Isolation of *Escherichia coli* and *Staphylococcus aureus* in raw milk from refrigeration tanks: identification and antimicrobial resistance profiles

Isolamento de *Escherichia coli* e *Staphylococcus aureus* em leite cru de tanques de refrigeração: identificação e perfis de resistência antimicrobiana

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ABSTRACT: *Escherichia coli* and *Staphylococcus aureus* in milk cooling tank reflects a hygienic deficit in animal management, production environment, and milk obtainment. With implications for public health as agents of infection and food poisoning, and the presence of antimicrobial-resistant strains. Therefore, were investigated in cooling tanks with high counts of somatic cells and total bacteria in milk. Microorganisms, in which a profile of resistance to antimicrobials was investigated, and whether there was a similarity in this profile between the strains of the eight dairy properties. Therefore, eighty-eight samples were obtained, and inoculated on Compact Dry® plates. Of this total, 27.27% (24/88) samples tested positive for *E. coli* and 56.81% (50/88) for *S. aureus*. Among 24 *E. coli* strains subjected to disk-diffusion antibiograms, 70.83% were resistant to rifampicin, 50% to ampicillin and 41.67% to cefoxitin and erythromycin, while of the 51 *S. aureus* strains, 94.32% expressed resistance to azetroanam, 86.27% to ampicillin and nalidixic acid, 76.47% to rifampicin and 47.06 % to erythromycin and cefoxitin. A criterion of resistance to over three antibiotics was observed for 8.33% (2/24) of the isolated *E. coli* strains and 17.65% (9/51) of the *S. aureus* strains, characterizing them as multidrug resistant (MDR) strains. Resistance phenotypes displayed high similarity between properties F5 and F6 for *S. aureus*, and properties F6 and F8 for *E. coli* when applying the Jaccard index. The presence of these antibiotic-resistant pathogenic microorganisms indicate flaws in milk production handling and sanitary conditions, representing risk to milk consumers.

KEYWORDS: Raw milk; etiological mastitis agents; antimicrobial resistance.

RESUMO: *Escherichia coli* e *Staphylococcus aureus* no tanque de resfriamento de leite refletem um déficit higiênico no manejo animal, ambiente de produção e obtenção de leite. Com implicações para a saúde pública como agentes de infecção e intoxicação alimentar e presença de cepas resistentes a antimicrobianos. Portanto, foram investigados em tanques de resfriamento com altas contagens de células somáticas e bactérias totais no leite. Microrganismos, nos quais foi investigado o perfil de resistência aos antimicrobianos e se havia semelhança nesse perfil entre as cepas das oito propriedades leiteira. Para tanto, oitenta e oito amostras foram coletadas inoculadas em placas de Compact Dry®, destas 27,27% (24/88) amostras revelaram contaminação com *E. coli*, e 56,81% (50/88) com *S. aureus*. Entre 24 cepas de *E. coli* submetidas a antibiograma por disco-difusão 70,83% foram resistentes a rifampicina, 50% ampicilina, 41,67% cefoxitina e eritromicina, enquanto das 51 cepas de *S. aureus* 94,32% expressaram resistência a azetroanam, 86,27% a ampicilina e nalidixico ácido, 76,47 % a rifampicina, e 47,06% a cefoxitina e eritromicina. O critério de resistência a mais de três antibióticos caracterizou 8,33% (2/24) das cepas de *E. coli*, e 17,65% (9/51) de *S. aureus* como multidroga resistente (MDR). O fenótipo resistência mostrou elevada similaridade entre as propriedades (F5 e F6) para *S. aureus*, e das propriedades (F6 e F8) para *E. coli* aplicando-se o índice de Jaccard. Estes microrganismos patogênicos resistentes a antibióticos, indicam falhas no manuseio e obtenção higiênica do leite, e que estes representam risco aos consumidores do leite.

PALAVRAS-CHAVE: Leite cru; agentes etiológicos de mastite; resistência antimicrobiana.
INTRODUCTION

The world’s milk production was of 851.8 million tons in 2019 in milk equivalents, with an average consumption of 111.6 kg of milk equivalents per inhabitant (FAO, 2020). In Brazil, a total of 24.46 billion liters were produced in the same year, with an average of 734 million liters/year was obtained in the state of Mato Grosso alone, ranking 11th among the most important milk producing states in the country (IBGE, 2019; BRASIL, 2019).

The quality and/or quantity of produced milk are influenced by several factors, such as those linked to milk obtention, transportation and storage, or associated to the producing animals, such as genetic herd potential, management and feeding, while also being influenced by general animal health and that of their mammary glands (COSTA et al., 2019; ARAÚJO et al., 2017; GUIMARÃES et al., 2017). Clinical and subclinical mastitis are noteworthy among animal health alterations. Microorganisms of contagious and environmental origins, respectively, cause this disease (OSTERAS, 2018). Coagulase negative Staphylococcus, S. aureus, Escherichia coli, Streptococcus uberis and S. dysgalactae are frequently reported as bacterial clinical mastitis agents, and S. aureus and Corynebacterium bovis as the agents responsible for subclinical mastitis cases (BETTANIN et al., 2019; OSTERAS, 2018; BI et al., 2016).

Regarding mastitis diagnoses, mastitic milk indicators comprise Somatic Cell (SCC) and Total Bacteria (TBC) counts, with cohort limits established at 500,000 cells/cm³ for SCC and 300,000 CFU/cm³ for TBC, respectively (BRASIL, 2018a). These parameters are, therefore, considered milk hygiene and/or intramammary infection indicators worldwide by official milk control and animal health agencies (EUROPEAN UNION, 2017; BRASIL, 2018a; OSTERAS, 2018).

In addition to conventional microbiological analyses, quick analysis methods like Readycult™ -LMX (BELOTI et al., 2002), Rida Count [Coliforms R 1009] (VASALLO; REYES; CAMBAS, 2013), and 3MTM PetrifilmTM Staph (SOUZA et al., 2015) are routinely applied to microbiological milk analyses. Among these methods, 3MTM PetrifilmTM products are recognized and regulated for foods of animal origin by the Brazilian Ministry of Agriculture, Livestock and Supply-MAPA (BRASIL, 2005). Compact Dry® system products, similar to 3MTM PetrifilmTM products, in these systems, chromogenic substrates are used, are also applied in the microbiological analyses of products of animal origin, such as milk (CASAROTTI et al., 2009).

Regarding the Compact Dry EC® kit, E. coli metabolizes the chromogenic substrate 5-bromo-4-chloro-3-indolyl-β-D-Glycuronic acid (X-Gluc), resulting in light blue colonies (MIZUOCCHI et al., 2016), while the Compact Dry X-SA® kit indicates Staphylococcus aureus as dark blue colonies, resulting from the action of acid phosphatase and β-glucosidase on mannitol and the chromogenic substrate (TERAMURA; MIZOUCHI; KODAKA, 2010).

Several antimicrobials are available for the treatment of mastitis, and failures in this process lead to increased bacterial resistance against usual antibiotics (KRÖMKER; LEIMBACH, 2017; KREWER et al., 2013; CAZOTO et al., 2011). In this regard, studies have been implemented to detect antimicrobial resistance and its mechanisms in several microorganisms, such as E. coli and S. aureus strains isolated from the milk production chain, classifying them as either resistant or multi-drug resistant (MDR) (MOREIRA et al., 2008; MORITZ; MORITZ, 2016). These strains, when present in milk, can lead to dairy products able to trigger difficult to treat toxifications.

The percentages of clinical and subclinical mastitis in dairy cows were reported as 37.5% (30/80), 74.2% (23/31) and 85.2% (92/108) in animals from the cities of Carlinda, Cuiabá and Nossa Senhora de Livramento, in the state of Mato Grosso, Brazil (MARTINS et al., 2006; MARTINS et al., 2010; SILVA; SILVA; BETT, 2017). Concerning S. aureus, this microorganism was the causal agent of 44% of clinical mastitis cases, and 21.51% of subclinical mastitis cases in the Cuiabá microregion (MARTINS et al., 2010), and of 17.2% of subclinical mastitis cases in the municipality of Nossa Senhora de Livramento (MARTINS et al., 2006).

In 2013, Cáceres, a municipality located in the Central-South mesoregion of the state of Mato Grosso, Brazil, was responsible for the production of 9710 liters of cow’s milk/year (SOARES et al., 2017). In this context, the present study aimed to investigate cooling tanks in the dairy region of the municipality of Cáceres presenting high Somatic Cell (SCC), and Total Bacteria Counts (TBC) detected over six months concerning the occurrence of E. coli and S. aureus. The Compact Dry® kit was employed to this end, and the antimicrobial resistance profiles and the similarities between strain resistance profiles, among the eight investigated milk-producing properties were verified for the isolated strains.

MATERIAL AND METHODS

This study was carried out in eight milk production properties located in the municipality of Cáceres, in the central-southern mesoregion of the state of Mato Grosso, Brazil. Raw milk presenting Somatic Cell Counts and Total Bacteria counts (SCC and TBC) higher than the maximum MAPA limit (BRASIL, 2018a) for six months (08/2018 to 01/2019) were analyzed. After 01/2019, weekly samples were collected from the cooling tanks with the aid of a sterile shelf for eleven weeks, from 02 to 04/2019. Three hundred-mL aliquots of raw milk were placed in a sterilized polyvinyl chloride bottle, which was then sealed, identified and maintained at 5°C in an isothermal box and sent to the Food Molecular Microbiology Laboratory, belonging to the Faculty of Nutrition, Federal University of Mato Grosso, for bacteriological analyses. At the time of collection, milk temperature in the sampled cooling tanks of the eight assessed properties was determined with the aid
of a calibrated dipstick thermometer (MINIPA, São Paulo, Brazil - [0 to 100° C]).

At the laboratory, following container asepsis, the samples were homogenized by inversion bottle movements, and a 1 mL- aliquot of the milk diluted in 9 mL of 0.1% Peptone Saline Solution (0.1% SSP), at 10⁻¹ and 10⁻² dilutions of the first 1 mL aliquot dilution, were inoculated onto EC-Compact Dry® plates (CapLab, Brazil), and 1 mL of the 10⁻² dilution were inoculated on X-SA Compact Dry® plates (CapLab, Brazil), which were then incubated at 35 °C for 24 hours. Reddish colonies were characterized as total coliforms, and light blue colonies, as E. coli (MIZUOCHI et al., 2016) on the EC-Compact Dry® plates. Characteristic S. aureus colonies were dark blue (TERAMURA; MIZOUCHI; KODAKA, 2010) on the X-SA-Compact Dry® plates, which were then measured, and the results expressed as Colony Forming Unit per mL (CFU/mL).

The disk diffusion technique was used to analyze in vitro antimicrobial susceptibility. E. coli and S. aureus strains representing property (F) and collection (C) were sown by swarming on Müller-Hinton agar, and disks containing 20 antimicrobial susceptibility.

| Disk Content (µg) | Zone diameter Breakpoints (mm) for each serotype |
|-------------------|-----------------------------------------------|
|                   | *Escherichia coli* | *Staphylococcus aureus* |
|                   | S | I | R | S | I | R |
| Ampicillin        | 10 | ≥17 | 14 – 16 | ≤13 | ≥26 | 21 – 25 | ≤22 |
| Aztreonam         | 30 | ≥21 | 18 – 20 | ≤17 | NR | NR | NR |
| Cefepime          | 30 | ≥25 | 19 – 24 | ≤18 | ≥18 | 15 – 17 | ≤14 |
| Cefotaxin         | 30 | ≥18 | 15 – 17 | ≤14 | ≥22 | ≤21 |
| Ceftiofur         | 30 | ≥21 | 18 – 20 | ≤17 | ≥18 | 15 – 17 | ≤14 |
| Chloramphenicol   | 30 | ≥18 | 13 – 17 | ≤12 | ≥18 | 13 – 17 | ≤12 |
| Florfenicol       | 30 | ≥19 | 15 – 18 | ≤14 | ≥18 | 13 – 17 | ≤12 |
| Imipenem          | 10 | ≥23 | 20 – 22 | ≤19 | ≥16 | 14 – 15 | ≤13 |
| Gentamicin        | 10 | ≥15 | 13 – 14 | ≤12 | ≥15 | 13 – 14 | ≤12 |
| Tetracycline      | 300 | ≥15 | 12 – 14 | ≤11 | ≥19 | 15 – 18 | ≤14 |
| Nalidixic acid    | 30 | ≥19 | 15 – 18 | ≤14 | NR | NR | NR |
| Ciprofloxacin     | 5 | ≥31 | 21 – 30 | ≤20 | ≥21 | 16 – 20 | ≤15 |
| Enrofloxacin      | 5 | ≥21 | 17 – 20 | ≤16 | ≥18 | 15 – 17 | ≤14 |
| Sulfamethoxazole/Trimethoprim | 25 | ≥16 | 11 – 15 | ≤10 | ≥32 | 25 – 31 | ≤24 |
| Sulphonamides     | 300 | ≥19 | 15 – 18 | ≤14 | ≥17 | 13 – 16 | ≤12 |
| Trimethoprim      | 5 | ≥16 | 11 – 15 | ≤10 | ≥16 | ≤10 |
| Nitrofurantoin    | 300 | ≥17 | 15 – 16 | ≤14 | ≥17 | 15 – 16 | ≤14 |
| Azithromycin      | 15 | ≥19 | ≤18 | ≥18 | 14 – 17 | ≤13 |
| Erythromycin      | 15 | NR | NR | NR | ≥23 | 14 – 22 | ≤13 |
| Rifampicin        | 5 | ≥10 | ≤8 | ≥20 | 17 – 19 | ≤16 |

Legend: (NR) Naturally resistance; (S) Susceptible; (I) Intermediary; (R) Resistant.
(E. coli indicators) set in the Brazilian Normative Instruction (IN) N° 76 of 26 November 2018 (BRASIL, 2018b), was applied, while the maximum acceptable limit (LMA) standard recommended by the Institute of Medicine National Research/Council of the National Academies (2003), of 500 or 2.70 Log_{10} CFU/mL was applied for S. aureus.

Similarities were observed regarding strain resistance to the tested antibiotics (Table 1) among the eight evaluated properties. For this assessment, the antimicrobial susceptibility data were converted into a binary matrix, where 1 indicates resistance and 0 indicates absence of resistance or susceptibility. The data regarding the strains (E. coli and S. aureus) from each property (F1, ..., F8) were grouped, and the sets were compared ([F1 x F2], [F1 x F3],...) to verify phenotype similarities applying the Jaccard similarity coefficient, calculated using the PAST software (Unweighted Pair Group Method with Arithmetic Mean). The score for this similarity coefficient ranges from 0 (different) to 1 (similar) according to Sahu; Swain and Kar (2019).

**RESULTS AND DISCUSSION**

Among the eighty-eight raw milk samples obtained from the cooling tanks of the eight investigated farms with high Somatic Cells and Total Bacteria counts for six months, 67.04% (59/88) were contaminated, 27.27% (24/88) with Escherichia coli, and 56.81% (50/88) with Staphylococcus aureus (Table 2). Mixed contamination (E. coli and S. aureus) was observed in 25.42% (15/59) of the positive samples. The exclusive occurrence of only one species was also verified, where 59.32% (35/59) of the samples were contaminated with S. aureus and 15.25% (9/59) with E. coli (Table 2).

It was assumed that 100% of the herd of properties with high SCC and TBC counts in the cooling tanks had subclinical mastitis, similar to the percentages historically observed in other Mato Grosso cities, such as 74.2% in Nossa Senhora do Livramento (MARTINS et al., 2006) and 85.2% in Cuiabá (MARTINS et al., 2010). A high incidence of subclinical and clinical mastitis may be due to a number of factors, such as deficient or non-existent mastitis control programs, cattle overcrowding, unhygienic milking practices and variations in farm locations (DEVI; DUTTA, 2018). Concerning the evaluated properties, inaccuracies such as poor environment hygiene, manual milking, failure to perform pre- and post-dipping processes, or incorrect performance, lack of milker and cooling tank hygiene were observed. Failures of this type were also observed in other dairy properties in the state of Mato Grosso, such as in Nossa Senhora de Livramento (MARTINS et al., 2006), Cuiabá (MARTINS et al., 2010) and Carlinda (SILVA; SILVA; BETT, 2017).

*Staphylococcus aureus* was present in over 50% of the evaluated milk samples (Table 2). Costa et al. (2019) reported a moderate relationship between high somatic cell counts (>700,000 SCC/mL), and mastitis caused by *S. aureus*. The main identified factors associated with mastitis caused by this microorganism are handling deficiencies during milking, in addition to being linked to teat infection; *S. aureus* may be present on milker hands and in their nostrils (GUIMARÃES et al., 2017; KREWER et al., 2013). Bi et al. (2016) observed that *S. aureus* was significantly more prevalent in small properties compared to large ones in China. The present study was carried out on small farms, which may justify the obtained results (Table 2).

**Table 2.** Count in Log_{10} UFC/mL of *Staphylococcus aureus* and *Escherichia coli* in the cooling tanks of milk-producing properties in the central-southern mesoregion of the State of Mato Grosso.

| Farm | F01 | F02 | F03 | F04 | F05 | F06 | F07 | F08 |
|------|-----|-----|-----|-----|-----|-----|-----|-----|
| Collect | AS | EC | SA | EC | SA | EC | SA | EC | AS | EC | SA | EC | AS | EC | SA | EC | AS | EC | SA | EC | AS | EC |
| C01 | 3.91 | 2.95 | 2.78 | 0 | 0 | 0 | 2.76 | 2.48 | 3 | 0 | 3.94 | 2.9 | 3.46 | 0 | 3.19 | 2.67 |
| C02 | 0 | 0 | 3.48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2.26 | 3 | 0 | 3.09 | 2.26 |
| C03 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| C04 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 3.78 | 0 | 3.2 | 0 |
| C05 | 0 | 0 | 0 | 0 | 3 | 2.3 | 0 | 2.6 | 0 | 2.48 | 3.84 | 2 | 0 | 4 | 3.7 | 0 |
| C06 | 0 | 0 | 3.7 | 2 | 3.3 | 2.6 | 0 | 0 | 0 | 2.48 | 2.95 | 2 | 2.11 | 2 | 3.7 | 0 |
| C07 | 3.3 | 0 | 0 | 0 | 3.3 | 0 | 0 | 0 | 2 | 2.3 | 3.04 | 2 | 3.7 | 0 | 3 | 0 |
| C08 | 0 | 0 | 0 | 2.95 | 3.3 | 0 | 0 | 0 | 3 | 4 | 0 | 3.78 | 0 | 2.95 | 0 |
| C09 | 0 | 0 | 3.3 | 0 | 3.3 | 0 | 0 | 0 | 2 | 3 | 0 | 3.7 | 0 | 2.78 | 0 |
| C10 | 3 | 0 | 3 | 0 | 3 | 0 | 0 | 0 | 2.3 | 0 | 3.48 | 2 | 4.34 | 0 | 3.9 | 2 |
| C11 | 3.48 | 0 | 2.04 | 2 | 3 | 0 | 0 | 0 | 2.3 | 0 | 3.3 | 2 | 3.95 | 0 | 4.04 | 0 |

(F) = Farm; (CO) = collect; SA = *Staphylococcus aureus*, and EC = *Escherichia coli*.  

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The occurrence percentages of *E. coli* (29.54%) in the present study are similar to those observed in dairy farms in China (28.6%) (BI et al., 2016), indicating unsatisfactory hygienic conditions (MARTINS et al., 2016). As a pathogen acquired from the environment the main sources of *E. coli* are contact with humidity, mud and animal feces (BETTANIN et al., 2019). A lack of hygiene at the assessed properties may result in contact with fecal material, the main water and raw milk contamination source by this microorganism. Therefore, water quality and effective hygienic practices during milking are crucial in order to avoid raw milk contamination (RIBEIRO et al., 2019).

Property F4 was displayed the lowest number of contaminated samples (Table 2), two, one by *E. coli* and *S. aureus* (CO1), and the other by *E. coli* alone (CO5). This property presented the best hygiene and general state of conservation. The rest of the properties were hygienically deficient concerning milking, milking utensils and cooling tanks, with predominant *S. aureus* detection (Table 2). At F5, in addition to hygienic deficits, one mastitis case was reported, and at F6, milk during the collection period presented strange characteristics, containing odor and dirt. A high detection of both *S. aureus* and *E. coli* isolates were sub- jected to a susceptibility test to 20 antimicrobials belonging to 13 different chemical classes (Table 1). *E. coli* strains isolated herein (51) were sensitive to imipenem, ciprofloxacin and sulfonamide, as well as resistant to 17 other antibiotics, displaying high percentages of resistance to aztreonam (94.12%), ampicillin and nalidixic acid (86.27%), rifampicin (76.47%) cefoxitin (58.85%) and erythromycin (47.06%) (Figure 1). Among the antibiotics employed herein, enrofloxacin, tetracycline, sulfamethoxazole/trimethoprim, ampicillin, gentamicin, ceftiofur, chloramphenicol, erythromycin and sulfonamide are the most reported concerning resistance expressed by *S. aureus* isolated from bovine milk in Brazil (GIRARDINI et al., 2016; BEURON et al., 2014; SILVEIRA FILHO et al., 2014; COSTA et al., 2013; KREWER et al., 2013). Genes encoding different resistance mechanisms (*ermA*, *ermB*, *ermC*, *msrA*, *mecA*, *icaA*, *icaB*, *blaZ*, *tetL*, *tetK*, *tetM*, *aac*, *mepA*, *grrA*, and *gyrA*) have also been reported for *S. aureus* isolated from milk in Brazil (PEREZ et al., 2020; ARAÚJO et al. 2017; GIRARDINI et al., 2016). The presence and circulation of these genes among *S. aureus* isolated from milk samples justify the results presented in Figure 1.
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Figure 1. Distribution of the frequency of resistance to antibiotics, such as: Amoxicillin (AMP), Aztreonam (ATM), Cefepime (CPM), Cefoxitin (FOX), Ceftiofur (TIO), Chloramphenicol (CL), Florfenicol (FFN), Imipenem (IPM), Gentamicin (GEN), Tetracycline (TET), Nalidixic Acid (NAL), Ciprofloxacin (CIP), Enrofloxacin (ENR), Sulfamethoxazole/Trimethoprim (SXT), Sulfonamides (SSS), Trimethoprim (TMP), Nitrofurantoin (NIT), Azithromycin (AZM), Erythromycin (E), and Rifampicin (RD). In 24 strains of E. coli and 51 of S. aureus isolated from milk of cows with subclinical mastitis.

Multidrug-resistant (MDR) strains were also observed, at 8.33% (2/24) among the 24 E. coli isolates, displaying resistance to 11 antibiotics belonging to 10 different chemical classes. Concerning S. aureus, 17.65% (9/51) were MDR to 13 antibiotics belonging to 12 different chemical classes. The appearance of MDR strains in milk is attributed to the indiscriminate use of antibiotics in the treatment of mastitis (KRÖMKER; LEIMBACH, 2017). The presence of these isolates reinforces the importance of choosing the most adequate antimicrobial agents in order to successfully treat mastitis (KREWER et al., 2013).

The detected MDR E. coli and S. aureus strains displayed common resistance to rifampicin, cefoxitin, tetracycline, chloramphenicol, ampicillin, azithromycin and nitrofurantoin. Resistances to imipenem, cefepime, and gentamicin were detected exclusively in E. coli, and resistances to erythromycin, trimethoprim, ceftiofur, sulfamethoxazole/trimethoprim, enrofloxacin and florfenicol were detected only in S. aureus. Resistance to erythromycin in E. coli and to aztreonam and nalidixic acid in S. aureus were not categorized as MDR, which could lead to bias concerning MDR classification, as these species are naturally resistant to these antibiotics.

The Jaccard similarity coefficient was employed to compare similarities or differences in E. coli, and S. aureus strain behavior regarding their phenotypic resistance to the tested antibiotics among the eight investigated properties. The findings indicate that properties F5 and F6 displayed the greatest similarity (0.91) concerning S. aureus antimicrobial resistance (Figure 2, A), differentiated only by resistance to sulfamethoxazole/trimethoprim in strains isolated from property F5. On the other hand, E. coli displayed low similarity among the eight properties, with a maximum of 0.60 among strains isolated from properties F6 and F8 (Figure 2, B). The low similarity among these strains was due to resistance to only chloramphenicol and sulfamethoxazole/trimethoprim, and to azithromycin and tetracycline, expressed respectively, by E. coli strains isolated from F6 and F8. Properties F5 and F6 are physically distant, and properties F6 and F8 are physically close.

The differences and similarities observed between the eight milk producing properties regarding the resistance expressed by the isolated E. coli and S. aureus strains to antibiotics is due to lack of technical assistance from veterinarians and the empirical use of antibiotics by the farm owners. This lack of technical assistance concerning mastitis control also affected the sanitary conditions of the investigated properties, which mostly exhibited hygienic and general conservation deficits, as well as hygienic deficiencies concerning milking, utensils and cooling tanks. Thus, a vicious cycle develops, resulting in reinfections, with high somatic cell and total bacteria counts in raw milk, as well as the presence and high counts of microorganisms like S. aureus and E. coli.
CONCLUSION
The findings reported herein confirm a hygienic deficit in the production of the evaluated dairy basin and potentially mastitic milk. This was indicated by high Somatic Cell (SCC), and Total Bacteria (TBC) counts and confirmed by the presence of *E. coli* and *S. aureus* detected by the Compact Dry® kit. The susceptibility profiles of the isolates indicate incorrect handling of animals presenting mastitis, the indiscriminate use of antibiotics, as the isolates were resistant to 18 antibiotics belonging to 13 different chemical classes, and a high resistance similarity expressed by *S. aureus* strains, representing public health risks.

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DECLARATION OF CONFLICT OF INTEREST
The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

AUTHORS’ CONTRIBUTIONS
All authors contributed equally to the conception and writing of the manuscript. All authors critically revised the manuscript and approved the final version.

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