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Antimicrobial Resistance of *Escherichia coli* Isolated from Ground Beef in Huasca de Ocampo, Hidalgo, Mexico

A. P. Cordero-López, V. Vega-Sánchez, V. M. Martínez-Juárez, J. I. Olave-Leyva, F. R. Gómez-De Anda, & N. E. Reyes-Rodríguez*
Academic Area of Veterinary Medicine and Zootechnics, Institute of Agricultural Sciences,
Autonomous University of the State of Hidalgo, Mexico
*Corresponding author: nydia_reyes@uaeh.edu.mx
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ABSTRACT

The various pathotypes of *Escherichia coli* cause gastrointestinal infections and diarrhea in humans. Cattle have been reported as reservoirs of different strains of pathogenic *E. coli*, where the origin of animal-human transmission is usually based on the food chain. Therefore, the study of different food matrices plays an important role, especially in foods of high demand and consumption worldwide, such as beef and beef products. The present study determined the antimicrobial resistance profile of *E. coli* in ground beef marketed in the municipality of Huasca de Ocampo, Hidalgo, Mexico. In the present study, 10 ground beef samples were collected. The isolated strains were identified by traditional means and molecular by the 16S rRNA gene, the antibiotic sensitivity profile was identified by the Kirby-Bauer method and genotypic identification was performed for the type 1 integrase gene. All strains showed multidrug resistance to different classes of antimicrobials, and the resistance profile yielded a MAR index of 0.64. Of the 13 isolates, 6 (45.15%) were amplified in the presence of the type 1 integrase gene. This cross-sectional study showed a high prevalence of multidrug resistant *E. coli* recovered from ground beef. In addition, the bacterial resistance profile showed that all the isolated strains were resistant to antibiotics of the β-lactam family, while some antibiotics, such as fluoroquinolones, are highly sensitive drugs for the treatment of possible *E. coli* infections in the area studied.

Keywords: food-borne diseases; ground beef; multi-drug resistance; one health

INTRODUCTION

Beef is a high-demand source of protein, ranking third in production worldwide with a contribution of 72 446 000 tons (FAO, 2023). However, the high demand for this protein entails greater risks of biological contamination at different stages of primary processing (Tarekegn *et al.,* 2023). Ground beef, in particular, is one of the products that present the greatest risk due to the mixture of bacteria from the surface of the carcass, the addition of trimmings left over from other carcasses, or the lack of hygienic processes in the equipment (Abayneh *et al.,* 2019). These situations promote ground beef contamination with bacteria of public health importance, such as *Escherichia coli* (including serotype O157:H7), *Listeria monocytogenes*, *Salmonella* spp., and *Campylobacter* spp. (Kaesbohrer *et al.,* 2019; Kassem *et al.,* 2020). Unfortunately, although there is the development of increasingly permeable technologies and hygienic practices in the livestock production industry, there are still developing geographic areas that produce farm animals where food is public health (Ejikeugwu *et al.,* 2021; Moawad *et al.,* 2017).

Escherichia coli is considered a commensal-type bacterium that is related to the microbiota of both animals and humans; however, some strains are considered pathogenic and can cause gastroenteritis, cystitis, meningitis, peritonitis, or even septicemia in the host (Ajuwon *et al.,* 2021; Jamil *et al.,* 2022; Yassin *et al.,* 2017). Furthermore, *E. coli* has the ability to harbor genes that confer antimicrobial resistance, reinforcing the problem that it implies for public health. Only in 2019, *E. coli* was the first pathogen for deaths associated with antimicrobial resistance, being responsible for more than 250,000 deaths associated with antimicrobial resistance, especially third-generation cephalosporin-resistant *E. coli* and fluoroquinolone-resistant *E. coli* (Antimicrobial Resistance Collaborators, 2022).

The presence of pathogenic strains of *E. coli* in animals represents a risk of infection in humans, especially when consuming undercooked meat (Llorente *et al.,* 2014; Martínez-Vázquez *et al.,* 2018). Moreover, meat products have been declared by the CDC (Centers for Disease Control and Prevention) as a route of transmission of antimicrobial resistance between animals and humans, mainly due to the indiscriminate use of antibiotics in the production of food of animal origin (Ghodousi *et al.,* 2015; Vikram *et al.,* 2018). In addition, antimicrobial resistance is increasingly expanding in trophic networks, which

represents an emerging danger due to the therapeutic deficiencies that this implies for the treatment of infections (Kaesbohrer *et al.,* 2019; Obaidat, 2020).

The objective of the present study was the determination of multidrug resistance *E. coli* and the characterization of the isolates in their antimicrobial resistance profile in ground beef samples in the municipality of Huasca de Ocampo, Hidalgo, since there are no previous records in this geographic area, to generate information that will help health authorities to improve the use of antibiotics in beef production.

MATERIALS AND METHODS

Study Area

Huasca de Ocampo, Hidalgo is located at 20° 12′ 10″ north latitude and between 98° 35′ 55″ west longitude, has a production volume of 3977.360 tons of cattle and 2452.020 tons of beef carcasses with an approximate value of $ 4341.41 USD per ton (SIAP, 2023). Huasca de Ocampo is adjacent to Mexico City, a characteristic that allows the exploitation of environmental goods and services related to tourism (OECD, 2019). It has the distinction of "Pueblo Mágico" (Magic Town), a status that grants the area a high flow of tourists related to cultural and gastronomic aspects, a situation that denotes the importance of food safety in the region (Velázquez-García & Bautista-Moedano, 2021; Winiarczyk-Raźniak & Raźniak, 2021).

Sample Collection

Sampling corresponded to cross-sectional monitoring. Ten samples of 50 g of ground beef were collected from 10 sampling points (one sample per point of sale), covering the 10 butcher shops established in Huasca de Ocampo. Samples were collected in November 2021, and the meat was placed in sterile containers and kept at 4 °C for transport (Pungpian *et al.,* 2021), then transferred to the Parasitology and Bacteriology Teaching Laboratory of the Institute of Agricultural Sciences of the Autonomous University of the State of Hidalgo, for processing.

Bacterial Isolation

It was performed as reported by Abayneh *et al.* (2019) with some modifications. 1 g of ground beef was weighed and placed in 15 mL falcon tubes, 3 mL of peptonized water sterile 1% was added to each tube, and the samples were homogenized with vortex and incubated at 37 °C for 24 hours. The sample was then seeded on MacConkey agar MCD LAB® (Mc) and MacConkey agar with sorbitol BD DifcoTM® (McS) at 37 °C for 24 hours. Colonies with morphology corresponding to *E. coli* according to each media were selected (Crecencio *et al.,* 2020; Ajuwon *et al.,* 2021). Presumptive colonies from both agars were seeded on DIBICO® eosin and methylene blue (EMB) agar (Bhoomika *et al.,* 2016). The isolates were incubated at 37 °C for 24 hours and blue-black colonies that showed metallic green luster were selected. Gram staining was performed (Saida *et al.,* 1998) with the HYCEL® Gram stain train for observation by light microscopy at 100x. Isolates were confirmed by standard biochemical tests, such as indole, SIM Agar (Sulfite Indole Motility, DIBICO®), methyl red and Voges-Proskauer (MR-VP DIBICO®), Simmons citrate (DIBICO®) (Ghodousi *et al.,* 2015) and TSI (Triple Sugar Iron Agar, DIBICO®) (Crecencio *et al.,* 2020).

Antimicrobial Resistance Profile

E. coli isolates (n=13) were evaluated using the Kirby-Bauer disk diffusion method (Hudzicki, 2009), Multibac I.D. Gram-negative sensidisks were used (IDlab, Mexico), with test profiles for 12 antibiotics: amikacin (AK) 30 μg, ampicillin (AM) 10 μg, carbenicillin (CB) 100 μg, cephalothin (CF) 30 μg, cefotaxime (CFX) 30 μg, ciprofloxacin (CPF) 5 μg, chloramphenicol (CL) 30 μg, gentamicin (GE) 10 μg, netilmicin (NET) 30 μg, nitrofurantoin (NF) 300 μg, norfloxacin (NOF) 10 μg, and sulfamethoxazole/trimethoprim (STX) 25 μg. The analysis was performed according to the Clinical and Laboratory Standards Institute (CLSI) (Weinstein & Lewis, 2020). The results were expressed by categories of sensitive (S), intermediate (I), and resistant (R), according to the parameters provided by the manufacturer.

DNA Extraction

DNA was obtained using the methodology described by Ribeiro *et al*. (2016). The isolates were inoculated in thioglycolate broth at 37 °C. 1 mL of bacterial culture was taken and centrifuged at 14500 rpm. The pellet was suspended in TE (Tris-HCl [10 mM]: EDTA [1 mM]) buffer. The suspension was lysed in heat for 15 minutes at 100 °C and frozen for 15 minutes at -20 °C, then centrifuged for 10 minutes at 14500 rpm to obtain the supernatant with the bacterial genetic material, which was preserved in freezing at -20 °C for later use.

Presence of Integron

The following primers were used for type I integrase (Intl-1): IntI1F 5' CCTCCCGCACGATGATC 3' and IntI1R 5' TCCACACGCATCGTCAGGC 3' (280 bp) and for the variable region of the integron 5'_CS 5' GGCATCCAAGCAAGCAGCAAG 3' and 3'_CS 5' AAGCAGACTTGACCTGA 3' (Henriques *et al.,* 2006). Previously established PCR conditions were implemented (Henriques *et al.,* 2006; Vega-Sánchez *et al.,* 2014), and amplicons were visualized on 1.5% agarose gel (Miranda-Estrada *et al.,* 2017). The band obtained from the variable region was purified with the Wizard® SV Gel and PCR Clean-Up System purification kit for sequencing, following the supplier's methodology.

Sequencing Identification

To identify the isolates, the sequence of 16S rRNA gene was analyzed. The 16S rRNA gene was amplified

with the primers and the PCR reactions described by Zepeda-Velazquez *et al.* (2023); the presence of an amplicon was verified in 1.5% agarose gels. Purification of the amplified product was carried out using the kit Wizard® SV Gel and PCR Clean-Up System (Promega) and sequenced using the Sanger method at the National Laboratory of Genomics for Biodiversity of the Center for Research and Advanced Studies of the National Polytechnic Institute, Mexico.

Phylogenetic Analysis

The sequences obtained were analyzed with the DNAstar SeqMan software (Lasergene), and compared with the National Center for Biotechnology Information database using the basic local alignment search tool (BLAST).

Data Analysis

The descriptive analysis of the antimicrobial resistance was carried out using Microsoft Excel 2019, and the data were represented in percentages. The multiple antibiotic resistance index (MARI) was calculated from the resistance designations of the isolates, which is calculated using the formula *a/b* where a= the number of antibiotics to which the strain showed resistance and b= the number of antibiotics used in the test (Hadžić-Hasanović *et al.*, 2020). The MARI indicates values close to 1 with greater relevance of the resistance and close to 0 with lesser relevance of the resistance presented by each strain.

RESULTS

A total of 13 isolates were obtained and identified according to morphology, biochemical characteristics, and sequence analysis (Table 1). The total number of isolates (13/13) presented 100% resistance to ampicillin (AM), carbenicillin (CB), cephalothin (CF), cefotaxime (CFX), and nitrofurantoin (NF). An 84.62% (11/13) of the isolates were resistant to Netilmicin (NET) and 69.23% (9/13) to chloramphenicol (CL), while other antibiotics such as amikacin (AK), trimethoprim (STX) presented 46.15% (6/13) and 38.46% (5/13) of resistance respectively. In contrast, gentamicin (GE) presented 46.15% (6/13) sensitivity and only 30.77% (4/13) resistant isolates. Finally, the antibiotics ciprofloxacin (CPF) and norfloxacin (NOF) showed a sensitivity of 53.85% (7/13) and 84.62% (11/13) respectively (Figure 1). As many as 100% (13/13) of isolates were resistant to β-lactams (AM, CB, CF, and CFX) and nitrofuran family (NF), in contrast to fluoroquinolones (CPF and NOF) presented the highest percentage of sensitive strains, and no isolate with resistance to these antibiotics' family. In the case of aminoglycosides (AK, GE, and NET), *E. coli* isolates showed greater resistance activity of 53.85%

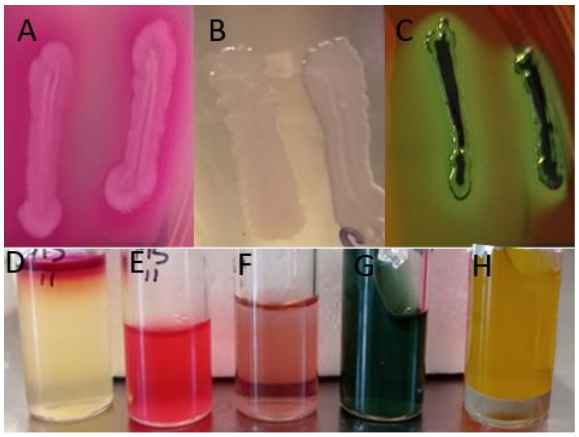

Figure 1. Morphological and biochemical characteristics of *Eschericia coli* obtained from ground meat from butcher shops in Huasca de Ocampo Hidalgo, Mexico. A) Lactose positive colony on MacConkey agar. B) Sorbitol negative colony on sorbitol MacConkey agar. C) Colony with a metallic green glow on EMB agar. D) Positive motility and indole on SIM agar. E) Positive methyl red. F) Negative Vogues-Proskauer. G) Negative citrate. H) TSI: acid-acid surface and gas production.

Table 1. Molecular identification of *Eschericia coli* through analysis of 16S rRNA obtained from ground meat from butcher shops in Huasca de Ocampo Hidalgo, Mexico

Sampled butcher's shop (1 to 10)*	Id strain	Identification	% identity to type strain	GenBank nucleotide accession code
2	Mc2	*Escherichia coli*	98.34	OQ073501
	McS2	*Escherichia coli*	99.81	OQ344332
3	Mc3	*Escherichia coli*	99.46	OP740807
5	Mc5	*Escherichia coli*	99.67	OP986071
	McS5	*Escherichia coli*	99.57	MT427668
6	Mc6	*Escherichia coli*	99.06	MN208223
	McS6	*Escherichia coli*	98.75	KY856932
7	Mc7	*Escherichia coli*	99.93	OP986844
	McS7	*Escherichia coli*	100	OQ344332
8	Mc8	*Escherichia coli*	98.77	MW026012
9	Mc9	*Escherichia coli*	99.48	OP363870
	McS9	*Escherichia coli*	99.25	MK784807
10	Mc10	*Escherichia coli*	99.41	OP740807

Note: *1 to 10= butcher shops sampled in this study. The butcher's shop 1 and 4 do not have any isolates of *E. coli*. Id= Identification of the strain, %= percentage.

than sensitivity of 28.21%. In the phenicol (CL) and sulfonamide potentiated (STX) families, the isolates showed sensitivity activity of 23.08% and 15.38%, respectively. In 100% percent (13/13) of the isolates showed multi-resistance to 3 or more families of the antibiotics evaluated. The resistance patterns with the highest frequency were profile 1 (McS2 and McS7) and profile 11 (Mc7 and Mc10); the rest of the patterns presented only one isolate with this profile. From the resistance profile, the MARI was calculated, which indicates the ratio of the number of antibiotics to which a strain is resistant between the number of antibiotics included in the test. The mean MARI was 0.64; the values indicated that the two strains presented the highest MARI with 0.83. These corresponded to Mc7 and Mc10; conversely, the lowest resistance values were 0.50 for strains McS2, McS7, and Mc9 (Table 2).

Out of the 13 *E. coli* isolates, 6 (45.15%) amplified in the presence of the type 1 integrase enzyme, the amplicon presents a band of 280 bp, and the isolates correspond to Mc3, Mc5, Mc6, Mc7, Mc8, and McS9 (Figure 2). From the sequencing of the variable region of the integron of 3 isolates, we were able to determine the presence of 3 plasmids. The data from the blast search are reported in Table 3. Isolate Mc3 presented the plasmid psh13D178-2, with the InCFII skeleton and harboring the genes *mphA*, bla_{TEM-1}, *aac(3)-IId*, *dfrA1*, *aadA5* and *sul1*. Strain Mc7 presented the plasmid pLSB54-mcr-1, which presents the $bla_{CTX-M-14}$, *oqxA*, *oqxB*, *fosA3*, *floR*, *cmlA1*, *sul1*, *sul2*, *sul3* and *dfr12* genes. And

Table 2. Multidrug resistance patterns and class 1 integron gene arrangement of *Eschericia coli* obtained from ground meat from butcher shops in Huasca de Ocampo Hidalgo, Mexico

Profile	Antibiotic resistance profile	n (%) of isolates	MDR n (%)	MAR index	Integrase (*Intl-1*)	Gene cassettes
1	AM - CB - CF - CFX - NET - NF	2 (15.38)	2 (15.38)	0.5	-	-
2	AM - CB - CF - CFX - CL - NF	1 (7.69)	1 (7.69)	0.5	-	-
3	AM - CB - CF - CFX - AK - NET - NF	1 (7.69)	1 (7.69)	0.58	-	-
4	AM - CB - CF - CFX - NET - CL - NF	1 (7.69)	1 (7.69)	0.58	+	*mphA*, bla_{TEM-1}, *aac(3)-IId*, *dfrA1*, *aadA5* y *sul1*
5	AM - CB - CF - CFX - NET - NF - SXT	1 (7.69)	1 (7.69)	0.58	+	-
6	AM - CB - CF - CFX - AK - CL - NF	1 (7.69)	1 (7.69)	0.58	+	*aac(6')-Ib*, *aada2*, *aph(3')-1a*, bla_{KPC-2}, bla_{OXA-9}, bla_{TEM-1A}, *catA1*, *dfrA12*, *mph(A)*, *sul1*-
7	AM - CB - CF - CFX - NET - CL - NF - SXT	1 (7.69)	1 (7.69)	0.67	+	-
8	AM - CB - CF - CFX - AK - NET - CL - NF	1 (7.69)	1 (7.69)	0.67	-	-
9	AM - CB - CF - CFX - AK - GE - NET - CL - NF	1 (7.69)	1 (7.69)	0.75	-	-
10	AM - CB - CF - CFX - GE - NET - CL - NF - SXT	1 (7.69)	1 (7.69)	0.75	+	-
11	AM - CB - CF - CFX - AK - GE - NET - CL - NF - SXT	2 (15.38)	2 (15.38)	0.83	+	$bla_{CTX-M-14}$, *oqxA*, *oqxB*, *fosA3*, *floR*, *cmlA1*, *sul1*, *sul2*, *sul3* y *dfr12*
	Total	13 (100%)	13 (100%)	0.64	6 (46.15%)	-

Note: AK= amikacin, AM= ampicillin, CB= carbenicillin, CF= cephalothin, CFX= cefotaxime, CPF= ciprofloxacin, CL= chloramphenicol, GE= gentamicin, NET= netilmicin, NF= nitrofurantoin, NOF= norfloxacin, STX= sulfamethoxazole/trimethoprim, n= number of isolates, %= percentage, MDR= Multidrug resistance, Intl-1= Primer selection for class 1 integron integrase gene.

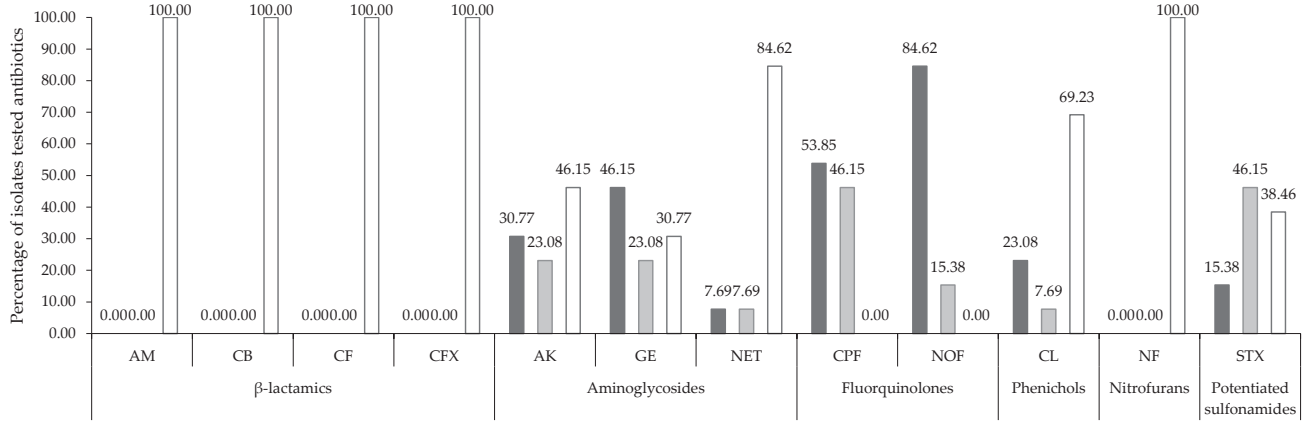

Figure 2. Antibiotic resistance profile by Kirby-Bauer technique in the 13 *Eschericia coli* isolates obtained from ground meat from butcher shops in Huasca de Ocampo Hidalgo, Mexico. AK= amikacin, AM= ampicillin, CB= carbenicillin, CF= cephalothin, CFX= cefotaxime, CPF= ciprofloxacin, CL= chloramphenicol, GE= gentamicin, NET= netilmicin, NF= nitrofurantoin, NOF= norfloxacin; STX= sulfamethoxazole/trimethoprim; S= sensitive, I= intermediate and R= resistant. ■S ■I □R

Table 3. Molecular identification of plasmids by Blast of class 1 integron variable region in *Eschericia coli* isolates

Id strain	Plasmid	Identity (%)	GenBank nucleotide accession code
Mc3	pKL00221_2	98.05	ON461900
Mc7	pLSB54-mcr-1	97.84	MG773376
McS9	pKL00221_2	97.70	OP378664

Note: Id= Identification of the strain, %= percentage.

in the McS9 isolate, the plasmid pKL00221_2 was found, which encodes for the genes: *aac(6')-Ib*, *aada2*, *aph(3')-1a*, *blaKPC-2*, *blaOXA-9*, bla_{TEM-1A}, *catA1*, *dfrA12*, *mph*(*A*), *sul1* (Table 2).

DISCUSSION

The presence of *E. coli* along the meat production chain represents a biological risk of relevance (Kim *et al.,* 2018). The occurrence of this pathogen in livestock production plays an important role in the transmission of foodborne diseases (Castro *et al.,* 2019). In the present study, isolates of *E. coli* were recovered, a relevant situation due to the nature of the samples since meat is considered a perishable food, even more so when the presentation is ground, which allows the homogenization of bacterial loads throughout the product (Abayneh *et al.,* 2019; González-Gutiérrez *et al.,* 2019). However, other authors report a lower prevalence of *E. coli* in similar meat matrices. Petternel *et al*. (2014) reported a lower prevalence of ground beef collected in Austria, with 20% prevalence of *E. coli*. Similarly, Hamed *et al*. (2017) reported 8% prevalence for shiga toxin-producing *E. coli* in ground beef. In this case, the authors determined that these values were higher than those found for other products, such as sausages or beef hamburgers. Some studies even report the absence of *E. coli* in ground beef that has been minced in restaurants, indicating that the finding of this pathogen is related to hygiene deficiencies in meat handling (Beyi *et al.,* 2017). These findings are important because ruminants are one of the main reservoirs of *E. coli* and cause outbreaks of diarrheal diseases (Blount, 2015; Nobili *et al.,* 2017). Therefore, it is necessary to understand transmission and its bacterial resistance to improve animal and human health care (Darphorn *et al.,* 2021). Of the 13 isolates tested, 13 showed multi-resistance; the high frequency of resistance in the strains may result from the widespread use of antibiotics in livestock production farms (Liu *et al.,* 2015). The Kirby-Bauer test showed in our study that 100% of the strains were resistant to antibiotics of the β-lactam family, including ampicillin, carbenicillin, cephalothin, and cephatoxime. These results demonstrate that the isolates maintain a close relationship with the production of extended-spectrum β-lactamases encoded by bla_{TEM}, $bla_{SHV,}$ and bla_{CTX-M} genes, mainly (Galvis & Moreno, 2019). Previously, resistance of *E. coli* to ampicillin has been reported in Peru and Mexico, with values up to 90% in chicken meat (Ruiz-Roldán *et al.,* 2018), cephalothin in up to 75% of isolates recovered from bovine carcasses (Reyes-Rodríguez *et al.,* 2013), resistance up to 80% of cefatoxime in chicken

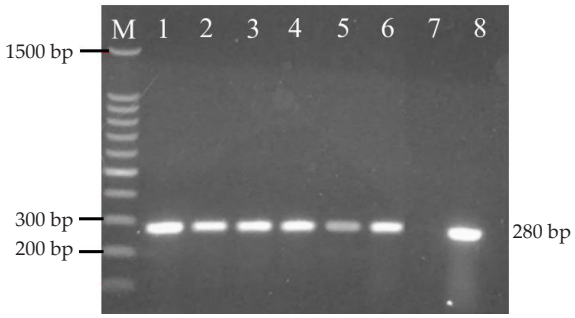

Figure 3. Agarose gel electrophoresis (1.5%) of PCR amplification of the integrase gene in isolates of *Eschericia coli* (280 bp) obtained from ground meat from butcher shops in Huasca de Ocampo Hidalgo, Mexico. Lane M= molecular weight marker, Lane 1-6= isolated from E. coli positive for the integrase gene, Lane 7= control negative, Lane 8= control positive.

meat (Del Rio-Avila *et al.,* 2016), and in carbenicillin up to 72.2% (Fuentes *et al.,* 2013).

In *E. coli*, the presence of genes, such as *aadA*, *aadA5*, *aadA2*, *aac(3)-I*, *aac(3)-IId*, *aac(3)-IV*, *aac(6')-Ib*, *aphA-1*. *aph(3')-1a* and *strA-strB* in *Enterobacteriaceae* isolated from animal foods, such as meat (Liu *et al.,* 2015; Racewicz *et al.,* 2022). In this study, high sensitivity to drugs of the fluoroquinolone family was evidenced; however, in other studies, *E. coli* strains have shown high resistance to these drugs, with values of up to 91.3% in *E. coli* isolates obtained from chicken, beef, and pork meat collected in Italy (Caruso *et al.,* 2018). These results show the genetic diversity of the bacterium in relation to its biogeography, supported by gene transmission strategies such as the acquisition of resistance by plasmids. In beef, plasmid-mediated quinolone resistance has been reported in *E. coli* associated with the presence of genes such as *qnrA1*, *aadA2*, *blaCARB-1*, *mphA*, *floR*, *sul1(3x)*, *tetA* and *dfrA1* (Tyson *et al.,* 2019). The presence of type 1 integrons denotes resistance to sulfonamides, recalling that within the conserved region of these genetic elements, the *sul1* gene is located (Wan & Chou, 2015). In addition, more than 70 cassette genes have been considered in the variable region that can harbor and confer resistance to most β-lactams, aminoglycosides, trimethoprim, rifampicin, chloramphenicol, quinolones, erythromycin and quaternary ammonium compounds (Kaushik *et al.,* 2018). In addition, type 1 integrons have already been reported in meat *E. coli* isolates. Rebbah *et al*. (2018) analyzed 102 *E. coli* isolates, 69 presented class 1 integrons; Sunde *et al.* (2015) found the presence of class 1 integrons in 29 of 241 isolates; and Chen *et al*. (2017) analyzed bovine carcass meat, managing to isolate 28 with presenting the integron. In addition, the presence of integrons detonates anthropogenic contamination, as they are used as an indicator as it is common to find them in human-dominated environments, with prolonged exposure to different selective agents such as antibiotics (An *et al.,* 2018), suggesting that the acquisition of resistance in *E. coli* isolates is a result of interaction between organisms present from human activities. The MARI indices in this study presented maximum values of 0.83 in three strains evaluated in

the antimicrobial resistance profile (Mc7 and Mc10); the values obtained for all strains was >0.2, an indicator of the frequent use of antibiotics in the environment from which the isolates were obtained (Jaja *et al.,* 2020). The results of the present study were similar to those reported by Sadat *et al*. (2022) in *E. coli* isolates from chicken meat, which presented MARI index values in an interval of 0.5-1; however, *E. coli* isolates from beef meat have shown lower MARI index values of 0.13 (Adzitey *et al.,* 2020), indicating considerable variability in the behavior of antibiotic resistance by species.

In all cases, it is relevant to consider that different enterobacteria have diverse mechanisms to respond to environmental pressures to cope with antibiotic treatments, where the gene set is determinant for the development of antibiotic resistance (Alonso *et al.,* 2018; El-Demerdash *et al.,* 2018; Wang *et al.,* 2020). In addition, practices in the livestock production chain play a highly relevant role, where transparency of antibiotic use could improve production processes (Davis *et al.,* 2018). Likewise, the development of public policies focused on antibiotic regulation is necessary in different geographical areas to reduce the spread of antibiotic multidrug-resistant bacteria (Ejikeugwu *et al.,* 2021; Hossain *et al.,* 2022; Nekouei *et al.,* 2018).

CONCLUSION

This cross-sectional study showed a high prevalence of multidrug resistant *E. coli* recovered from ground beef, which places this food as a reservoir of microbiological loads involved in disseminating antimicrobial resistance genes and pathogenic potential in an area of high tourist traffic. In addition, the bacterial resistance profile showed that all the isolated strains were resistant to antibiotics of the β-lactam family, while some antibiotics, such as fluoroquinolones, are highly sensitive drugs for the treatment of possible *E. coli* infections in the area studied.

CONFLICT OF INTEREST

We certify that there is no conflict of interest with any financial, personal, or other relationships with other people or organization related to the material discussed in the manuscript.

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