Prevalence of *Escherichia coli* O157:H7 in foods of animal origin in Ethiopia: A meta-analysis

Ayalew Assefa*

Abstract: *Escherichia coli* O157 is one of the causes of gastrointestinal diseases in developed countries causing millions of illness annually. The occurrence of *Escherichia coli* in foods of animal origin in Ethiopia is arguably high due to many reasons like illegal slaughtering of animals in open fields, unhygienic slaughter practices in the abattoirs, and the risk of disease due to this organism is high because of a widespread tradition of raw meat consumption. The objective of this systematic review and meta-analysis was to pool estimates of the prevalence of the organism in different foods of animal origin which is the first of its kind in the country. The literature search was conducted to identify all published articles reporting the prevalence of *Escherichia coli* in foods of animal origin. From all screened articles, nine studies were eligible for final systematic review and meta-analysis. Because substantial heterogeneity was expected, random-effects meta-analyses were carried out to pool the prevalence of the organism from different foods of animal origin. Prevalence of the organism was found to be 4% (95% CI = 3%—5%) in foods of animal origin. This systematic review and meta-analysis showed the level of contamination of foods of animal origin in Ethiopia is high indicating the need for immediate planning of mitigation strategies and detection methods to reduce its level and impact throughout the country.

Subjects: Microbiology; Nutrition; Epidemiology

Keywords: *E. coli* o157; Ethiopia; meta-analysis; prevalence

1. Introduction

Foodborne pathogens are the leading causes of foodborne human illness and death in the world (Agüeria, Terni, Baldovino, & Civit, 2018). The reason for the increased risk can be due to many reasons; changes in eating habits, mass catering, complex and lengthy food supply procedures...
with increased international movement and poor hygiene practices are few of them (Bevilacqua, Corbo, & Sinigaglia, 2017; Lopez-Campos, Martinez-Suarez, Aguado-Urda, & Alonso, 2012). *Escherichia coli* O157 is one of the virulent strain under the species *Escherichia coli*. It is the leading cause of hemorrhagic colitis, hemolytic-uremic syndrome (HUS) and thrombotic thrombocytopenic purpura (TTP) in man. These illnesses may lead to death due to improper absorption of nutrients and destruction of certain tissues in the target organs (Cobbaut, Houf, Buvens, Habib, & De, 2009; Earley & Leonard, 2006).

Epidemiology of foodborne pathogens especially that of *Escherichia coli* O157: H7 was not well studied in Ethiopia in the past years. However, recently there is an increasing trend of reporting occurrence level of the organism in beef and dairy products (Abebe et al., 2014; Desta, Donata, Gabriella, & Martino, 2016; Haileslassie, Taddele, Adhano, & Kalayou, 2013; Hiko, Asrat, & Zewde, 2008; Tassew, Abdissa, Beyene, & Gebre-Selassie, 2010; Taye, 2013). This may be because beef and dairy products are considered the risk for *E. coli* due to close contact with cattle manure. However, studies showed that the organism had been isolated from mutton, chicken, fish, and vegetables.

*Escherichia coli* O157: H7 is a well-known Shiga toxin-producing bacterium that belongs to the family Enterobacteriaceae. They are reasonably tolerant to different extreme conditions like; minimum pH for growth, heating, irradiation, antimicrobials, ruminant gastrointestinal tract fluids, and even cool nutrient-dilute water as well (Karmali, Gannon, & Sargeant, 2010; Yoon et al., 2004). The organism has gained recognition as an essential food-borne pathogen in recent years. Most strains of *E. coli* isolated from natural sources are harmless commensals, but the O157: H7 serotype had a highly virulent character and regarded as the ugliest *Escherichia coli* strain by WHO (Ayscue, Lanzas, Ivanek, & Gro, 2009; Berry & Wells, 2010). Nomenclature of *Escherichia coli* O157: H7 has been variously described as verotoxigenic *E. coli* (VTec), Shiga like toxin-producing *E. coli* (SLTEC), and currently, Shiga toxin-producing *E. coli* (STEC) (Soeddi et al., 2017). Unlike any other non-pathogenic strains of *E. coli*, *E. coli* O157 has no ability to ferment sorbitol, unable to produce β-glucuronidase, has an attaching and effacing gene (eae) and, produces Shiga toxins (Stxs) that inhibit host protein synthesis (Duffy, Cummins, Nally, O’ Brien, & Butler, 2006; Pennington, 2010; Wilson et al., 2018).

A handful of studies have been conducted in Ethiopia that reports the occurrence level of *Escherichia coli* in foods of animal origin mostly in meat and milk in recent years (Atnafie et al., 2017; Dulo et al., 2015; Mengistu, Abayneh, & Shiferaw, 2017; Mersha, Asrat, Zewde, & Kyule, 2010; Taye, 2013). Most of the studies were conducted in central Ethiopia due to extensive animal farming practices in those areas. There are also studies throughout the country that estimate the prevalence of the organism in foods of animal origin. National level estimation and quantification of *Escherichia coli* occurrence can help responsible bodies for the prevention and control of its occurrence in foods before reaching end users ultimately reducing its impact. To the best of our knowledge, this review is the first of its kind in estimating the pooled prevalence of *Escherichia coli* in foods of animal origin in Ethiopia. The objective of the study was to pool estimates of proportions of occurrence of *Escherichia coli* O157:H7 in foods of animal origin to have a national estimate of the occurrence level of the organism.

2. Materials and methods

2.1. Literature search strategy

The literature search was conducted to identify all published studies reporting the prevalence of *Escherichia coli* O157 in foods of animal origin. It was conducted in electronic databases of PubMed, google scholar, and African Journals Online from April to May 2018. The specific search medical subject heading (MeSH) terms include “*Escherichia coli and Ethiopia*”, “*Escherichia coli prevalence and Ethiopia*”, “*Escherichia coli O157: H7 and Ethiopia*”, “*Escherichia coli O157 and meat in Ethiopia*”, “*Escherichia coli O157 in milk in Ethiopia*”, “*Escherichia coli O157*” AND “Ethiopia” AND “prevalence”. Based on the intensive literature search, a total of 187 pieces of literature that report
the prevalence of *Escherichia coli* in Ethiopia were retrieved. However, only 30 reports on the prevalence of *Escherichia coli* in meat, milk, and related working environmental samples were screened, and nine of them reported the pathogenic strain *E. coli* O157 made it to the final meta-analysis procedure. Study screening strategy and exclusion reasons are presented in Figure 5.

### 2.2. Eligibility criteria and data extraction procedure

All Articles that report the prevalence of *Escherichia coli* O157 in meat and milk in Ethiopia were downloaded and added to Mendeley reference manager. Duplicates were rigorously checked and removed. Quality criteria were developed before starting the review of full papers. Inclusion/exclusion criteria were defined regarding the relevance of the articles to the research questions of interest. The inclusion criteria include an observational study that reports prevalence of the diseases, published article or MSc thesis in University online repositories, reporting the prevalence of the organism only in foods of animal origin from 2000 to 2017, diagnostic methods that employed one of the diagnostic approaches (culture, Latex agglutination, and molecular methods). Articles that met the above criteria were considered for the final meta-analysis and systematic review. Titles were checked twice in both excluded and included databases of the Mendeley reference manager before the start of the data extraction process to avoid missing a valuable report. Those papers considered relevant were retained, and their results were extracted to a prepared data extraction excel sheet. Data extracted from valuable papers include study area, study year, sample size, number of positives, food type examined, diagnosis method used, author’s name, article title, and year of publication.

### 2.3. Statistical analysis

Statistical analyses were done using Stata 14 (StataCorp. 2015. Stata Statistical Software: Release 14. College Station, TX). A simple summary of reports with the prevalence of *Escherichia coli* O157 was done with descriptive statistics. Meta-analysis of prevalence data was analyzed, pooled the estimates and the 95% confidence intervals. Due to the natures of studies, substantial heterogeneity was expected, and a random-effects meta-analysis was done with the estimate of heterogeneity being taken from an inverse-variance model (DerSimonian & Laird, 1986). Between-study heterogeneity was assessed using Higgins’ 1² and Cochran’s Q method. 1² values of 25%, 50%, and 75% were considered low, moderate and high heterogeneity, respectively (Higgins & Thompson, 2002). Subgroup analysis was also conducted by food type sampled, the location of study and diagnosis method used.

### 3. Results

#### 3.1. Descriptive results of eligible studies

From all screened studies, nine articles were eligible for the final systematic review and meta-analysis. Literature was heterogeneous, had inappropriate study designs, unrepresentative sample size, and unreliable diagnostic methods that cannot identify pathogenic strain O157. This diversity, together with the lack of data on other required variables, reduced the datasets substantially. Descriptive summary statistics were calculated to determine the total number of sampled foods and the range of prevalence estimates in different foods. Accordingly, the overall apparent prevalence in all studies estimated 4.91% in all samples examined. A detailed summary of the studies can be found in Table 1.

#### 3.2. Meta-analysis

Due to the expected variation between studies, a random-effects meta-analysis was carried out using the total sample size and number of positives (effect size and standard error of the effect size). The result of the meta-analysis indicated that individual study prevalence estimates ranged from 0% to 10% with an overall random pooled prevalence of 4% (95% CI = 3%—5%). Figure 1 presents the Forest plot derived from the meta-analysis. Between-study variability was high (τ² = 0.01; 1² = 89.06% with Cochran’s Q statistics value of 146.28). Studies weighted approximately equal with weights on individual studies due to high heterogeneity between studies.
Table 1. Summary of studies included in the systematic review and meta-analysis

<table>
<thead>
<tr>
<th>Study (references)</th>
<th>SS</th>
<th>NP</th>
<th>AP (%)</th>
<th>Region</th>
<th>Diagnosis method</th>
<th>Sample Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Abdissa et al., 2017)</td>
<td>1235</td>
<td>6</td>
<td>0.49</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Beef</td>
</tr>
<tr>
<td>(Abdissa et al., 2017)</td>
<td>1247</td>
<td>10</td>
<td>0.80</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Environmental samples</td>
</tr>
<tr>
<td>(Atnafie et al., 2017)</td>
<td>300</td>
<td>8</td>
<td>2.67</td>
<td>Southern Ethiopia</td>
<td>Serological</td>
<td>Beef</td>
</tr>
<tr>
<td>(Atnafie et al., 2017)</td>
<td>330</td>
<td>7</td>
<td>2.12</td>
<td>Southern Ethiopia</td>
<td>Serological</td>
<td>Environmental samples</td>
</tr>
<tr>
<td>(Bekele, Zewde, Tefera, Feleke, &amp; Zerom, 2014)</td>
<td>384</td>
<td>39</td>
<td>10.16</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Beef</td>
</tr>
<tr>
<td>(Beyi et al., 2017)</td>
<td>195</td>
<td>5</td>
<td>2.56</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Beef</td>
</tr>
<tr>
<td>(Beyi et al., 2017)</td>
<td>330</td>
<td>4</td>
<td>1.21</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Environmental samples</td>
</tr>
<tr>
<td>(Dulo et al., 2015)</td>
<td>235</td>
<td>6</td>
<td>2.55</td>
<td>Eastern Ethiopia</td>
<td>Serological</td>
<td>Chevon</td>
</tr>
<tr>
<td>(Haile, Kebede, &amp; Wubshet, 2017)</td>
<td>150</td>
<td>14</td>
<td>9.33</td>
<td>Western Ethiopia</td>
<td>Serological</td>
<td>Beef</td>
</tr>
<tr>
<td>(Haile et al., 2017)</td>
<td>150</td>
<td>11</td>
<td>7.33</td>
<td>Western Ethiopia</td>
<td>Serological</td>
<td>Environmental samples</td>
</tr>
<tr>
<td>(Hiko et al., 2008)</td>
<td>243</td>
<td>6</td>
<td>2.47</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Mutton</td>
</tr>
<tr>
<td>(Hiko et al., 2008)</td>
<td>245</td>
<td>5</td>
<td>2.04</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Chevon</td>
</tr>
<tr>
<td>(Hiko et al., 2008)</td>
<td>250</td>
<td>20</td>
<td>8.00</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Beef</td>
</tr>
<tr>
<td>(Mersha et al., 2010)</td>
<td>120</td>
<td>8</td>
<td>6.67</td>
<td>Central Ethiopia</td>
<td>Molecular</td>
<td>Chevon</td>
</tr>
<tr>
<td>(Mersha et al., 2010)</td>
<td>224</td>
<td>21</td>
<td>9.38</td>
<td>Central Ethiopia</td>
<td>Molecular</td>
<td>Mutton</td>
</tr>
<tr>
<td>(Mersha et al., 2010)</td>
<td>344</td>
<td>13</td>
<td>3.78</td>
<td>Central Ethiopia</td>
<td>Molecular</td>
<td>Environmental samples</td>
</tr>
<tr>
<td>(Bedosa, Shiferaw, Abraha, &amp; Mages, 2018)</td>
<td>200</td>
<td>24</td>
<td>12</td>
<td>Central Ethiopia</td>
<td>Serological</td>
<td>Milk</td>
</tr>
</tbody>
</table>

SS sample size, NP number of positives, AP apparent prevalence.
3.3. Subgroup analysis
Subgroup analyses were done for sample types (beef, milk, mutton, chevon, and environmental swabs like hand swab, knife swab, and working water samples), study location (Eastern, Central, Southern and Western Ethiopia), and diagnosis method used (latex agglutination (serological test) and molecular techniques). Results of the subgroup analysis are depicted in Figures 2, 3, and 4 respectively with forest plot and in Table 2 for the overall statistics.

4. Discussion
This is the first systematic review and meta-analyses on the status of *Escherichia coli* O157 in foods of animal origin in Ethiopia. The review process was limited to foods of animal origin to lower heterogeneity between studies and absence of enough studies in other foodstuffs. This report was from the analysis of data obtained through a systematic review of scientific publications on the organism between 2008 to 2017. Literature was very heterogeneous, had inappropriate study designs, unrepresentative sample size, and different diagnostic methods. Lack of data on the required variables and other factors reduced the number of studies to be included in the final meta-analysis substantially. The final systematic review and meta-analyses were done with nine studies. According to this review, the first published result that reported *Escherichia coli* in foods of animal origin was in 2008 (Hiko et al., 2008). However, from that year onwards an incredible effort has been noted to report the organism’s occurrence in different foods. Studies increased these days regarding number and quality by applying the latest diagnostic techniques like molecular (PCR) methods. The other qualities of studies were sampling not only the food but also working environment like swabs of workers hand, knife and handling equipment. These sampling approaches are appreciated because they are helpful in identifying sources of contamination.

The overall pooled prevalence of *Escherichia coli* O157 was 4% across all samples. This prevalence might seem low; however, the organism is responsible for severe infections and series
Figure 2. Forest plot of sub-group analysis by sample type on the prevalence of Escherichia coli.

Figure 3. Forest plot of sub-group analysis by study location.
Figure 4. Forest plot of subgroup analysis by diagnosis method.

Figure 5. Flowchart of literature search and inclusion/exclusion process.
attention should be given. Ethiopians have controversial raw meat and milk consumption habit (Avery, 2004). The occurrence of the organism in these foods coupled with these habits can be a factor in causing infections in the country. Raw meat consumption like (birndo, dulet, and kitfo) should be handled with caution.

Most of the eligible studies retrieved were conducted in central Ethiopia. This can be due to most milk and meat processing plants are found in this area which can attract the attention of researchers and funders in investigating the occurrence of the organism. Even though this approach may not be wrong at all, it is wise to involve a broader area of research as the condition is worse in rural households where poor hygienic practice and raw food consumption are imminent. According to studies included, the overall pooled prevalence of the organism in central Ethiopia was 4% (95% confidence interval of 3%—5%).

Based on diagnostic techniques used, the prevalence of the organism was lower in molecular diagnostic technique than latex agglutination test. This can be attributed to serologically reactive organisms yet may fail to possess toxins unique to O157 strain detectable by molecular diagnosis approach.

5. Conclusion
In light of the above findings planning of mitigation strategies to reduce the impact of the organism is mandatory. If the country wants to achieve the long-awaited membership to world trade organization, it needs to reduce the occurrence of this and other foodborne pathogens to an acceptable level. Escherichia coli O157: H7 and other known pathogenic strains should be well studied by applying modern methods of diagnosis to precisely estimate the true status in foods of animal origin. Besides, future studies need to bear in mind to include rural households of the country where the level of hygienic practices is expected to be low.

<table>
<thead>
<tr>
<th>Region</th>
<th>Prevalence (95%CI)</th>
<th>I²</th>
<th>Heterogeneity test</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Q</td>
<td>DF</td>
</tr>
<tr>
<td>Eastern Ethiopia</td>
<td>3 (1–5)</td>
<td>*</td>
<td>1</td>
</tr>
<tr>
<td>Southern Ethiopia</td>
<td>21–4</td>
<td>*</td>
<td>1</td>
</tr>
<tr>
<td>Central Ethiopia</td>
<td>4 (3–5)</td>
<td>90.8%</td>
<td>119.61</td>
</tr>
<tr>
<td>Western Ethiopia</td>
<td>8 (5–11)</td>
<td>*</td>
<td>1</td>
</tr>
<tr>
<td>Overall</td>
<td>4 (3–5)</td>
<td>89.06%</td>
<td>146.28</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Sample type</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Beef</td>
<td>5% (2–8)</td>
<td>75.93</td>
<td>5</td>
<td>0.00</td>
</tr>
<tr>
<td>Chevon</td>
<td>3% (1–5)</td>
<td>*</td>
<td>1</td>
<td>0.00</td>
</tr>
<tr>
<td>Environmental sample</td>
<td>2% (1–4)</td>
<td>18.39</td>
<td>4</td>
<td>0.00</td>
</tr>
<tr>
<td>Milk</td>
<td>12 (8–17)</td>
<td>-</td>
<td>0</td>
<td>*</td>
</tr>
<tr>
<td>Mutton</td>
<td>4% (2–6)</td>
<td></td>
<td>2</td>
<td>*</td>
</tr>
<tr>
<td>Overall</td>
<td>4% (3–5)</td>
<td></td>
<td>0.00</td>
<td></td>
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</table>

<table>
<thead>
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<th>Diagnosis method</th>
<th></th>
<th></th>
<th></th>
<th></th>
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</thead>
<tbody>
<tr>
<td>Latex Agglutination</td>
<td>3 (2–5)</td>
<td>88.79%</td>
<td>115.98</td>
<td>13</td>
</tr>
<tr>
<td>Molecular Diagnosis</td>
<td>6 (3–10)</td>
<td>*</td>
<td>2</td>
<td>*</td>
</tr>
<tr>
<td>Overall</td>
<td>4 (3–5)</td>
<td>89.06%</td>
<td>146.28</td>
<td>16</td>
</tr>
</tbody>
</table>

*Indicates omitted results due to lack of enough observations (few studies).
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Conflicts of Interest
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Data Availability
Data Available on Request from the author

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