Short communication

Isolation and characterization of multidrug-resistant bacteria from minced meat in Austria

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A R T I C L E  I N F O

Article info
Introduction: Resistant bacteria are a well-known public health problem. This study was conducted to investigate the prevalence and genetic characteristics of extended spectrum β-lactamase (ESBL) producing enterobacteria, methicillin-resistant Staphylococcus aureus (MRSA) and vancomycin-resistant Enterococci (VRE) in mixed minced meat from pork and beef.

Methods: One hundred samples of mixed minced meat were collected from supermarkets (n = 70) and local butcher shops (n = 30) in the city of Graz (Austria). After enrichment and inoculation on selective media, bacteria were identified with MALDI-TOF MS or Vitek2 systems, tested for antibiotic resistance and further characterized with PCR and sequencing.

Results: In 20 of the 100 meat samples 24 ESBL positive Escherichia coli isolates were found. The most common ESBL among the isolates was CTX-M-1. Other detected bla genes contained CTX-M-14, CTX-M-32, SHV-12 and TEM-52 types. Nine samples were tested positive for MRSA and spa-typed. Detected spa-types were hospital-acquired t3928, as well as livestock-associated t011, t034 and t2241. No VRE were found.

Conclusion: A contamination of meat with ESBL-producing E. coli and MRSA was confirmed in this study. The large diversity of ESBL producing E. coli could indicate a growing dissemination of ESBL genes in E. coli found in meat products from porcine and bovine origin.

1. Introduction

Contamination of raw meat with pathogens, such as Salmonella spp., Campylobacter spp., Listeria monocytogenes, Staphylococcus aureus or Escherichia coli, can result in adverse effects on human health, these being potential sources for food borne infections or food poisoning. The contamination of food with zoonotic bacteria is just one of many issues in this respect, yet well monitored by national surveillance laboratories. However, resistant bacteria with medical relevance are not monitored. These certainly could carry a risk for consumers, as well as for food handlers working in abattoirs to get colonized or infected (Marshall and Levy, 2011; Seiffert et al., 2013).

Although the use of antibiotics as growth promoters was banned in food animal production in the EU in 2006 (European Parliament and European Council, 2003), resistant bacteria are still detected in meat of livestock animals; however numbers are decreasing (Marshall and Levy, 2011). Nonetheless today antibiotics are still used in veterinary medicine for treatment of sick animals or prophylactic purposes. These antibiotics are occasionally identical to those used in human medicine and are often of high clinical importance. Therefore resistant bacteria in animals can be regarded as an underrated threat for human medicine. Recent studies show that resistant bacteria are not only present in livestock animals, but also in the environment (Reinthaler et al., 2010); even in the open air (Gandolfi et al., 2011). In the worst case scenario these bacteria are resistant to multiple antibiotics, leaving only few agents susceptible and classifying them as multidrug-resistant (MDR). MDR bacteria are by definition resistant to at least one antibiotic drug of three or more antibiotic classes (Canton and Ruiz-Garbajosa, 2011). They represent a huge problem in public health care. The most prevalent MDR bacteria are extended-spectrum-β-lactamase (ESBL) producing Enterobacteriaceae and methicillin resistant S. aureus (MRSA). Less common, but still clinical important pathogens are vancomycin-resistant Enterococci (VRE).
ESBLs are enzymes that are able to hydrolyze third and fourth generation cephalosporins and aztreonam. Usually they are successfully inhibited by beta-lactamase inhibitors like clavulanic acid. Associated resistances to quinolones, tetracyclin and aminoglycosides are common among ESBL-producers (Morosini et al., 2006).

MRSA evades beta-lactam antibiotics by production of the modified penicillin-binding protein 2a (PBP2a) encoded by the meca gene. MRSA are classified according to their origin. Hospital-acquired (HA) MRSA mainly infect older people with long medical records in health care facilities. Community-acquired (CA) MRSA can be found outside hospitals and tend to infect younger people, who are healthy until infection. While coresistance rates are higher in HA-MRSA, CA-MRSA often produce the virulence factor Pantone-Valentine Leukocidin (PVL). Livestock-associated (LA) MRSA are frequently found in nasal swabs from pork and beef (David and Daum, 2010).

VRE are frequent pathogens of nosocomial infections in hospitals. Although other resistance phenotypes exist in VRE, usually the presence of vanA or vanB gene is responsible for their multidrug-resistance.

Apart from increasing mortality, infections caused by MDR bacteria prolong the average length of patients’ hospital stays and raise costs for health care facilities (Lautenbach et al., 2001). Overuse of antibiotics breeds new resistance mechanisms not only in human but also in animal pathogens. This can lead to new ways of spreading drug resistant bacteria by means of the food chain to humans. Resistance genes localized on highly mobile genetic elements are prone to be transferred to other bacteria, e.g. in the human gut (Rolain, 2013).

The research goals of this study were to determine the prevalence of ESBL-producing Enterobacteriaceae, MRSA and VRE in mixed minced meat from porcine and bovine origin. Instead of investigating different kind of meat products, this study focused on minced meat as various animal parts are used for production. Thus getting an extensive picture of the contamination of food products from pork and beef with MDR bacteria was possible.

2. Material and methods

2.1. Sample collection

Between September 2011 and September 2012 one hundred samples of mixed minced meat produced from pork and beef were collected from supermarkets (n = 70) and butcher shops (n = 30) in the city of Graz. Minced meat samples from supermarkets were bought in styrofoam bowls packaged either within or without protective environment or in foil-coated paper. Meat bought from butcher shops was wrapped in foil-coated paper. The samples were transported in coolers to the Institute of Hygiene, Microbiology and Environmental Medicine, Medical University Graz within one hour, stored in a refrigerator at a temperature between 4 and 8 °C and processed for further examination within 24 h.

2.2. Enrichment and identification

The preparation of the food samples was based on the European standard ISO 6887-2:2003 (International Organization for Standardization (ISO), 2003). In order to screen for the maximum amount of MDR bacteria, we selected two enrichment methods: one with peptone broth, the other with thioglycolate bouillon. For the first method 25 g of the meat samples were randomly selected, mixed with 225 mL peptone broth 1% (Oxoid Ltd, Basingsoke, England) and homogenized in a Stomacher® 400 Lab Blender for two minutes. The solution was poured into an Erlenmeyer flask and enriched overnight (16–24 h) in an incubator shaker (Innova 4000, New Brunswick Scientific, Enfield, USA) at 150 rpm at 37 °C. Afterwards a decimal dilution series up to 10–3 (1:1000) was made. Therefore 0.5 mL of the solution was diluted in 4.5 mL sterile, saline solution. Then 0.1 mL from the appropriate dilution was inoculated on chromID™ ESBL (bioMérieux, Marcy-l’Etoile, France), chromID™ VRE (bioMérieux, Marcy-l’Etoile, France) and OXA agar (Oxoid Ltd, Basingsoke, England). ChromID™ ESBL agar was incubated for 24 h at 37 °C; chromID™ VRE and OXA agar for 48 h at 37 °C. Colonies were chosen as described in the manufacture’s manual and identified with MALDI-TOF MS Axima™ Assurance (Shimadzu, Japan) system. For the second enrichment method 1 g of each meat sample was inoculated in 5 mL thioglycolate bouillon and incubated overnight (16–24 h) at 37 °C. A sterile cotton swab was dipped into the thioglycolate bouillon and inoculated on the selective agar mentioned above. Bacteria were identified as described above.

2.3. Genotypic characterization

Phenotypic ESBL-producers were screened for three different beta-lactamase gene families, blao TAM, blao TXY, and blaoCTX M, by PCR and sequencing as described previously (Eckert et al., 2004; Kiratinsri et al., 2008; Zarfel et al., 2013). The ESBL gene family blaoCTX M was screened for the subgroups 1, 2, 8 and 9. MRSA were spa-typed by sequencing according to Ruppitsch et al. (Ruppitsch et al., 2006) and further characterized with Identibac MRSA bacterial genotyping system (Identibac, UK; StaphyType, Alere Technologies GmbH, Germany) as described previously (Monecke et al., 2011).

Furthermore, MLST typing was performed according to the Pasteur Institute schema as described previously (Jauregui et al., 2008). The schema is based on eight housekeeping genes (dinB, icaA, pabB, polB, putP, spa, and icaD). Used Primers are freely accessible at the Institut Pasteur’s homepage (http://www.pasteur.fr; last accessed February 2014).

2.4. Plasmid replicon typing

Plasmid replicon typing was performed using PCR as described previously (Carattoli et al., 2005), which allowed detection of plasmid incompatibility (inc) groups FIA, FIB, FIC, HII, HII-1, I/II, M, N, P, W, T, A/C, F, K, B/O, X, Y, and FIA. 

2.5. Antimicrobial susceptibility testing

For all identified Enterobacteriaceae and S. aureus resistance testing was performed as recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST). For Enterobacteriaceae ampicillin (10 μg), amoxicillin/clavulanic acid (20 μg/10 μg), piperacillin/tazobactam (100 μg/10 μg), cefalexin (30 μg), cefuroxime (30 μg), cefoxitin (30 μg), cefotaxime (30 μg), ceftriaxone (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepime (30 μg), cefepi...
TM paper discs. The inhibition zone diameters were interpreted according to EUCAST guidelines (The European Committee on Antimicrobial Susceptibility Testing, 2013), except for tetracycline and nalidixic acid, which were evaluated in conformity with Clinical Laboratory Standards Institute (CLSI) guidelines (Clinical and Laboratory Standards Institute (CLSI), 2011), since these antibiotics are considered as inappropriate drugs by EUCAST. Isolates tested intermediate to an antibiotic were considered resistant. Phenotypic ESBL-production in Klebsiella spp., E. coli and Proteus spp. were screened with double disc diffusion tests according to CLSI guidelines, using ceftazidime (30 μg), ceftazidime/clavulanic acid (30 μg/10 μg), cefotaxime (30 μg) and cefotaxime/clavulanic acid (30 μg/10 μg). Enterobacter spp. were screened for ESBL production with the combined disc test as described previously (Apfalter et al., 2007).

2.6. Statistical analysis

A two-sample test for equality of proportions with continuity correction was performed with the statistical program R (R version 2.15.2, The R Foundation for Statistical Computing).

3. Results

3.1. ESBL-producing Enterobacteriaceae

E. coli was the only species of ESBL-producing Enterobacteriaceae, found in 20 of the 100 (20%) samples. Genotypic ESBL production was confirmed in 24 isolates with distinct resistance patterns (Fig. 1). All ESBL-producing E. coli isolates were found after enriching the meat samples in peptone broth. The most common CTX-M type, found in 18 of 24 (75%), was CTX-M-1, one of those contained TEM-1 as an additional β-lactamase. Two isolates harbored CTX-M-14 and one CTX-M-32. Genes from other ESBL gene families were TEM-52, found in two isolates, and SHV-12, found in one isolate. One meat sample contained three different types of ESBL-producing E. coli, one carrying CTX-M-1, one CTX-M-14 and one SHV-12. Another meat sample contained two E. coli isolates, one with CTX-M-32 and the other with genes encoding for CTX-M-1. The CTX-M-32 producing isolate also carried genes for the production of the non-ESBL TEM-1.

Resistance to second, third and fourth generation cephalosporins was characteristic among the ESBL-producing E. coli (Table 1). It was unusual that four isolates were susceptible to the first generation cephalexin, but resistant to third generation cephalosporins. All isolates were resistant to ampicillin (100%, 24 of 24), cefuroxime (100%, 24 of 24) or cefotaxime (100%, 24 of 24). Penicillin-inhibitor combinations, like amoxicillin/clavulanic acid (4%, 1 of 24) and piperacillin/tazobactam (4%, 1 of 24), showed excellent efficacy against the ESBL producing E. coli. The same applies to the cephalexin cefoxitin (0%, 0 of 24). No ESBL producing E. coli was resistant to the tested carbapenems, imipenem (0%, 0 of 24) and meropenem (0%, 0 of 24). Coresistance rates to quinolones and aminoglycoside compounds were low. Three cefoxitin (12.5%, 3 of 24), three moxifloxacin (12.5%, 3 of 24), two gentamicin (8.3%, 2 of 24) and no amikacin (0%, 0 of 24) resistant E. coli were found. The coresistance rate among the ESBL producing E. coli isolates was 29.2% (7 of 24) for the drug combination trimethoprim/sulfamethoxazole and 20.8% (5 of 24) for nalidixic acid. The coresistance for tetracycline was as high as 58.3% (14 of 24).

With one exception (5.6%, 1 of 18) all E. coli isolates expressing CTX-M-1 were susceptible to ciprofloxacin and moxifloxacin. One CTX-M-14 producing E. coli isolate (50%, 1 of 2) was resistant to the tested quinolones. Another TEM-52 producing E. coli (50%, 1 of 2) was only intermediately resistant to moxifloxacin and ciprofloxacin. Resistance rates to tetracyclines were high in E. coli with bla genes expressing CTX-M-1 (66.7%, 12 of 18), TEM-52 (50%, 1 of 2) and SHV-12 (100%, 1 of 1). This did not apply to E. coli with CTX-M-14 (0%, 0 of 2) or CTX-M-32 (0%, 0 of 1).

Eleven ESBL-producing E. coli isolates were resistant to three and seven of the isolates were resistant to more than three antibiotic classes, which summarizes to 18 MDR E. coli isolates. One E. coli carrying blaCTX-M-1 and additionally blatem-1 was resistant to twelve tested antibiotics out of seven antibiotic categories and was only susceptible to carbapenems, aminoglycosides and tigecycline.

The E. coli isolates could be assigned to 21 different sequence types (ST). ST7, ST88 and ST539 were each found twice, the remaining 18 STs were only found once.

Plasmid replications of the E. coli isolates revealed ten different inc/rep groups (Table 1). The most common inc/rep groups were FIB (75%, 18 of 24), F (70.8% 17 of 24), II-1y (62.5%, 15 of 24) and Y (29.2%, 7 of 24). The remaining groups were N (four isolates), FIA (three isolates), K (three isolates), B/O (two isolates), H1 (one isolate) and P (one isolate). The number of detected rep/inc groups within the E. coli isolates ranged from one to five. E. coli isolates producing CTX-M-1 were highly associated with inc/rep group FIB and F.

3.2. MRSA

Nine samples (9%, 9 of 100) were tested positive for MRSA. Altogether ten different MRSA isolates were found (Fig. 2), due to the fact that one sample harbored two different MRSA isolates (t011 and t2241). Two of the ten MRSA isolates were detected after enrichment in thioglycolate bouillon and the remaining eight after enrichment in peptone broth. The meca gene was confirmed in all isolates. None of the isolates carried genes for production of Pantone-Valentine Leukocidin (PVL) or Toxie Shock Syndrome Toxin (TSL). Detected spa types were t011, t034, t2241 and t3928. The first three spa types were characterized as LA-MRSA of MLST ST398. The MRSA carrying t3928 was confirmed as an epidemic, HA-MRSA of MLST ST45. In total, nine LA MRSA isolates and one HA MRSA isolate were detected. The most common spa type t011 was found in six (60%, 6 of 10) MRSA isolates, t034 in three (30%, 3 of 10), t2241 in one (10%, 1 of 10) and t3928 in another one (10%, 1 of 10).

While all (n = 9) LA-MRSA isolates with ST398 were resistant to tetracycline, the single HA-MRSA was susceptible to this antibiotic (Table 2). All MRSA isolates were susceptible to norfloxacin, gentamicin, rifampicin, fusidic acid, linezolid and muipirocin.

![Fig. 1. Distribution of the detected ESBL members in the 24 E. coli isolates.](Image)
Four MRSA isolates were resistant to three and five of them to more than three antibiotic classes, defining nine tested MRSA isolates as MDR. One MRSA with MLST ST45 and spa type t3928 was only resistant to two antibiotic classes.

In three samples (MM-15, MM-95 and MM-100 in Tables 1 and 2) both ESBL-producing _E. coli_ and MRSA were found. Two samples had been bought from supermarkets and one from a butcher shop.

### 3.3. VRE

VRE were not found in the meat samples.

### 4. Discussion

This study found ESBL-producing _E. coli_ in 20% of all minced meat samples, which is a significantly higher prevalence than found in a different Austrian study, having previously only rarely found ESBL-producing _E. coli_ in minced beef (3.7%) and pork (3.6%) (Springer and Bruckner, 2012). The ESBL-genes found in the _E. coli_ isolates are from the plasmid encoded ESBL families CTX-M, TEM and SHV. To our knowledge this large diversity of ESBL-producing _E. coli_ has only been described in poultry and retail chicken meat (Leverstein-van Hall et al., 2011), but not in mixed minced meat. Surprisingly no other ESBL producing enterobacteria than _E. coli_ have been found in the meat samples.

The most frequently detected ESBL in this study were members of the CTX-M family, of which 19 (CTX-M-1 and CTX-M-32) belonged to the CTX-M-1 cluster and two (CTX-M-14) to the CTX-M-9 cluster (Canton et al., 2012). The large amount of detected _bla_CTX-M genes shows, that this specific ESBL gene did not only succeed in the human health care sector over _bla_TEM and _bla_SHV, but also in livestock animals. On closer examination the _E. coli_ isolates could be assigned to numerous different MLST sequence types, which reflects the high diversity of strains found in the meat samples.

The rate of ESBL-producing _E. coli_ found in stool samples of healthy volunteers ranges from 3.7% (Valverde et al., 2004) to 4.9% in our region (unpublished results, manuscript under preparation) and some of these _E. coli_ share the same _bla_ESBL_ genes ( _bla_SHV-12_ and _blaCTX-M-14_) as _E. coli_ isolated from minced meat.

The main reservoir for the ESBL gene _bla_TEM-52_ detected in two _E. coli_ isolates, was thought to be _Salmonella_ spp. isolated from humans (Carattoli, 2008). The fact that TEM-52 producing _E. coli_ was found in the meat samples could indicate a horizontal transfer of _bla_TEM-52_ from _Salmonella_ spp. to _E. coli_.

Human urinary tract infections (UTI), which usually begin as an ascending infection from the bowel, are often caused by ESBL-producing _E. coli_ frequently carrying CTX-M-15 (76%) and CTX-M-1 (22%) (Huemer et al., 2011; Pobiega et al., 2013; Zarfel et al., 2013). Both CTX-M genes were found in the ESBL-producing _E. coli_ from minced meat. Compared to CTX-M-15 producing _E. coli_ isolates from human origin (Shibl et al., 2012) resistance rates to quinolones were low in the CTX-M-1 producing _E. coli_ from

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**Table 1**

Antimicrobial resistance pattern (AMR), ESBL gene products, _bla_ESBL_ genes and plasmid rep/loc groups of all 24 _E. coli_ isolates.

<table>
<thead>
<tr>
<th>isolate</th>
<th>sample</th>
<th>AMR pattern</th>
<th><em>bla_ESBL</em> gene</th>
<th>Plasmid replicon types</th>
<th>MLST</th>
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<td>MM-15</td>
<td>AM, CN, CXM, CTX, CAZ, FEP, TE</td>
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<td>ST645</td>
</tr>
<tr>
<td>ESBL-24</td>
<td>MM-100</td>
<td>AM, CN, CXM, CTX, CAZ, FEP</td>
<td>CTX-M-14</td>
<td>11-ty, FIA, FIB, F</td>
<td>ST19</td>
</tr>
</tbody>
</table>

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*a* ESBL, ESBL producing _E. coli_.  
*b* MM, minced meat.  
*c* AM, ampicillin; AMC, amoxicillin/clavulanic acid; TZIP, pipercillin/tazobactam; CN, cephalexin; CXM, cefuroxime; CTX, cefotaxime; CAZ, ceftazidime; FEP, cefepime; CIP, ciprofloxacin; MXF, moxifloxacin; GM, gentamicin; SXT, trimethoprim/trimethoprim; TE, tetracycline; NA, nalidixic acid; C, chloramphenicol.
minced meat. Furthermore all ESBL-producing E. coli isolates were susceptible to imipenem and meropenem. This could be interpreted as a sign that carbapenemase producing Enterobacteriaceae have not yet found their way into meat products in Austria.

There have been also previous reports of MRSA in food products in Europe (van Loo et al., 2007), but to our knowledge HA-MRSA was isolated from meat samples for the first time during the course of this study. The MRSA isolate with MLST ST45 and spa type t3928 was previously detected in a Spanish hospital (Menegotto et al., 2012), but unlike other HA-MRSA this isolate was only resistant to β-lactam antibiotics and aminoglycosides. Nevertheless, it is an alarming scenario that MRSA has entered our food chain, taking into consideration that so far there has been one food borne outbreak involving MRSA (Kluytmans et al., 1995).

Nine of the ten (90%) MRSA isolates belong to MLST ST398, a MRSA strain with the ability to colonize and infect humans (Graveland et al., 2011). The high resistance rates to tetracycline of the MRSA isolates with ST398 found in minced meat are conform to those found in human and non-human MRSA isolates with ST398 (Argudin et al., 2011; Zarfel et al., 2012) Generally, the high resistance rates to tetracycline of the MRSA (90%) and ESBL-producing Enterobacteriaceae is limited to genes in the blaCTX-M family, taking into consideration that so far there has been one food borne outbreak involving MRSA (Menegotto et al., 2012), but unlike other HA-MRSA this isolate was only resistant to β-lactam antibiotics and aminoglycosides. Nevertheless, it is an alarming scenario that MRSA has entered our food chain, taking into consideration that so far there has been one food borne outbreak involving MRSA (Kluytmans et al., 1995).

Aminoglycosides are generally used as a growth promoter and is highly associated with the occurrence of VRE, has been forbidden in the EU since 1997 as a feed additive in all antibiotics used in veterinary medicine in Austria. Therefore all ESBL-producing E. coli isolates from meat products are monitored for bacteria causing zoonosis on a regularly basis. Resistance rates of all antibiotics used in veterinary medicine in Austria are monitored for bacteria causing zoonosis on a regularly basis, MDR bacteria are not covered by this, which could leave the rise of new resistant bacteria in our food chain unnoticed.

5. Conclusions

Resistant bacteria found in minced meat share the same genetic traits as bacteria isolated from humans. The large diversity of ESBL genes in E. coli isolated from minced meat could be evidence of a growing dissemination of ESBL genes in E. coli from meat products from porcine and bovine origin in Austria, although the variety of ESBL producing Enterobacteriaceae is limited to E. coli. Albeit food products are monitored for bacteria causing zoonosis on a regularly basis, MDR bacteria are not covered by this, which could leave the rise of new resistant bacteria in our food chain unnoticed.

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