Prevalence and antimicrobial resistance profile in Salmonella spp. isolates from swine food chain

Carlotta Lauteri,1 Anna Rita Festino,1 Mauro Contar,1 Alberto Vergara1
1Post-Graduate Specialization School in Food Inspection “G. Tiecco”, Faculty of Veterinary Medicine, University of Teramo; 2Doctor in Veterinary Medicine, Parma, Italy

Abstract
The aim of this survey was to examine the prevalence and the antimicrobial resistance (AMR) of Salmonella spp. isolated from swine food chain. A total of 435 samples were collected: 360 from slaughterhouse (150 carcasses, 30 carcass samples, 180 environmental samples) and 75 from Italian traditional pork dry sausages. Thirty-six Salmonella were isolated and identified by Polymerase Chain Reaction (PCR): 13.3% (4/30) in fecal samples, 5.5% (10/180) in environmental samples, 7.3% (11/150) in carcasses, and 14.6% (11/75) in Italian traditional dry sausages. Salmonella serotypes were: S. Typhimurium (44.4%), S. Typhimurium monophasic variant (8.3%), S. Typhi (2.8%), S. Enteritidis (22.2%), S. Rissen (16.6%) and S. Derby (5.5%). Phenotypic and genotypic characterization of AMR Salmonella spp. isolates was executed through automatic system (VIETEK 2, bioMéreux) and PCR assays. Salmonella spp. showed phenotypical and genotypical resistance to at least one or more classes of antibiotic. All Salmonella spp. were resistant to aminoglycoside (amikacin and tobramycin) and gentamicin, 86.1% strains were resistant to tetracycline, 55.5% strains were resistant to ampicillin and piperacillin, 25% strains to trimethoprim, 5.5% strains to chloramphenicol, 2.8% strains to amoxicillin/clavulanic acid, and nitrofurantoin. Among Salmonella isolates, the most detected AMR genes were catA for chloramphenicol (94.4%), nitrofurin nfxA (77.7%), nfxB (86.1%) and, for fluoroquinolone par C (100%) and gyrA (94.4%). This study reported epidemiological data regarding Salmonella spp. and AMR’s circulation in the swine food chain. This phenomenon (AMR) has critical repercussions on the final consumer health; therefore, it represents a crucial One-Health issue.

Introduction
In 2019 Salmonellosis was the second reported zoonotic disease in the European Union (EU), affecting about 88,000 people (Molla et al., 2003; Astorga et al., 2007; Wang et al., 2013; EFSA, 2021).

In swine, it is caused by S. Choleraus and, occasionally, may be responsible for human disease. However, ubiquitous Salmonella serovars are the unrestricted serovars that can cause symptomatic disease in a wide range of hosts, but more frequently cause self-limiting gastroenteritis. Typical symptoms in pigs are enteric and even fatal diseases; asymptomatic infected animals frequently carry these serovars in tonsils, gut, and gut-associated lymphoid tissue (Fedorka-Cray et al., 2000). These latent carriers could begin to shed Salmonella after leaving livestock, a process that might be triggered by stress factors such as transportation, holding pens at the slaughterhouse (Hurd et al., 2002).

Pork is the most frequently consumed meat in Europe (especially in Northern countries), and parallelly to this trend, Mediterranean nations have increased its consumption (Valero et al., 2014).

Italians are specialized in “heavy pig” livestock, which means that animals weight ranges between 150-160 kg with an age of 9 months (Di Cicco et al., 2016).

In Europe, contaminated pork and pork products are important sources for Salmonellosis in human cases (EFSA, 2021). The risk of infection is exacerbated by the high prevalence of Salmonella spp. in livestock, slaughterhouses, and asymptomatic animal acting as healthy carrier (Baptista et al., 2010).

Since 2005, the EU has established strict microbiological criteria for pig carcasses (Regulation EU No. 2073/2005). Focusing on Salmonella carcasses’ contamination, the European Legislator introduced new hygienic criteria (Regulation EU No. 217/2014) to reduce its prevalence.

Antibiotics’ administration in animals has different aims: disease treating, metaphylaxis, and prophylaxis, especially in stress periods such as before slaughtering (Aarestrup, 2005). Antimicrobial resistances have increased AMR phenomenon’s diffusion, and for this reason Regulation EC No. 1831/2003 was introduced to ban antibiotics usage for growth promotion.

In many countries the most used antibiotic in swine livestock were penicillin and tetracyclines. During pig production, suckling and post-weaning are periods in which there is a wide administration of oral medication (Lekagul et al., 2019).

Antimicrobial resistance in pigs and pig products is an increasing global concern, with resistance to at least one antimicrobial observed in 92% of Salmonella isolates in the UK (Miller et al., 2011). Treatment options of Salmonellosis in animal and humans has become more difficult due to the emerging of multidrug-resistant Salmonella spp. strains (Alcaine et al., 2006; Hur et al., 2012).

From a microbiological perspective, our investigation wants to provide data regarding Salmonella spp. prevalence, AMR and antibiotic resistance genes circulation in swine food chain.

Materials and methods
Sample collection
Samples were collected from six slaughterhouses located in North-Central Italy. These structures had different capabilities, as reported in Table 1. Each slaughterhouse was visited three
times. Twenty-five carcasses and thirty environmental sites (15 before and 15 during slaughtering activities) were sampled on each sampling day. Finally, a total of 75 total of 150 carcasses, 180 environmental samples, and 30 cecal samples were collected. A total of 75 traditional pork dry sausages were collected.

**Carcasses**

A total of 150 carcasses (weight range: 140-160 kg) were randomly selected for sampling by using pre-hydrated sponges (International PBI S.P.A Milan, Italy) with Buffered Peptone Water (BPW; Oxoid, Milan, Italy) from different sites (4×100 cm²): hind limb, abdomen lateral (belly), midsdorsal region (mid-back) and jowl. All samples were sent to the laboratory in cooled containers within the same day of analysis.

**Cecal contents**

A total of thirty pooled cecal samples (225 gr) were taken after evisceration. Every sample was collected aseptically from different pigs. All samples were individually packed and kept at a temperature of +4°C during storage and transportation to the laboratory.

**Environmental samples**

A total of 30 environmental samples (15 before slaughter activities and 15 during slaughter activities) were collected in each slaughterhouse. Evaluation included floor after bleeding, gut container, and run-off pit/drain well. The first sampling round was done before the starting of activities, and one at the end. A 100 cm² surface per site using a template, was sampled using sponges pre-soaked in 10 ml of Buffered Peptone Water (BPW; Oxoid, Milan, Italy) by collecting surface swabs in the floor after the bleeding stage, in runoff pit and gut container. All samples were stored at +4°C and returned to the laboratory within the same day for the analysis.

**Traditional dry sausages samples**

A total of 75 traditional pork dry sausage samples were collected, they had an average weight of 150 gr and 3 week of curing time. The screened products were manufactured by a farmer, or a butcher or a small workshop. In the analyzed area all samples were stored at +4°C and returned to the laboratory within the same day for the analysis.

**Salmonella isolation, identification, and serotyping**

Environmental and carcass samples were then pre-enriched in Buffered Peptone Water (BPW; Oxoid, Milan, Italy) and incubated at 37°C for 24h. Pools of fecal samples (25 gr) and dry sausages (25 gr) were transferred to 225 ml of sterile BPW solution and homogenized for 120 s in a stomacher machine and incubated at 37°C for 24h. All samples were analyzed following the ISO6579:2002 0.1 ml of the sample were transferred in 10 ml of Rappaport-Vassiliadis (RVS Oxoid, Milan, Italy) and incubated in 42°C for 24h. Xylose Lysine Deoxycholate (XLD, Oxoid, Milan, Italy) was used as selective media than suspected colonies were transported in Tryptone Soy Agar (TSA, Oxoid, Milan, Italy) and they were performed by slide agglutination with Salmonella Rapid Latex Test (Oxoid, Milan, Italy).

All Salmonella spp. were differentiated biochemically and serologically by VITEK 2 system (bioMérieux, France), according to the manufacturer’s instructions (bioMérieux, 2013).

The Identification Gram-Negative Bacteria (GNB) cards were used for the identification of bacterial strains, according to the manufacturer’s instructions (bioMérieux, 2013).

Confirmation of serotyping was performed by qualitative Polymerase Chain Reaction (PCR) assay (Kikuvi et al., 2010), while genomic DNA was analyzed by pulsed-field gel electrophoresis (PFGE), using XbaI (50U/sample), BlnI/AvaII (30U/sample) as restriction enzymes, according to the PULSENET protocol (PULSENET, 2010) (Di Cicco, et al.,2016).

**Antimicrobial susceptibility testing**

Card VITEK 2 AST GN-65 was performed for antibiograms susceptibility and Minimum Inhibitory Concentrations (MICs) detection according to the manufacturer’s instructions (bioMérieux, 2013). Fifteen antimicrobial agents were tested: ampicillin, amoxicillin and clavulanic acid, imipenem, cefpodoxime, cefotiofur, tobramycin, piperacillin, gentamicin, amikacin, enrofloxacine, marbofloxacine, chloramphenicol, tetracycline, nitrofurantoin, trimethoprim-sulfamethoxazole.

**Detection of antibiotic resistance genes**

According to the manufacturer’s instructions, genomic DNA was extracted from the above-mentioned bacterial isolates by using High Pure PCR Template Preparation Kit (Roche, Indianapolis, Ind.).

Antimicrobial resistance genes were examined using conventional PCR reaction (Table 2), which was performed in a final reaction volume of 25 μl: containing purified DNA 1 μl, DreamTaq Green PCR Master Mix (Thermo Fisher Scientific, US) 12.5 μl, forward primers 0.25 μl, reverse primers 0.25 μl, Nuclease-free water 11 μl. Twelve antimicrobial resistance genes were tested: tetA, tetB, tetC for tetracycline, catA1 for chloramphenicol, aadA2, aac(3)IV, aadB for aminoglycoside, bla TEM and bla PSE for beta-lactamase, nfsA and nfsB for nitrofurantoin and par C and gyrA for fluoroquinolone, dfrA1, dfrB, dfrA14 for trimethoprim-sulfamethoxazole.

**Results**

In the present study, microbiological screenings permitted to identify different Salmonella serovars, as reported in Table 3. The isolated Salmonella displayed a high spectrum of antibiotic resistance. All strains (100%) showed phenotypically and genotypically resistance to at least one or more examined classes of antibiotic.

All samples (100%) were resistant to amikacin, tobramycin, and gentamicin; 20 strains (55,5%) showed resistance to ampicillin and piperacillin; 31 strains (86%) were resistant to tetracycline, one strain was resistant to amoxicillin-clavulanic acid and nitrofurantoin, 2 strains (5,5%) were resistant of chloramphenicol and 9 strains were resistant of trimethoprim.

A lot of strains showed a multiple antimicrobial resistance: 27,8% (10/36) was resistant to 3 antimicrobial classes; 25% (9/36) to 4 antimicrobial classes, 2,8% (1/36) to 6 antimicrobial classes (Table 3).

All 36 Salmonella isolates, belonging to five different serovars recovered from the swine food chain, were investigated for antimicrobial resistance genes detection by uniplex PCR. The resistance genes most detected were parC (100%), gyrA (94,4%), catA (94,4%), nfsB (86,1%), nfsA (77,7%), bla TEM (47,2%), tetA (47,2%) and tetB (41,6%), tetC, aac(3)IV, aadB and dfrA1 showed a presence of 2,8%.

AadA2, bla PSE , dfrAB and dfrA14 genes resistance were not detected in Salmonella selected (Table 4).

**Discussion**

In swine food chain, Salmonella spp. prevalence has been extremely studied in all Europe (Bonardi, 2017); indeed, international agencies underlined high variability of Salmonella isolation data in different Member States (EFSA, 2021).

Our survey showed that 14,6% (11/75) of Salmonella was recovered from traditional dry sausages, 7,3% (11/150) from carcasses, 13,3% (4/30) from cecal pools, 5,5% (10/180) from environmental samples.
The different results observed could be attributed to different factors: slaughterhouses’ capabilities, good hygiene standards, cross-contaminations between carcasses and equipment, presence of resident slaughtering microflora, and inappropriate food handling (Bonardi, 2017). For this reason, the European Legislative ((Regulation EU No 1474/2015) purposed a new approach to reduce prevalence, apply-

### Table 1. Sampled slaughterhouses and their productive capabilities.

| Slaughterhouse | Slaughtered animals / time |
|----------------|---------------------------|
| S 1            | 350 animals / 1 hour      |
| S 2            | 450 animals / 1 hour      |
| S 3            | 55 animals / 1 hour       |
| S 4            | 115 animals / working day |
| S 5            | 1000 animals / working day|
| S 6            | 350 animals / 1 hour      |

### Table 2. Target antibiotic, PCR primers, forward and reverse sequence, annealing temperature of the primers, amplicon size and reference used to evaluate the presence of antibiotic resistance genes.

| Antibiotic       | Gene | Sequence (5’-3’) | Annealing | Amplicon | Reference temp (°C) |
|------------------|------|------------------|-----------|----------|--------------------|
| Tetraacycline    | tetA | F- GTAACTTGACGCTGATTG | 45        | 954      | Kikuvi et al., 2010 |
| Tetraacycline    | tetB | F- AAGTTTTCTGATACCGGCTG | 48        | 1170     | Kikuvi et al., 2010 |
| Tetraacycline    | tetC | F- AACAATCCGCAGCTGTTT | 50        | 1138     | Kikuvi et al., 2010 |
| Chloramphenicol  | catA | F- GGTGGGCAGCTG | 50        | 551      | Kikuvi et al., 2010 |
| Aminoglycosides  | ada2 | F- CGGATGACCAGAAATTCG | 54        | 250      | Prasertsee et al., 2016 |
| Aminoglycosides  | aac(3)-IV | F- TGTCGTCGACCAGCTCTTC | 63        | 653      | Koak et al., 2009 |
| Aminoglycosides  | adaB | F- GAGGATTGAGTTGATTGATT | 55        | 208      | Koak et al., 2009 |
| Ampicillin       | blaTEM | F- CGCTCCTGGTCTACATATATTT | 51        | 780      | Kikuvi et al., 2010 |
| Ampicillin       | blaPSE | F- CGTTTGCAGGCTTATACATATAGG | 58        | 465      | Kikuvi et al., 2010 |
| Nitrofurantoin   | nfxA | F- CTGCCGTCGTCGCTCGATT | 60        | 964      | Garcia et al., 2017 |
| Nitrofurantoin   | nfxB | F- ATCCGGCGCGGTCTCGATT | 58        | 921      | Garcia et al., 2017 |
| Quinolone        | parC | F- CTATTGCGATATATACCCG | 62        | 270      | El-Tayeb et al., 2017 |
| Quinolone        | gyrA | F- AAATCTGGGCTGTCGATTG | 55        | 343      | El-Tayeb et al., 2017 |
| Trimethoprim     | dfrA | F- GTGAACTAATCATATATG | 50        | 474      | El-Tayeb et al., 2017 |
| Trimethoprim     | dfrB | F- GATCGTCAGCGGAAAGATC | 60        | 141      | El-Tayeb et al., 2017 |
| Trimethoprim     | dfrA14 | F- GAGCAGCTCTTCTTTAAAGC | 58        | 393      | El-Tayeb et al., 2017 |

### Table 3. Prevalence of Salmonella.

| Source               | N. Salmonella isolates | Serovar (%) |
|----------------------|------------------------|-------------|
| Environmental sample | 10                     |             |
| Traditional dry sausage | 11                  |             |
| Carcass              | 11                     |             |
| Caecal sample        | 4                      |             |

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ing hot waters to remove microbiological surface contamination from carcasses.

It was also found that Salmonella also persist in slaughterhouses environment. In our study, one Salmonella Typhimurium, detected from gut container, presented monophasic Salmonella Typhimurium were isolated from runoff pit.

Therefore, the implementation of good manufacturing practice (GMP) is a crucial factor that allows to decrease environmental cross-contamination multi-drug resistance Salmonella.

Monophasic Salmonella Typhimurium is strongly associated with swine food chain, especially in Europe. This consideration permits to suggest a potential link between human infections with contaminated pork products consumption (de la Torre et al., 2003; Mossong et al., 2007; Hauser et al., 2010; Lucarelli et al., 2010; Mourao et al., 2014).

Pork and dry ready-to-eat products are an important source of disease in southern Europe, where human Salmonellosis prevalence, derived from these products, is higher than in the rest of Europe (Bonardi, 2017). In fact, in our study, prevalence of Salmonella in traditional dry sausages is higher than in other groups of samples.

Our results, obtained from antimicrobial tests, showed that Salmonella is more resistant to ampicillin, piperacillin, tetracycline, gentamicin, amikacin, and tobramycin.

Table 4. Sources of sample, serovar, resistant antibiotic class, phenotypic resistance.

| Source                     | Serovar             | Resistance phenotype | Resistance pattern | Resistance genotype |
|----------------------------|---------------------|----------------------|--------------------|---------------------|
| Traditional dry sausage    | S. Typhimurium      | AMI, AMP, GEN, PIP, TOB | 2                  | gyrA, parC          |
| Traditional dry sausage    | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | catA1, gyrA, parC, tetA, tetB |
| Environmental sample       | S. Typhimurium      | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetA, tetB |
| Caecal sample              | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB | 3                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetB |
| Carcass                    | S. Typhimurium      | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetA |
| Environmental sample       | S. Typhimurium      | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetB |
| Caecal sample              | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB | 3                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetB |
| Carcass                    | S. Typhimurium      | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetA |
| Environmental sample       | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB | 3                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetB |
| Carcass                    | S. Typhimurium      | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetA |
| Environmental sample       | S. Typhimurium      | AMI, AMP, AMX, CLO, GEN, NIT, PIP, TET, TOB | 6                  | catA1, gyrA, parC, tetB |
| Environmental sample       | Monophasic Variant  | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB | aadB, blaTEM, catA1, nsfA, nsfB, parC, tetB |
| Environmental sample       | Monophasic Variant  | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB | aadB, blaTEM, catA1, nsfA, nsfB, parC, tetB |
| Environmental sample       | Monophasic Variant  | S. Typhimurium      | AMI, AMP, GEN, PIP, TET, TOB | blaTEM, gyrA, nsfA, nsfB, parC, tetB |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Traditional dry sausage    | S. Enteritidis      | AMI, AMP, GEN, PIP, TET, TOB, TRI | 4                  | blaTEM, catA1, gyrA, nsfA, nsfB, parC, tetA |
| Carcass                    | S. Enteritidis      | AMI, GEN, TET, TOB   | 1                  | catA1, gyrA, nsfA, nsfB, parC |
| Environmental sample       | S. Rissen           | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetA |
| Environmental sample       | S. Rissen           | AMI, GEN, TET, TOB   | 2                  | catA1, gyrA, nsfA, nsfB, parC, tetA |
| Carcass                    | S. Rissen           | AMI, CLO, GEN, TET, TOB, TRI | 4                  | catA1, gyrA, nsfA, nsfB, parC, tetA |
| Carcass                    | S. Derby            | AMI, GEN, TET, TOB   | 1                  | catA1, gyrA, nsfA, nsfB, parC |
| Carcass                    | S. Derby            | AMI, GEN, TET, TOB   | 1                  | catA1, gyrA, nsfA, nsfB, parC |

AMP: ampicillin, AMX-amoxicillin and clavulanic acid, CEF-Cefibiof, TOB-Tobramycin, PIP-Piperacillin, GEN-Gentamicin, AMI-Amikacin, CLO-Chloramphenicol, TETRA-Tetracycline, NIT-Nitrofurantoin, TRI-Trimethoprim Sulfaethionamide
Ampicillin and tetracycline are commonly used in swine livestock as first-choice antibiotics to cure disease. Ampicillin and tetracycline are commonly used in swine livestock as first-choice antibiotics to cure disease worldwide (Prasertsee et al., 2016, Kozak et al., 2009). In devolving country such as China, antibiotics have been used as growth promoter (Yang et al., 2019), in Europe instead they had been banned since 2006 (Regulation EC No 1831/2003). For this reason, it is crucial detect the prevalence of AMR, especially in a global trade perspective. Indeed, microbiological and genetic evaluation are powerful tools to investigate Salmonella spp. prevalence, AMR and antibiotic resistance genes circulation in swine food chain.

The highest priority critically important antimicrobials are still used in pig production, for treatment and prevention of infection. This evidence requires global efforts for a prudent use of antibiotics to reduce the emergence of AMR in agricultural, veterinary, and foodborne sectors (Lekagul et al., 2019).

The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals, and food in 2018/2019 shows resistance to ampicillin, sulfonamides, and tetracyclines >20% (in Italy 68-72 % of the isolates were resistant), while the resistance to third generation cephalosporins was <10% (in Italy this resistance was <2% in human isolates and <5% in animal isolates).

In our study, AMR against third generation cephalosporins and fluoroquinolones, classified as “Criticallly important antimicrobials” (CIA), were not discovered. All examined strains were susceptible to cepodoxime, marbofloxacin, and enrofloxacin, and only 2.8% resulted resistant to ceftriaxone.

On the other hand, the presence of gene par C has been detected in all sample and, gyrA has been detected in 94.4% of samples.

The fluoroquinolone ciprofloxacin and the third-generation cephalosporin ceftriaxone are now the recommended drugs to treat human invasive Salmonella infections or patients at risk of developing an invasive infection (Shane et al., 2017).

For the strategic importance of fluoroquinolones, it could be useful investigate the presence of mutation and sequencing DNA.

In our study, antimicrobial resistance phenotype more present in the swine food chain are ampicillin, streptomycin, tetracycline, and chloramphenicol, in agreement with previous research papers (Calayag et al. 2017, Lekagul et al., 2019).

Two strains are phenotypic resistant to chloramphenicol, and 94.4% of strains showed catA gene typical antimicrobial resistance gene of this antibiotics. In European Union, it is not authorized for use in food-producing animals (EFSA, 2014). Deekshit demonstrated in his study that the ubiquitous strain of non-typhoidal Salmonella can have a silent gene of antimicrobial resistance and there isn’t a correlation between phenotypic and genotypic resistance (Deekshit et al., 2012).

Previous studies demonstrated that the main important resistance factor to chloramphenicol is in an auto-transmissible plasmid (IncHI). This type of plasmid carries other resistance genes responsible for streptomycin, sulfonamide, and tetracycline (Crump et al. 2015).

All strains are phenotypically resistant to at least three antibiotic classes. It is an important concern for human health. The resistance genes most commonly detected were parC (100%), gyrA (94.4%), catA (94.4%), nfxB (86,1%), nfxA (77,7%), bla TEM (47,2%), tetA (47,2%) and tetB (41,6%). Tetracycline (TetC), acr (3)Ib and aadB, dfrA1 show a presence of 2.8%.

Conclusions

In accordance with EU Regulation No 2160/2003, all Member States elaborated national control plans for Salmonella serovars in poultry and pig’s food chains. The aim of these plans is to guarantee human health.

The findings in this survey may suggest that there is a strict correlation between the prevalence of Salmonella spp. and antimicrobial resistance for human and animal health. Pig products could be an important carrier of AMR and a potential risk for public health.

The data relating to the frequency of isolation and presence of multiple resistances in the isolates of dry products demonstrate that problem must be carefully evaluated, especially in those situations where the domestic slaughter of pigs and the preparation of traditional products are used.

The monitoring of antimicrobial resistance and the rapid identification of trends that could further reduce the effectiveness of therapeutic antibiotics require a comprehensive and integrated One-Health approach.

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