Review

Shiga-Toxin Producing Escherichia Coli in Brazil: A Systematic Review

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Abstract: Shiga-toxin producing E. coli (STEC) can cause serious illnesses, including hemorrhagic colitis and hemolytic uremic syndrome. This is the first systematic review of STEC in Brazil, and will report the main serogroups detected in animals, food products and foodborne diseases. Data were obtained from online databases accessed in January 2019. Papers were selected from each database using the Mesh term entries. Although no human disease outbreaks in Brazil related to STEC has been reported, the presence of several serogroups such as O157 and O111 has been verified in animals, food, and humans. Moreover, other serogroups monitored by international federal agencies and involved in outbreak cases worldwide were detected, and other unusual strains were involved in some isolated individual cases of foodborne disease, such as serotype O118:H16 and serogroup O165. The epidemiological data presented herein indicates the presence of several pathogenic serogroups, including O157:H7, O26, O103, and O111, which have been linked to disease outbreaks worldwide. As available data are concentrated in the Sao Paulo state and almost completely lacking in outlying regions, epidemiological monitoring in Brazil for STEC needs to be expanded and food safety standards for this pathogen should be aligned to that of the food safety standards of international bodies.

Keywords: STEC; food microbiology; food-borne diseases; VTEC; EHEC; shiga-toxigenic Escherichia coli; bloody diarrhea

1. Introduction

Brazil is one of the largest producers and exporters of food in the world. Animal products, such as beef, poultry, pork, fish, and crops such as corn, soybeans, and rice represent Brazil’s major exports [1]. However, it is a challenge to maintain both high production efficiency and control physical, chemical and microbiological contamination [2]. In addition, the production of different animals and crops may
be carried out in the same geographic region and the use of animal manure as a fertilizer may promote the contamination of fruits and vegetables [3].

The main microorganisms involved in food contamination belong to the Enterobacteriaceae, with Escherichia coli representing a major species. This bacterium represents one of the most extensively studied and was one of the first to be sequenced [4,5]. In addition, Escherichia coli is the main bacterium involved in food contamination in Brazil [6]. It possesses seven pathogenic groups, namely enterotoxigenic (ETEC), enteroinvasive (EIEC), enteropathogenic (EPEC) diffusely adherent (DAEC), invasive adherent (AIEC), enteroaggregative (EAEC), and Shiga-toxin producing (STEC) [7].

These pathogenic groups are involved in outbreaks related to food consumption, and STEC in particular are of importance to public health, potentially causing diarrhea, bloody diarrhea (hemorrhagic colitis), hemolytic uremic syndrome (HUS) and renal injury [8–10]. STEC strains may produce two immunologically distinct toxins: Shiga-toxin type 1 and 2. In addition, STEC strains may have a pathogenicity island, LEE (Locus of Enterocyte Effacement), which encodes the proteins that include those responsible for induction of attaching-and-effacing lesions [11,12].

In Brazil, there are no reports of outbreaks involving STEC. The hypothesis is that: (i) Disease outbreaks are not being recorded due to lack of a centralized reporting system or (ii) disease outbreaks are not being recognized as there is no surveillance system for STEC. Farm animals have been shown to be carriers and contamination of food as well as sporadic STEC infections in humans have been reported [13,14]. In addition, STEC infections have been reported in several South American countries, including an endemic issue in Argentina, which borders on Brazil. The possible reasons for this contrast are the differences in cattle breeds, surveillance systems, more livestock confinement system or a combination of these factors. Moreover, Brazil’s large cattle populations pose a direct risk, as STEC infections are mainly linked to beef and milk consumption. Furthermore, understanding the relationships among the STEC serogroups in the different Brazilian regions and sources (livestock, food, humans) in recent years is crucial for the future monitoring and control strategies concerning this relevant pathogen [4]. There are some documents that have compiled global STEC data based on sites of health institutions and overview by continent [15,16]. However, the prevalence and distribution of STEC serogroups in Brazil remains unclear. In this context, the aim of the present study was to conduct the first systematic review of Escherichia coli STEC with a focus on Brazil and to compare the presence of serogroups detected in food products, animals and humans.

2. Materials and Methods

Data were obtained from online databases PubMed, Scielo, Lilacs, Web of Science and Cochrane BVS. The date interval filter was set from January 2000 to December 2018, accessed between 10 September 2018 and 2 January 2019. Papers were selected according to the Prisma guidelines and flow diagram [17]. Therefore, from each database using the Mesh term entries: “Verotoxigenic Escherichia coli” OR “Verotoxigenic” OR “STEC” OR “Shiga Toxigenic E. coli” OR “Shiga Toxigenic Escherichia coli” OR “Shiga Toxin-Producing Escherichia coli” OR “VTEC” OR “Vero Cytotoxin-Producing Escherichia coli” OR “Verotoxigenic E. coli” OR “Verotoxigenic Escherichia coli” OR “Verotoxin-Producing Escherichia coli” AND “Brazil”. Papers in both English and Portuguese were included in this review. Duplicates were traced and excluded. A total of 161 papers were collected, independent of sample size or culture/detection methods. The full text for each paper was obtained and evaluated individually (Figure 1). Papers were excluded when reporting the characterization of strains isolated from another published article, when assessing decreases in intentional contamination (inactivation methods), and when composed of literature reviews or experimental infection. After the application of these criteria, a total of 80 papers were selected.
3. Results

3.1. Animals

Data on livestock were evaluated in 35 scientific articles, analyzing the presence of STEC through the collection of feces from healthy animals and those with diarrhea (Table 1). The frequency of STEC was heterogeneous and determination of the presence of STEC in herds presents a challenge. STEC contamination rates in cattle ranged from 17.5% to 71.0%, and relevant serogroups O157:H7, O113:H21 and O111 were detected.

In calves, STEC prevalence rates ranged from 12.0% to 20.9%, and serogroups O26, O103 and O111 were detected. These serogroups are monitored in meat by control agencies, such as the EFSA (European Food Safety Authority) and USDA-FSIS (Food Safety and Inspection Service), which require their absence in meat products. In addition, STEC were isolated from 2.7% to 78.3% of sheep and O111 were detected. These serogroups are monitored in meat by control agencies, such as the EFSA and other agencies.

In other species that could possibly act as vectors, STEC rates were 0.7% to 20.4% in wild birds and 0.4% to 1.5% in humans. Other animals were also positive for STEC such as pigs (2.2%) and rabbits (5.1%). In chickens, a study evaluated 110 strains of avian pathogenic *Escherichia coli* (APEC) and noted that stx1 and stx2 were present in 30.9% of the strains, indicating possible dispersion of the stx genes between STEC and APEC. In addition, stx1 and stx2 were detected in 4.7% of poultry litter samples in the south of Brazil (Table 1).

Table 1. Prevalence of Shiga toxin-producing *Escherichia coli* (STEC) isolated in animals reared in Brazil.

| Host          | State                  | Number of Samples | Prevalence | Serotype or Genes Amplified                                      | Author |
|---------------|------------------------|-------------------|------------|-----------------------------------------------------------------|--------|
| Bovine and Buffaloes | Rio Grande do Sul       | 243 feces from dairy cattle | 49%        | O157:H-, O91:H-, O125:H-, O19:H-, O112:H-, O29:H-          | [19]   |
|                | São Paulo              | 182 *E. coli* isolated from milk samples | 12.08%     | stx1 and stx2                                                | [20]   |
|                | São Paulo              | 153 fecal samples  | 25.5%      | O113:H21, O157:H7, O111:H-, O22:H8                          | [13]   |
|                | Rio Grande do Sul      | 243 feces from dairy cattle | 48.9%      | O157, O157:NM, O91:NM, O112:NM                               | [21]   |
|                | Minas Gerais           | 100 water buffaloes | 37%        | O137:H41, O71:H25, O159:H21, O41, O77:H18, O88:H25, O116:H21, O141:H49, O178:H19, O23:H7, O32:H8, O93:H19, O59:H8, O113:H21, O93:H19, O156:H21, O22:H16, O49, O49:H21, O77:H41, O176:H2, O93:H16, O99:H14 | [22]   |
| Host       | State                  | Number of Samples | Prevalence | Serotype or Genes Amplified | Author |
|------------|------------------------|-------------------|------------|-----------------------------|--------|
| Minas Gerais | 205 healthy beef and dairy cattle, and 106 reared goats | 57.5% (goats) 39.2% (beef cattle) 17.5% in dairy cattle | O181:H4, O22:H8, O104:H2, O161:H21, O105:H8, O157:H7, O98:H14, O22:H16, O22:H4, O156:H8, O179:H8, O79:H14, O6:H49, O191:H7, O91:H21, O141:H49, O178:H19, O174:H21, O174:H8, O19:9:H4, O124:H21 | [23] |
| Paraná    | 190 healthy cattle     | 36%               | O6:H34, O10:H42, O22:H8, O22:H16, O41:H2, O74:H42, O79:H1, O82:H8, O98:H41, O110:H2, O113:H21, O117:H8, O124:H11, O159:H21, O174:H21, O175:H21, O178:H19, O179:H8, O181:H4 | [24] |
| Goiás     | 198 rectal swabs      | 72.73%            | stx1, stx2, eaeA | [25] |
| Rio Grande do Sul | 108 carcass swabs | 20.37%            | O157:H7 | [26] |
| São Paulo | 171 fecal samples     | 19.4%             | stx1 and stx2 | [27] |
| São Paulo | 516 fecal samples     | 0.74%             | stx2      | [28] |
| São Paulo | 466 fecal samples     | 9.8%              | O6, O48   | [29] |
| Minas Gerais | 100 fresh fecal samples | 2%              | stx1 and stx2 | [30] |
| Ceará     | Case report            | -                 | stx1      | [31] |
| São Paulo | 118 pigeons and 38 great egrets | 2.5% (pigeons) | stx2      | [32] |
| São Paulo | Case report            | -                 | O137:H6   | [33] |
| São Paulo | 48 sheep               | 52.1%             | O5:H-, O16:H-, O75:H-, O75:H8, O87:H16, O91:H-, O146:H21, O172:H-, OR:H-, ONT:H-, ORT:H16 | [34] |
| São Paulo | 330 feces and 99 carcass samples | 2.72% (Feces), 1.01% (Carcass) | O5, O75, and O91 | [35] |
| Paraná    | Case report            | -                 | O103:H2   | [36] |
| Paraná    | 130 fecal samples      | 50%               | O76:H19 and O65:H- | [37] |
| Goiás     | 115 E. coli strains    | 78.3%             | stx1, stx2 | [38] |
| Mato Grosso do Sul | 205 E. coli strains | 9.75% (stx1), 6.34% (stx2) | O26:H, O111:H, O118:H16 | [39] |
| São Paulo | 139 diarrheic and 205 non-diarrheic fecal samples | 12.7% | O113:H21, O118:H16, O123:H2, O111:NM, O111:H8 | [40] |
| São Paulo | 264 diarrheic and 282 healthy fecal samples | 12% | O71:H7, O71:H10, O48:H17, O111:H19, O121:H2, O132:H51, O173:H-4, O175:H49 | [41] |
| Paraná    | 29 diarrheic and 21 healthy fecal samples | 101 strains | O1, O3, O7, O8, O17, O23, O78, O144, O46, ONT, O26, O35, O103, O117, O123, O124, O153, O15, O128, O175, O119, O4, O156 | [42] |
| Minas Gerais | 850 fecal samples | 20.9% | stx1, eae, fla, toxR, eaeA, eae-1, saa, astA | [43] |
| Chickens  | São Paulo              | 110 APEC E. coli samples | 30.90% | stx1, stx2 | [44] |
| Pigs      | Mato Grosso            | 74 lumen content samples | 2.2% | stx2 | [45] |
| Dogs      | São Paulo              | 25 feces from diarrheic dogs | 48% | O157:H7 and stx1, stx2, eaeA | [46] |
| Cats      | São Paulo              | 40 feces samples and 3 urine infection samples | 0% | - | [47] |
| Dogs and Cats | Paraná               | 50 cat feces and 50 dogs | 0% | - | [48] |
| Rabbits   | São Paulo              | 178 E. coli isolates | 5.05% | O20:H28, O41:H1, O103:H19, O110:H6, O126:H11, O126:H12, O128:H2, O132:H2, O135:H7 | [49] |
| Avian Organic Fertilizers | Paraná    | 40 fertilizers | 4.7% | stx1, stx2 | [50] |
| Stomoxys calcitrans | Rio de Janeiro | 40 Stomoxys calcitrans flies | 15% | stx1, stx2 and eae | [51] |
In other species that could possibly act as vectors, STEC rates were 0.7% to 20.4% in wild birds and 15% in stable flies (*Stomoxys calcitrans*). Prevalence rates in dogs ranged between 0 and 48%, but to date there are no reports of STEC in cats in Brazil.

### 3.2. Food

The Shiga toxin-producing contamination in food was evaluated in 23 scientific articles (Table 2). In six studies, the presence of STEC in beef was assessed, with prevalence rates ranged from 0 to 27.5%, the serogroups O157 and the “big six” (O26, O45, O103, O111, O121, and O145) were not isolated. In milk, the presence of stx1 and stx2 in *E. coli* ranged from 0 to 31.1%, but isolates were not serotyped in these studies [52–54]. However, STEC were detected in 0 to 14% of cheese samples. In addition, the presence of O111, O55, and O157:H7, serogroups frequently linked to food-borne disease outbreaks worldwide [55] were also found in Brazilian cheese.

Contaminated water is increasingly linked to STEC outbreaks associated with fruits and vegetables in Europe [56]. Although STEC contamination is usually related to products of animal-origin, contamination of plant products occurs as a result of cross-contamination [57]. In Brazil, STEC prevalence rates in water ranged from 0.65 to 5.93% with only a single sample testing positive for O157:H7. Water can also be a source of contamination of plant products. For example, in a study with lettuce, 0.76% of samples were contaminated with O157:H7.

### Table 2. Prevalence of Shiga toxin-producing *Escherichia coli* isolated in food produced in Brazil.

| Matrix    | State             | Number of Samples | Prevalence          | Serotype or Genes Amplified | Author |
|-----------|-------------------|-------------------|---------------------|----------------------------|--------|
| Beef      | São Paulo         | 204 bovine carcass swabs | 27.5% (rainy season), 17.5% (dry season) | stx1 and stx2 | [58] |
|           | São Paulo         | 250 raw ground beef samples | 1.6% | O93:H19, O174:HNT | [59] |
|           | São Paulo         | 91 beef samples | 2.1% | stx2 | [60] |
|           | São Paulo         | 70 raw kibe samples | 2.8% | O125:H19, O149:H8 | [61] |
|           | São Paulo         | 552 meat products samples | 0% | - | [62] |
|           | Rio Grande do Sul | 5 beef jerky samples | 0% | - | [63] |
| Milk      | Mato Grosso       | 80 samples | 10% | O83:H19, O26:HNT, O73:H45, O6:H21, O79:H7, O113:H21, O22:H16, O117:H7, O21:H19, O132:H21 | [4] |
|           | São Paulo         | 30 milk samples | 3.3% | stx1, stx2 | [64] |
|           | Minas Gerais      | 670 bovine mastitis milk samples | 8.6% | stx1, stx2 | [65] |
|           | Rio Grande do Sul | 101 milk samples | 31.1% | stx1, stx2 | [52] |
|           | São Paulo         | 62 milk samples | 0% | - | [53] |
|           | Paraná            | 87 milk *E. coli* strains | 0% | - | [54] |
| Cheese    | Minas Gerais      | 50 cheese samples | 14% | O125, O111, O55, O119 | [66] |
|           | Minas Gerais      | 30 cheese samples | 0% | - | [67] |
|           | Goiás             | 60 cheese samples | 6.7% | O157:H7 | [68] |
|           | Minas Gerais      | 147 *E. coli* strains isolated from 38 cheeses | 9.5% | stx1 | [69] |
| Water     | São Paulo         | 133 *E. coli* isolates | 0.75% | stx3 | [70] |
|           | Paraná            | 1850 drinking water samples | 0.65% | rhxA, sla, lpf/A0111, lbt, subAB, cdTV | [71] |
|           | Rio de Janeiro    | 178 *E. coli* isolates | 2.8% | stx1 | [72] |
|           | São Paulo         | 25 water samples | 19 isolates | stx12, rfbE,O157:H7 | [73] |
|           | Rio Grande do Sul | 219 water samples | 5.93% | O157:H7 | [74] |
| Vegetable | Rio Grande do Sul | 260 lettuce samples | 0.76% | O157:H7 | [75] |
| Shrimp meat | São Paulo       | 42 chilled shrimp samples | 0% | - | [76] |
3.3. Human

The presence of STEC contamination in humans was evaluated in 22 scientific articles (Table 3). In five studies, STEC infection was reported in case reports or in samples collected from patients with hemolytic uremic syndrome, and was associated with O26:H11, O103:H2, O165, O157, O157:H7 and O104:H4 (enterohaemorrhagic group with the acquisition of the stx gene). Through whole genome sequencing, the O104:H4 strain in Brazil was found to be similar to a strain isolated from an American citizen diagnosed with hemolytic uremic syndrome (HUS) who had traveled to Germany during the 2011 HUS outbreak [14].

Table 3. Prevalence of Shiga toxin-producing Escherichia coli isolated in cases of foodborne disease in Brazil.

| State                      | Number of Samples | Prevalence | Toxin Type | Serotype                  | Author |
|----------------------------|-------------------|------------|------------|---------------------------|--------|
| São Paulo                  | 1010 children feces samples | 0.3%       | stx1, stx2 | O111:ac                  | [77]   |
|                            | 3 patient strain samples |            |            | O157:H7                  | [78]   |
|                            | 2607 samples from patients with diarrhea | 1.1%       | stx1, stx2 | O55:H9, O93:H9, O118:H16, O157:H7, O111:HNM, O111:H8, O26:H11 | [79]   |
|                            | 1 haemolytic anaemia and 2 faecal with diarrhea samples |            | stx1, stx2 | O103:H2                  | [18]   |
|                            | 377 stools from patients with diarrhea | 0.86%      | stx2       | O69:H11, O157:H7, O165:H7 | [80]   |
|                            | 13 post-diarrheal HUS cases |            | stx1, stx2 | O157:H7, O165:H7         | [82]   |
|                            | 5047 cases of human infection | 4.2%       | stx1, stx2 | O8:1:H19, O24:H14, O26:H11, O71:K8, O91:H14, O100:HNM, O103:HNM, O111:H11, O111:H8, O111:HNM, O118:H16, O123:H2, O123:HNM, O145:HSM, O153:H21, O153:H7, O157:H7, O177:HNM, O178:H19 | [84]   |
| Bahia                      | 1233 children feces | 1.6%       | stx1, stx2 | O26:H11, O21:H21         | [85]   |
|                            | 1233 children feces | 1.6%       |            | O26:H11, O21:H21         | [86]   |
|                            | 1207 children feces | 0.6%       | stx2       | O157:H7, O26:H11, O111:H7 | [87]   |
| Paraná                     | 306 culture stool samples | 0.6%       | stx1, stx2 | O91:H11, O178:H19        | [88]   |
|                            | 141 children fecal samples | 2.8%       | stx1, stx2 | O26:H11, O21:H21         | [89]   |
| Rio de Janeiro             | 307 children samples | 0%         |            | O157:H7                  | [90]   |
|                            | 2 strains          |             |            | O157:NM                  | [91]   |
|                            | 375 children feces samples |            | stx1, stx2 | O157                     | [92]   |
|                            | 400 children feces samples | 0.4%       |            | Not disclosed            | [94]   |
| Espírito Santo             | 560 children feces samples | 0.17%      |            | Not disclosed            | [95]   |
| Paraíba                    | 580 children feces samples | 0%         |            | Not disclosed            | [96]   |

In other studies of diarrhea or healthy subjects, the serogroups predominantly detected were O26:H11, O103:H2, O111 Not typeable (NT), O118:H16, O165:NT and O157:H7 (Figure 2).
Some of these serogroups were verified in animal and food studies in Brazil. For instance, the O111 and O157 serogroups were verified in all three groups. Our hypothesis is that the dispersion of the strains has contaminated all stages of the food chain (pre and post-processing). Moreover, the O103 strains in animals were linked to those found in humans. In contrast, stains O165 and O118:H16 were only detected in human clinical cases.

4. Discussion

The most frequent serogroups described in peer-reviewed papers in samples collected in Brazil are represented in Figure 2. As with studies in other countries, O157:H7 was the serotype most frequently linked to human cases and also had the highest occurrence rates in animal, food and humans in Brazil. However, due to the large-scale outbreaks related to this serotype in the USA in 1982 and 1993, much effort has been invested in methods to detect this specific serotype. It can be readily isolated as non-sorbitol fermenting colonies (the main O157 characteristic) and identified using PCR primers designed specifically for the O157 antigen or the flagellum H7. Consequently, a higher prevalence of O157:H7 in Brazil might also be related to its ease of detection.

Serogroup O111 was also reported in animals, food and humans and has been linked to clinical human cases in Brazil [13,66,77] and worldwide [55,97]. O111 is one of six non-O157 serogroups classified by the USDA-FSIS (2013) as foodborne pathogens that should be monitored during meat production. Considering the serogroups listed by the USDA-FSIS, three: O157, O111, O26:H11 and O103:H2 have been associated with foodborne disease in Brazil (Figure 2). However, two other non-O157 strains, O165 and O118:H16 are not part of the USDA-FSIS “big six”, but were linked to cases of diarrhea, hemolytic uremic syndrome or hemorrhagic colitis in Brazil.

Serogroup O165 has been reported in cases of hemolytic uremic syndrome in Japan [98], and Germany [99]. This serotype has also been identified in cattle in the United States [100]. In addition, its genome has recently been made available on the GenBank/NCBI platform [101] for comparisons and genetic investigations, emphasizing the increasing importance of this serogroup in food production and human infection. Serotype O118:H16 has been linked to foodborne diseases in Germany [102], the United States [103], and its genome sequence was included in GenBank/NCBI in 2014 [104]. Detection of other new STEC in future cases of human disease is likely.

Studies evaluating different cattle feeds indicate that different diets may increase the acid resistance of *Escherichia coli* strains, enabling the bacteria to survive during passage through the human stomach [105]. Strain resistance due to diet may be responsible for the selection of some strains of STEC in Brazilian herds. In addition, a recent study by Acquaotta [106] identified a correlation between STEC infections and climatic differences in North America, where more cases of contamination were reported during warm periods as compared to cold periods. This result emphasizes the need for monitoring and control during food production as Brazil’s tropical climate may increase the risk of STEC infections.
Foods showed the greatest diversity among serogroups, followed by animal sources (Figure 2). This diversity may be related to several factors, such as breeding and production heterogeneity, the nature of the animal and food carrier, the innate (animal) or initial (food) microbial load and the applied methodology (antibiotic use for pre-enrichment, colony morphology and analyzed genes). Moreover, serogroups detected in humans display greater homogeneity, perhaps related to toxin subtypes (stx2e) or other genetic factors including virulence [107,108].

Studies were concentrated mainly in Brazil’s most developed areas and especially in the state of Sao Paulo (Figure 3), with the southern and southeastern regions accounting for 69% of the Brazilian population [6]. However, the majority of animal and grain-production occurs in central Brazil, which is responsible for 34.4% of animal and 42% of grain production [109]. Differences in the number of STEC studies directly reflect national development and demographics. Further studies in the central region would provide a better description of STEC present in livestock and food and would aid in obtaining a more accurate national picture of foodborne STEC risks.

Figure 3. Distribution of STEC assessment studies carried out in Brazil from 2000 to 2018.

Currently, the main legislation in force in Brazil concerning food production is Resolution 12 of 2001 [110], which applies to coliforms in frozen or fresh meat. This resolution, however, does not call for STEC serogroup analyses in any food products. However, the Ministry of Livestock and Food Supply (MAPA) established an internal standard in 2013, requesting E. coli STEC tests for O157 and the “big six” non-O157 in beef destined for export [111]. However, any data about the frequency of STEC isolation has not been released.

The analysis procedure determined by MAPA is based on the methodology used by the USDA FSIS [112], comprising molecular screening followed by cultivation on Rainbow™ agar O157 (Biolog...
Inc, Hayward, USA) and serology of the positive isolates. The use of this methodology assists in production control and monitoring of the main STEC, followed by subsequent implementation of measures to combat contamination. However, this measure is only for beef, and it is necessary to extend the standard to other food matrices as the present review demonstrated high STEC contamination rates in milk and cheese, as well as water. The STEC causing infection and for which microbiological monitoring and control during production is required show some geographical variation and new STEC continually evolve. Instead of continuing to add new serogroups to a long list of food adulterants, microbiological monitoring could instead aim for the absence of strains that possess Shiga-toxin gene(s) in their genome.

Moreover, the improvement and cost reduction of molecular tools such as whole genomic sequencing (WGS), metagenomics, and others will facilitate the understanding of serotype epidemiology and the dispersion of these strains in neighboring countries and in other continents. Epigenetics advances will also improve the understanding of gene expression and the impact of good animal management practices, as well as possible genome mutations that may influence virulence and antimicrobial resistance profiles [113].

5. Conclusions

The epidemiological data presented in this review indicate that O157:H7, O26, O103 and O111 strains, classified as foodborne pathogens and monitored by the USDA-FSIS (USA), U.S. FDA, EFSA (European Food Safety Authority - EU) and MAPA (Ministry of Agriculture, Livestock and Supply - Brazil), are currently circulating in different regions of Brazil. Although no STEC outbreak cases in Brazil have been reported, several animal, food and human studies have indicated the presence of STEC in Brazil and it has been related to several foodborne outbreaks around the world. Thus, improved epidemiological monitoring and food production control is necessary. Novel studies should be financed in regions presenting significant agricultural production, such as Brazil’s central region in order to better assess potential threats and prevent human STEC infections.

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