium isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
MOTYPHIFATPIGD	Occurrence of resistance for selected antimicrobials in monophasic *Salmonella* Typhimurium isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
MOTYPHIFATPIGD2	Panel2: Occurrence of resistance for selected antimicrobials in monophasic *Salmonella* Typhimurium isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
DERBYPIGD	Occurrence of resistance for selected antimicrobials in *Salmonella* Derby isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
ENTERPIGD	Occurrence of resistance for selected antimicrobials in *Salmonella* Enteritidis isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
RISSENFATPIGD	Occurrence of resistance for selected antimicrobials in *Salmonella* Rissen isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
SALMCALVESD	Occurrence of resistance for selected antimicrobials in *Salmonella* spp. isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
TYPHICALVESD	Occurrence of resistance for selected antimicrobials in *Salmonella* Typhimurium from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
MOTYPHICALVESD	Occurrence of resistance for selected antimicrobials in monophasic *Salmonella* Typhimurium from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
ENTERCALVESD	Occurrence of resistance for selected antimicrobials in *Salmonella* Enteritidis from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values

Table abbreviation	Table name
DERBYCALVESD	Occurrence of resistance for selected antimicrobials in *Salmonella* Derby isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
AGONACALVESD	Occurrence of resistance for selected antimicrobials in *Salmonella* Agona isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
COMSALMPIGMEAT	Complete susceptibility, multiresistance and index of diversity in *Salmonella* spp. from pig meat in 2015
FREQSALMPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* spp. from meat from pigs in 2015
COMTYPHIPIGMEAT	Complete susceptibility and multiresistance in *Salmonella* Typhimurium from meat from pigs in 2015
FREQTYPHIPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Typhimurium from pig meat in 2015
COMMOTYPHIPIGMEAT	Complete susceptibility and multiresistance in monophasic *Salmonella* Typhimurium from meat from pigs in 2015
FREQMOTYPHIPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in monophasic *Salmonella* Typhimurium from meat from pigs in 2015
COMDERBYPIGMEAT	Complete susceptibility and multiresistance in *Salmonella* Derby from meat from pigs in 2015
FREQDERBYPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Derby from meat from pigs in 2015
FREQINFANTISPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Infantis from meat from pigs in 2015
COMINFANTISPIGMEAT	Complete susceptibility and multiresistance in *Salmonella* Infantis from meat from pigs in 2015
FREQINFANTISPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Infantis from meat from pigs in 2015
COMRISSENPIGMEAT	Complete susceptibility and multiresistance in *Salmonella* Rissen from meat from pigs in 2015
FREQRISSENPIGMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Rissen from meat from pigs in 2015
COMSALMBOVMEAT	Complete susceptibility and multiresistance in *Salmonella* spp. from meat from bovine animals in 2015
FREQSALMBOVMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* spp. from meat from bovine animals in 2015
COMTYPHIBOVMEAT	Complete susceptibility and multiresistance in *Salmonella* Typhimurium from meat from bovine animals in 2015
FREQTYPHIBOVMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Typhimurium from meat from bovine animals in 2015
COMDERBYBOVMEAT	Complete susceptibility and multiresistance in *Salmonella* Derby from meat from bovine animals in 2015
COMINFANTISBOVMEAT	Complete susceptibility and multiresistance in *Salmonella* Infantis from meat from bovine animals in 2015
FREQINFANTISBOVMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Infantis from meat from bovine animals in 2015

Table abbreviation	Table name
COMMONTYPHIBOVMEAT	Complete susceptibility and multiresistance in monophasic *Salmonella* Typhimurium from meat from bovine animals in 2015
FREQMONTYPHIBOVMEAT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in monophasic *Salmonella* Typhimurium from meat from bovine animals in 2015
COMENTERBOVMEAT	Complete susceptibility and multiresistance in *Salmonella* Enteritidis from meat from bovine animals in 2015
COMSALMFATPIG	Complete susceptibility and multiresistance in *Salmonella* spp. from fattening pigs in 2015
FREQSALMFATPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* spp. from fattening pigs in 2015
COMTYPHIFATPIG	Complete susceptibility, multiresistance and index of diversity in *Salmonella* Typhimurium from fattening pigs in 2015
FREQTYPHIFATPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Typhimurium from fattening pigs iin 2015
COMMOTYPHIPIG	Complete susceptibility and multiresistance in monophasic *Salmonella* Typhimurium from fattening pigs in 2015
FREQMOTYPHIPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in monophasic *Salmonella* Typhimurium from fattening pigs in 2015
COMDERBYFATPIG	Complete susceptibility and multiresistance in *Salmonella* Derby from fattening pigs in 2015
FREQDERBYFATPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Derby from fattening pigs in 2015
COMINFAFATPIG	Complete susceptibility and multiresistance in *Salmonella* Infantis from fattening pigs in 2015
COMRISSENFAFATPIG	Complete susceptibility and multiresistance in *Salmonella* Rissen from fattening pigs in 2015
FREQRISSENFATPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Rissen from fattening pigs in 2015
COMSALMCALV	Complete susceptibility and multiresistance in *Salmonella* spp. from calves (under 1 year) in 2015
FREQSALMCALV	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* spp. from calves (under 1 year) in 2015
COMTYPHICALV	Complete susceptibility and multiresistance in *Salmonella* Typhimurium from calves (under 1 year) in 2015
FREQTYPHICALV	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Typhimurium from calves (under 1 year) in 2015
FREQDERBYCALV	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in *Salmonella* Derby from calves (under 1 year) in 2015
HIGHSALMPIGMEAT	High-level ciprofloxacin resistance in *Salmonella* serovars from meat from pigs in 2015
HIGHSALMBOVMEAT	High-level ciprofloxacin resistance in *Salmonella* serovars from meat from bovine animals in 2015
HIGHSALMFATPIG	High-level ciprofloxacin resistance in *Salmonella* serovars from fattening pigs in 2015
HIGHSALMCALV	High-level ciprofloxacin resistance in *Salmonella* serovars from calves (under 1 year) in 2015

Table abbreviation	Table name
MULTISALMPIGMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* spp. from meat from pigs in 2015
MULTITYPHIPIGMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Typhimurium from meat from meat from pigs in 2015
MULTIMOTYPHIPIGMEAT	Multiresistance patterns of selected antimicrobials in monophasic *Salmonella* Typhimurium from meat from pigs in 2015
MULTIDERBYPIGMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Derby from meat from pigs in 2015
MULTIINFANTINSPIGMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Infantis from meat from pig in 2015
MULTIRISSENSPIGMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Rissen from meat from pig in 2015
MULTISALMBOVMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* spp. from meat from bovine animals in 2015
MULTISALMBOVMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* spp. from meat from bovine animals in 2015
MULTITYPHIBOVMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Typhimurium from meat from bovine animals in 2015
MULTIMONTYPHIBOVMEAT	Multiresistance patterns of selected antimicrobials in monophasic *Salmonella* Typhimurium from meat from bovine animals in 2015
MULTIDERBYBOVMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Derby from meat from bovine animals in 2015
MULTIINFANTISBOVMEAT	Multiresistance patterns of selected antimicrobials in *Salmonella* Infantis from meat from bovine animals in 2015
MULTISALMFATPIG	Multiresistance patterns in *Salmonella* spp. from fattening pigs in 2015
MULTITYPHIFATPIG	Multiresistance patterns in *Salmonella* Typhimurium from fattening pigs in 2015
MULTIMOTYPHIPIG	Multiresistance patterns in monophasic *Salmonella* Typhimurium from fattening pigs in 2015
MULTIDERBYFATPIG	Multiresistance patterns of selected antimicrobials in *Salmonella* Derby from fattening pigs in 2015
MULTIINFATPIG	Multiresistance patterns of selected antimicrobials in *Salmonella* Infantis rom fattening pigs in 2015
MULTIRISSENFATPIG	Multiresistance patterns of selected antimicrobials in *Salmonella* Rissen from fattening pigs in 2015
MULTITYPHICALV	Multiresistance patterns in *Salmonella* Typhimurium from calves (under 1 year) in 2015
MULTIDERBYCALV	Multiresistance patterns of selected antimicrobials in *Salmonella* Derby from calves (under 1 year) in 2015
MULTIAGONACALV	Multiresistance patterns of selected antimicrobials in *Salmonella* Agona from calves (under 1 year) in 2015
MULTISALMCALV	Multiresistance patterns of selected antimicrobials in *Salmonella* spp. from calves (under 1 year) in 2015
MULTIMONTYPHICALV	Multiresistance patterns in monophasic *Salmonella* Typhimurium from calves (under 1 year) in 2015
SALM1	Occurrence of resistance to cefotaxime among *Salmonella* spp. from fattening pigs and calves under 1 year in 2015, using harmonised ECOFFs and EUCAST CBPs
SALM2	Distribution of MICs of colistin by serovar in *Salmonella* spp. in carcases from fattening pigs

B.3.2. *Campylobacter* (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_campylobacter.zip

B.3.2.1. Antimicrobial resistance in *Campylobacter* isolates from humans

Table abbreviation	Table name
CAMPCOHUM	Antimicrobial resistance in *Campylobacter coli* from humans per country in 2015
CAMPJEHUM	Antimicrobial resistance in *Campylobacter jejuni* from humans per country in 2015
CAMPTRAVHUM	Proportion of tested *Campylobacter jejuni* and *C. coli* isolates from human cases associated with travel, domestic cases and cases with unknown travel information by country in 2015
COMCAMPCOHUM	Complete susceptibility, MDR and co-resistance in *Campylobacter coli* from humans in 2015
COMCAMPJEHUM	Complete susceptibility, MDR and co-resistance in *Campylobacter jejuni* from humans in 2015
CAMPCOPROP	Proportion of *Campylobacter coli* isolates from humans resistant to ciprofloxacin, erythromycin and tetracycline in 2015

B.3.2.2. Antimicrobial resistance in *Campylobacter* isolates from animals and food

Table abbreviation	Table name
CAMPCOOVERVIEW	Overview of countries reporting antimicrobial resistance data using MIC on *Campylobacter coli* from humans and various animal and food categories in 2015
CAMPJEOVERVIEW	Overview of countries reporting antimicrobial resistance data using MIC on *Campylobacter jejuni* from humans and various animal and food categories in 2015
CAMPCOPIGD	Decision: Occurrence of resistance for selected antimicrobials in *Campylobacter coli* from fattening pigs in 2015, using harmonised epidemiological cut-off values
COMCAMPCOFATPIG	Complete susceptibility and multiresistance in *Campylobacter coli* from fattening pigs in 2015
FREQCAMPCOFATPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to five antimicrobials in *Campylobacter coli* from fattening pigs in 2015
MULTICAMPCOFATPIG	Multiresistance patterns of selected antimicrobials in *Campylobacter coli* from fattening pigs in 2015
CAMP1	Occurrence of high-level resistance to erythromycin (MIC > 128 mg/L) in *Campylobacter coli* from fattening pigs in 2015
CAMP2	Number and proportions (%) of *Campylobacter coli*-positive caecal samples of fattening pigs, EU monitoring of AMR, 2015
CAMP3	Prevalence of resistance to selected antimicrobials in *Campylobacter coli* from fattening pigs in 2015, using harmonised ECOFFs

B.3.3. *Escherichia coli* (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_ecoli.zip

B.3.3.1. Antimicrobial resistance in indicator *Escherichia coli* isolates from animals

Table abbreviation	Table name
ESCHEOVERVIEWD	Decision Overview of countries reporting antimicrobial resistance data using MIC on indicator commensal *Escherichia coli* from various animal and food categories in 2015

Table abbreviation	Table name
ESCHEPIGD	Decision: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolate from fattening pigs in 2015, using harmonised epidemiological cut-off values
ESCHEPIGD2	Decision panel2: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
ESCHECALVD	Decision: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
ESCHECALVD2	Decision panel2: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
MULTIESCHEPIG	Multiresistance patterns of selected antimicrobials in commensal indicator *Escherichia coli* from fattening pigs in 2015
MULTIESCHECALV	Multiresistance patterns of selected antimicrobials in *Escherichia coli* from calves (under 1 year) in 2015
COMESCHECALV	Complete susceptibility and multiresistance in commensal indicator in *Escherichia coli* from calves (under 1 year in 2015
FREQESCHECATT	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in commensal indicator *Escherichia coli* from calves (under 1 year) in 2015
COMESCHEPIG	Complete susceptibility and multiresistance in commensal indicator *Escherichia coli* from fattening pigs in 2015
FREQESCHEPIG	Frequency distribution of completely susceptible isolates and resistant isolates to from one to eleven antimicrobials in commensal indicator *Escherichia coli* from fattening pigs in 2015
COESCHECATT	Co-resistance to fluoroquinolones and third-generation cephalosporins in commensal indicator *Escherichia coli* from calves (under 1 year) in 2015
COESCHEPIG	Co-resistance to fluoroquinolones and third-generation cephalosporins indicator *Escherichia coli* from fattening pigs in 2015
CIPESCHECATT	Ciprofloxacin resistance assessed at differing thresholds in commensal indicator *Escherichia coli* from calves (under 1 year) in 2015
CIPESCHEPIG	Ciprofloxacin resistance assessed at differing thresholds in commensal indicator *Escherichia coli* from fattening pigs in 2015
EC1	Resistance in indicator *E. coli* from fattening pigs assessed by the percentage of resistant isolates (Total) and 'summary indicator of resistance' (SIR) (weighted mean of the proportions of resistant isolates in the reporting MSs) in the EU, 27 MSs, 2015

B.3.4. Meticillin-resistant *Staphylococcus aureus* (MRSA) (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_mrsa.zip

B.3.4.1. Meticillin-resistant *Staphylococcus aureus* in food and animals

Table abbreviation	Table name
MRSAFOOD	MRSA in food, 2015
MRSAANIMAL	MRSA in food-producing animals (excluding clinical investigations), 2015
MRSAANIMALCLIN	MRSA in food-producing animals, clinical investigations, 2015
MRSACLINANIMAL	MRSA in companion animals, clinical investigations, 2015
MRSATRENDANIMAL	Temporal occurrence of MRSA in animals
MRSAAMR	Occurrence of resistance for selected antimicrobials in MRSA from food and animals in 2015, using harmonised epidemiological cut-off values
MRSAOVERVIEW	Overview of countries reporting data on MRSA in animals and food in 2015

B.3.5. Third-generation cephalosporin and carbapenem resistance in *Escherichia coli* and *Salmonella* (related tables are accessible by clicking the link below)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4694a_esbl.zip

Table abbreviation	Table name
ESCHEOVERVIEWESBL	ESBL: Overview of countries reporting antimicrobial resistance data using MIC on indicator commensal *Escherichia coli* from various animal and food categories in 2015
ESCHEPIGMEATESBL	Decision ESBL panel 1: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
ESCHEPIGMEATESBL2	Decision ESBL panel 2: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from meat from pigs in 2015, using harmonised epidemiological cut-off values
ESCHEBOVMEATESBL	Decision ESBL panel 1: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
ESCHEBOVMEATESBL2	Decision ESBL panel 2: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from meat from bovine animals in 2015, using harmonised epidemiological cut-off values
ESCHEPIGESBL	Decision ESBL Panel 1: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
ESCHEPIGDESBL2	Decision ESBL Panel 2: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from fattening pigs in 2015, using harmonised epidemiological cut-off values
ESCHECALVESBL	ESBL Panel 1: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
ESCHECALVESBL2	ESBL Panel 2: Occurrence of resistance for selected antimicrobials in *Escherichia coli* isolates from calves (under 1 year) in 2015, using harmonised epidemiological cut-off values
RESCEPH1	ESBL- and AmpC-phenotypes in *Salmonella* spp. isolates from humans by country, 2015
RESCEPH2	ESBL- and AmpC-phenotypes and genotypes in *Salmonella* spp. isolates from humans by serovar, 2015 (8 MSs and Norway)
RESCEPH3	Occurrence of resistance to beta-lactam compounds in *Salmonella* spp. isolates from fattening pigs and meat from pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015
RESCEPH4	Presumptive ESBL- and AmpC-producing *Salmonella* spp. isolates from meat from pigs and fattening pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015
RESCEPH5	Occurrence of resistance to beta-lactam and carbapenem compounds in indicator *E. coli* isolates from fattening pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015
RESCEPH6	Presumptive ESBL- and AmpC-producing indicator *E. coli* isolates from fattening pigs collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015
RESCEPH7	Occurrence of resistance to beta-lactam and carbapenem compounds in indicator *E. coli* isolates from calves under one year of age collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015
RESCEPH8	Presumptive ESBL- and AmpC-producing indicator *E. coli* isolates from calves under one year of age collected within the routine monitoring and subjected to supplementary testing (panel 2) in 2015

Table abbreviation	Table name
RESCEPH9	Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from pigs collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH10	Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from pigs collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH11	Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from bovine animals collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH12	Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from meat from bovine animals collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH13	Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from fattening pigs collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH14	Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from fattening pigs collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH15	Occurrence of presumptive ESBL- and AmpC-producing *E. coli* isolates from calves of less than one year of age collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH16	Prevalence of presumptive ESBL- and AmpC-producing *E. coli* isolates from calves of less than one year of age collected within the specific ESBL-/Ampc-/carbapenemase-producing monitoring and subjected to supplementary testing (Panel 2) in 2015
RESCEPH17	Prevalence of carbapenemase-producing *E. coli* from fattening pigs and calves under one year of age and meat thereof collected within the specific carbapenemase-producing monitoring in 2015