Review

Antimicrobial resistance patterns of *Salmonella* in Ethiopia: A review

Jelalu Kemal¹*, Berhanu Sibhat¹, Sissay Menkir², Yitagele Terefe¹ and Yimer Muktar¹

¹College of Veterinary Medicine, Haramaya University, Ethiopia.
²Department of Biology, Haramaya University, Ethiopia.

Received 19 September, 2015; Accepted 16 October, 2015

Foods of animal origin have been consistently implicated in sporadic cases and outbreaks of salmonellosis, and are widely acknowledged to be a significant reservoir for *Salmonella*. The usage of growth promoting agents (GPAs) in food animal production is a major public health threat that can contribute to the emergence of antimicrobial resistance bacteria. Extensive and improper use of antimicrobial drugs in food animal agriculture can also establish reservoirs of antimicrobial resistant bacteria, significantly impacting public health. There are an increased number of reports on antibiotic resistance and multiple drug resistant salmonellosis in developing countries caused by both *Salmonella typhi* and non-typhoidal *Salmonella* species. In Ethiopia, there have been studies conducted on salmonellosis which suggest an increase in the antimicrobial resistance of *Salmonella* to commonly used antimicrobials in both public health and veterinary sectors. For example, 31.8% of *Salmonella* isolates from sheep and goat, 44.4% of isolates from camels, 52% isolates from cattle and 87.2% isolates from minced beef and chicken were resistant to one or more antimicrobials commonly used to treat both human and animal infections. High proportion of *Salmonella* isolates developed resistance to the commonly prescribed antimicrobials and this may be a considerable risk in the treatment of clinical case. Therefore, isolation of drug resistant *Salmonella* strains from a wide range of sources, from humans, food animals and animal food products underlines the need for judicious use of antimicrobial agents in both clinical practice and animal husbandry, as well as the need for cooperative and coordinated surveillance and monitoring programs.

**Key words:** Antimicrobial resistance, Ethiopia, food animals, public health, *Salmonella*.

INTRODUCTION

Non-typhoidal salmonellosis is an important zoonotic ailment caused by the genus *Salmonella* which constitutes a major public health burden and represents a significant cost in many countries. The prevalence of the disease in animals is a continuous threat to human health (Murugkar et al., 2005; Razzaque et al., 2009).

*Corresponding author. E-mail: jelaluk@gmail.com. Tel: +251 911 953952.

Author(s) agree that this article remains permanently open access under the terms of the Creative Commons Attribution License 4.0 International License.
Salmonellae are widely distributed in nature and cause a spectrum of diseases in man, animal and birds. Animal origin foods and their products are the commonest vehicles of *Salmonella* to humans (Hoelzer et al., 2011; Abebe et al., 2014). Every year millions of *Salmonella* cases are reported worldwide and the disease results in thousands of deaths (Pui et al., 2011; Tadesse and Tessema, 2014).

The use of antibiotics in food animals selects bacteria which are resistant to antibiotics used in humans. These might be spread via the food to humans and cause human infection (Graham et al., 2007; Vanhoof et al., 2012). Amongst *Salmonella* species, antimicrobial resistance is a well confirmed phenomenon and antimicrobial-resistant *Salmonella* are increasingly associated with the use of antimicrobial agents. Antimicrobials are substances that have significantly contributed to the prevention and treatment of infectious diseases in humans, as well as to many animal species. However, the excess or overuse of antimicrobials can generate genomic selective pressures to enable microbes to adapt and acquire resistance (Yang et al., 2010; Mengistu et al., 2014). Ultimately, increases in bacterial antimicrobial resistance pose a considerable threat to public health, especially for vulnerable populations, including young children (Shea, 2003), the elderly and immunocompromised individuals (Hitti and Wolff, 2005).

Concentrated animal feeding operations (CAFOs) in agricultural practices have evolved to abode food consumption rates with increased agricultural output at the risk of introducing antimicrobial-resistant pathogens into the environment. In addition, several studies have suggested that characteristics of agricultural environmental settings, including animal crowding, CAFO hygiene, temperature, ventilation control and stress, can influence antimicrobial resistance and pathogen risk (Silbergeld et al., 2008). There have been studies conducted in Ethiopia on salmonellosis which suggest an increase in the antimicrobial resistance of *Salmonella* to commonly used antimicrobials in both public health and veterinary sectors (Mache, 2002; Molla et al., 2003; Alemayehu et al., 2004; Argaw et al., 2007; Zewdu, 2008; Beyene et al., 2011; Sibhat et al., 2011; Liyework et al., 2013; Abebe et al., 2014).

The presence of resistant organisms in food and food products for consumption is a safety concern to the population and therapeutic concern for the physicians which might pose prolonged treatment in cases of outbreaks, delayed recovery or treatment failure (Vanhoof et al., 2012; Silbergeld et al., 2008). Information on the antimicrobial resistance pattern of the *Salmonella* isolates could be useful for successful treatment, as well as planning strategic use of drugs to minimize resistance in the future. Although the disease being one of the most common zoonotic concern in the country, surveillance and monitoring systems are not in place and antimicrobial profile of the isolates has not been sufficiently studied and portrayed. The purpose of this paper is to review the prevalence and antimicrobial resistance patterns of *Salmonella* isolates conducted in Ethiopia.

**OVERALL VIEW OF SALMONELLOSIS**

**Evolution of Salmonella**

A non-human *Salmonella* spp., *Salmonella choleraesuis*, was isolated from a swine's intestine by Theobald Smith (1859-1934) under the direction of Daniel E. Salmon (1850-1914) in 1885 (Galantis et al., 2006). The genus *Salmonella* was named after Daniel E. Salmon who first reported the isolation of *Salmonella* from a pig in 1885 and named the organism Bacterium choleraesuis (currently known as *S. Choleraesuis*). It is conjectured that *Salmonella* and *Escherichia coli*, which evolved from a common ancestor emerged about the time of the emergence of mammals, and emerges as mammalian and avian pathogens through the acquisition of pathogenicity islands and of a virulence plasmid plus through variation in lipopolysaccharide antigens (Wray and Wray, 2001). It is hypothesized that accumulation of single mutations, insertions or deletions with the genome of modern-time *Salmonella* appears to have generated many pseudo genes, suggesting its recent evolutionary origin (Papagrigrorakis et al., 2007).

**Salmonellosis and pathogenesis**

The clinical manifestation of *Salmonella* infection presents as salmonellosis, an enteric condition which ranges in severity from self-limiting gastroenteritis to septicemia. The severity of disease depends heavily on the host susceptibility and the virulence of the serovar. Globally, *Salmonella* asymptomatic carriage is experienced in 5% of the human population (Perreten et al., 2005).

With association to disease outcome, strains of *Salmonella* are grouped as typhoidal and non-typhoidal organisms (Kohinur et al., 2010). Infections from specific human pathogens, *Salmonella typhi* and *Salmonella paratyphi*, result from the ingestion of fecal-contaminated consumables, e.g. food or water and contact with current or chronic carriers of typhoid fever. Typhoid fever is a global health issue of prominent public health concern. Worldwide, typhoid results in nearly 22 million cases each year with a case-fatality rate ranging from 10 to 35% (Maskalyk, 2003; Date et al., 2014).

*Salmonella* avoid host defense in the stomach and reach the intestines, and interact with the non-phagocytic cells such as the epithelial cells of the intestinal mucosa (Henselm, 2004). They adhere to the intestinal epithelial cells by adhesive structures (fimbriae) that promote
binding and invade epithelial cells to provoke gastroenteritis. The organisms have virulence factors such as virulence-plasmids, toxins, fimbriae and flagella that help in establishing an infection (Alphans et al., 2005). Pathogenicity is mediated by certain factors such as strain virulence, infectious dose, route of infection and host susceptibility. Microfold (M) cells are the target cells of Salmonella pathogenicity (Ohl and Miller, 2001). Some of the mechanisms of pathogenesis are bacterial mediated endocytosis, neutrophil recruitment and migration, epithelial cell cytokine secretion, fluid and electrolyte secretion, and systemic infection.

Salmonellosis in man

With respect to human disease, Salmonella serotypes can be divided into three groups that cause distinctive clinical syndromes, typhoid fever, bacteremia and enteritis (Santos et al., 2001). The non-typhoid Salmonella serotypes can cause protean manifestations in humans, including acute gastroenteritis, bacteremia and extra intestinal localized infections involving many organs (Chiu et al., 2004). Within Salmonella enterica subspecies I (S. enterica subspecies enterica), the most common O-antigen serogroups are A, B, C1, C2, D, and E. Strains within these serogroups cause approximately 99% of Salmonella infections in humans and warm-blooded animals. Serotypes in other subspecies are usually isolated from cold-blooded animals and the environment, but rarely from humans (Velge et al., 2005). The broad host-range Salmonella serovars are prevalent within warm-blooded animal populations that make up the human food supply and bacterial transmission generally results from consumption of raw or undercooked food products (Jones, 2005).

Salmonellosis in animals

Salmonella serotypes have a broad host range (Santos et al., 2001) and prevalent in the warm blooded animal population including rodents. Reptiles kept as pets, such as turtles, iguanas, other lizards and snakes, are often identified as non-food sources of infection. Some serotypes are highly adapted to animal hosts, such as Salmonella gallinarum in poultry and Salmonella abortus-ovis in sheep. Many non-typhoidal Salmonella strains, such as Salmonella typhimurium and Salmonella enteritidis, infect a wide range of animal host including poultry, cattle and pigs (Ohl and Miller, 2001). These serotypes generally cause self limiting gastrointestinal infections usually less severe than enteric fever in humans. However, they also have the capacity to produce typhoid-like infections in mice and in humans or asymptomatic intestinal colonization in chickens (Velge et al., 2005).

Salmonella in food animals in Ethiopia

Foods of animal origin, especially poultry and poultry products, including eggs, have been consistently implicated in sporadic cases and outbreaks of human salmonellosis, and chicken products are widely acknowledged to be a significant reservoir for Salmonella (Panisello et al., 2000).

In Ethiopia, there is no Salmonella serotype and antimicrobial resistance surveillance and monitoring system, therefore the available information are fragmented and made available through individual publications. One study, conducted on chicken and different chicken products in Ethiopia indicated the presence of different serotypes of Salmonella (Molla et al., 2003). In that study out of the total 80 Salmonella isolates, 8 different serotypes were identified of which Salmonella braenderup was the most frequent followed by S. typhimurium var. copenhagen, Salmonella anatum, Salmonella kottbus and Salmonella typhimurium. Other serotypes isolated include Salmonella bovismoribicans, Salmonella hadar and Salmonella infantis. S. braenderup, S. anatum and Salmonella newport appear to be the major Salmonella serotypes associated with chicken meat and chicken meat products around Addis Ababa (Zewdu, 2008).

Health impact of salmonellosis

Salmonella is one of the eight microorganisms in the European Union Zoonoses Monitoring Directive, which shows a disease considered to have a high impact on human health in the Union (Lazarus et al., 2007). S. enteritidis is transmitted to the human food supply through eggs of hens that appear healthy (Porwollik et al., 2005). Contamination with Salmonella in poultry products can occur at multiple steps along the food chain, which includes production, processing, distribution, retail marketing, handling and preparation (Cui et al., 2005).

In resource deprived settings of Africa, enteric fever is a public health concern (Kariuki, 2008) with an incidence of 10 to 100/100,000 cases per year (Crump et al., 2004). Of the non-typhoidal salmonellaosis, S. enteritidis and S. typhimurium are common (Gordon et al., 2008; Tadesse and Tessema, 2014), and in 2002 each accounted for approximately 25% of the human isolates (Galánis et al., 2006). As Salmonella was reported to be highly invasive (Beyene et al., 2011) and multi drug resistant (Beyene et al., 2011; Tadesse and Tessema, 2014), it could be a serious cause of morbidity and mortality in children. Of the total isolates obtained from stool samples of carriers, Salmonella could be of significant public health concerns which was a cause of an outbreak in Gondar College of Health Sciences, Ethiopia where 79 (23%) students had manifested the disease (Tadesse and Tessema, 2014). In Ethiopia as in other developing countries, it is difficult
to evaluate the burden of salmonellosis because of the limited scope of studies and lack of coordinated epidemiological surveillance systems. In addition, underreporting of cases and presence of other diseases considered to be of high priority may have overshadowed the problem of salmonellosis (Asrat, 2008).

Antimicrobial resistance and Salmonella

Global trends in antimicrobial resistance patterns

Feeds have been responsible for the infection of poultry with multidrug-resistant non-typhoid Salmonella in several industrialized countries. In food animal production, antimicrobials are administered for therapeutic means, for treatment of infection, prophylactic and non-therapeutic purposes for growth promotion and improved feed efficiency (Wegener, 2003). The use of growth promoting agents (GPAs) in feed preparations or water supplements illustrate the largest segment of antibiotic use in poultry production. The usage of GPAs in food animal production is a major public health threat, because this practice can contribute to the emergence of antimicrobial resistance worldwide (Silbergeld et al., 2008; Walsh and Fanning, 2008).

Chronic low-level doses of antibiotics and characteristic of GPAs administered in the animal production environment encourage the elimination of susceptible bacteria and yield the selections and expansion of resistant-bacterial population. Many drugs used in veterinary medicine have identical analogs that are used in human medicine (Smith et al., 2005). Animal-derived antimicrobial-resistant bacteria can colonize the intestinal flora of humans. Ultimately, extensive and improper use of antibiotic drugs in food animal agriculture can establish reservoirs of antimicrobial resistant bacteria, greatly impacting public health (Levy and Marshall, 2004; Afema et al., 2014).

In developing countries, household subsistence farming is common, which means that a large proportion of the population has close contact with food animals; therefore, if resistant organisms are common in animals, the chance that they will be transmitted to human beings is more likely (Okeke et al., 2005).

Resistance patterns in Ethiopia

Antimicrobial resistance is a global problem in general, but it might be more severe in Ethiopia where there is lack of antimicrobial resistance assessments of Salmonella and lack of rigorous regulations, but there is easy access of antimicrobials for purchase of people without prescription and incomplete treatment courses as the result of patient non-compliance (Beyene et al., 2011).

There have been studies conducted in Ethiopia on salmonellosis (Tables 1 and 2) which suggest an increase in the antimicrobial resistance of Salmonella to commonly used antimicrobials in both public health and veterinary sectors (Mache, 2002; Molla et al., 2003; Alemayehu et al., 2004; Argaw et al., 2007; Beyene et al., 2011; Sibhat et al., 2011; Liyuwork et al., 2013; Dagnew et al., 2013). A study by Beyene et al. (2011) detected multiple drug resistant Salmonella organisms in their study on aetiology of febrile and diarrheic illness in Ethiopian children focusing on Salmonella. According to Mache (2002), Salmonella was one of the major causes of diarrhoea in humans. This together with tradition of raw meat consumption and indiscriminate use of antimicrobials signifies the importance of salmonellosis in the country.

In a study conducted by Behailu and Mogessie (2009), about 70% of the isolates had varying resistance to the tested antibiotics. Multiple drug resistance was observed in over 30% of the Salmonella isolates. High proportion of Salmonella isolates developed resistance to the commonly prescribed antimicrobials and this may be a considerable risk in the treatment of clinical cases (Addis et al., 2011). In addition, according to Sibhat et al. (2011) out of the 87 isolates, 18 (20.7%) Salmonella serovars consisting of Newport (n = 14), Anatum (n = 3) and Eastbourne (n = 1) were resistant to two or more antimicrobials. Among the antimicrobial resistant Salmonella serovars, S. Newport was multidrug resistant (15.6%) and exhibited resistance to streptomycin, sulphisoxazole and tetracycline.

PREVENTION AND CONTROL OF SALMONELLOSIS

Prevention of salmonellosis by the implementation of hygiene measures is difficult and use of antibiotics may give rise to the emergence of resistance problems (Mastroeni and Menager, 2003). Reducing Salmonella prevalence requires a multi-hurdle approach at all stages of breeding, hatching, grow-out, transportation and processing. Attenuated DNA recombinant live Salmonella vaccines, combined with comprehensive control strategy in animals, feed and animal food stuffs will help to reduce salmonellosis. Additional measures to control secondary contamination could be prevention of contamination by cleaning and disinfection, hygiene of personnel and proper processing. Growth of micro-organisms in meat and poultry products can be controlled by maintaining a cold chain at 10°C, especially for Salmonella during transport and storage (Coleman et al., 2003).

CONCLUSION AND RECOMMENDATIONS

The multidrug resistance profile of reviewed studies indicated that many of the isolates were resistant to two
### Table 1. Antimicrobial resistance profiles of *Salmonella* isolates in animals, Ethiopia.

<table>
<thead>
<tr>
<th>Year</th>
<th>Location</th>
<th>Species</th>
<th>No. of sample</th>
<th>No. of isolates tested</th>
<th>Resistant No. (%)</th>
<th>MDR No. (%)</th>
<th>Predominant serovars isolated (No.)</th>
<th>Common resistance pattern (No.)</th>
<th>Maximum drug resisted</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>1999/2000</td>
<td>Debre Zeit</td>
<td>Cattle</td>
<td>1290</td>
<td>25 (1.93)</td>
<td>13 (52.0)</td>
<td>13 (52.0)</td>
<td>Mishmar HaEmek (11)</td>
<td>AMP, SMX, TIC</td>
<td>6</td>
<td>Alemayehu et al. (2004)</td>
</tr>
<tr>
<td>2001/2002</td>
<td>Dire Dawa, Jijiga</td>
<td>Camel</td>
<td>714</td>
<td>116</td>
<td>52 (44.80)</td>
<td>9 (33.62)</td>
<td>Braenderup (23), Typhimurium (5)</td>
<td>AMP, STR, SXT, SMX, TMP, SPC</td>
<td>8</td>
<td>Molla et al. (2004)</td>
</tr>
<tr>
<td>2003</td>
<td>Addis Ababa, Debre Zeit</td>
<td>Chicken, giblet</td>
<td>378</td>
<td>80</td>
<td>51 (63.7)</td>
<td>42 (52.5)</td>
<td>Typhimurium var Copenhagen (24), Anatum (15)</td>
<td>AMP, AMX-CAL, CHL, FEN, SPC, SMX, TET (18)</td>
<td>8</td>
<td>Molla et al. (2003)</td>
</tr>
<tr>
<td>2003/2004</td>
<td>Addis Ababa</td>
<td>Food item</td>
<td>1200</td>
<td>98</td>
<td>32 (32.7)</td>
<td>23 (23.5)</td>
<td>Newport (41), Braenderup (12)</td>
<td>STR, AMP, TET, SXT, SPC</td>
<td>8</td>
<td>Zewdu (2008)</td>
</tr>
<tr>
<td>2004/2005</td>
<td>Debre Zeit</td>
<td>Pigs</td>
<td>501</td>
<td>94</td>
<td>74 (78.7)</td>
<td>69 (73.4)</td>
<td>Hadrar (38), Kentucky (15)</td>
<td>TET, STR, NIT, NA, CIP, SXT</td>
<td>11</td>
<td>Molla et al. (2003)</td>
</tr>
<tr>
<td>2004/2005</td>
<td>Addis Ababa</td>
<td>Pigs</td>
<td>278</td>
<td>120</td>
<td>-</td>
<td>57 (32.9)</td>
<td>Hadrar (46), Eastbourne (39)</td>
<td>NIT, STR, TET</td>
<td>8</td>
<td>Argaw et al. (2007)</td>
</tr>
<tr>
<td>2009</td>
<td>Addis Ababa</td>
<td>Poultry, cattle</td>
<td>730</td>
<td>51</td>
<td>36 (70.0)</td>
<td>15 (29.4)</td>
<td>-</td>
<td>AMX, AMP, CIP, GEN, KAN</td>
<td>7</td>
<td>Behailu and Mogessie (2009)</td>
</tr>
<tr>
<td>2009</td>
<td>Debre Zeit</td>
<td>Cattle</td>
<td>800</td>
<td>87</td>
<td>18 (20.7)</td>
<td>-</td>
<td>Anatum (54), Newport (18)</td>
<td>STR, SXT, TET</td>
<td>3</td>
<td>Sibhat et al. (2011)</td>
</tr>
<tr>
<td>2010</td>
<td>Addis Ababa</td>
<td>Cattle</td>
<td>195</td>
<td>21</td>
<td>21 (100.0)</td>
<td>10 (47.6)</td>
<td>-</td>
<td>AMP, STR, TET, CEP</td>
<td>8</td>
<td>Addis et al. (2011)</td>
</tr>
<tr>
<td>2011</td>
<td>Bahir Dar</td>
<td>Cattle</td>
<td>186</td>
<td>28</td>
<td>11 (39.3)</td>
<td>4 (14.3)</td>
<td>Typhimurium (6), Newport (6)</td>
<td>AMP, GEN, NOR, STR, TET, TMP, CHL</td>
<td>8</td>
<td>Alemu and Molla (2012)</td>
</tr>
<tr>
<td>2011</td>
<td>Addis Ababa</td>
<td>Dairy items</td>
<td>384</td>
<td>6</td>
<td>6 (100.0)</td>
<td>3 (50.0)</td>
<td>-</td>
<td>TET, AMP, AMX, CHL</td>
<td>8</td>
<td>Liyuwork et al. (2013)</td>
</tr>
<tr>
<td>2013</td>
<td>Tigray</td>
<td>Cattle origin food</td>
<td>384</td>
<td>63</td>
<td>63 (100.0)</td>
<td>45 (71.4)</td>
<td>Typhimurium (40), Enteritidis (33)</td>
<td>CEP, CHL, TET, GEN, SUL, SXT, KAN, STR, NEO</td>
<td>12</td>
<td>Abebe et al. (2014)</td>
</tr>
</tbody>
</table>


Or more commonly used antimicrobials. Misuse and overuse of antimicrobial drugs creates selective evolutionary pressure that enables antimicrobial resistant bacteria to increase in numbers more rapidly than antimicrobial susceptible bacteria and thus increases the

---

Kemal et al.          2253
Table 2. Antimicrobial resistance profiles of *Salmonella* isolates in human, Ethiopia.

<table>
<thead>
<tr>
<th>Year</th>
<th>Location</th>
<th>No. of sample</th>
<th>No. of isolates tested</th>
<th>Resistance to one or more antibiotics No. (%)</th>
<th>MDR No. (%)</th>
<th>Predominant serovars isolated (No.)</th>
<th>Common resistance pattern</th>
<th>Maximum antibiotics resisted (No.)</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>1982/1983</td>
<td>Addis Ababa</td>
<td>1000</td>
<td>45</td>
<td>14 (31.0)</td>
<td>10 (22.0)</td>
<td>Serogroup C</td>
<td>SUL, STR, AMP, CAR, CEP, CHL, KAN, TET</td>
<td>8</td>
<td>Ashenafi and Gedebo (1985)</td>
</tr>
<tr>
<td>1995</td>
<td>Addis Ababa</td>
<td>700</td>
<td>45</td>
<td>31 (68.9)</td>
<td>29 (64.4)</td>
<td>Serogroup C</td>
<td>AMP, CEP, SXT, TET, KAN, CHL</td>
<td>8</td>
<td>Mache et al. (1997)</td>
</tr>
<tr>
<td>2000</td>
<td>Jimma</td>
<td>384</td>
<td>59</td>
<td>55 (93.22)</td>
<td>51 (86.44)</td>
<td>Serogroup B (15), Serogroup C (12), Typhi (11)</td>
<td>CEP, CHL, TET</td>
<td>6</td>
<td>Mache (2002)</td>
</tr>
<tr>
<td>2006</td>
<td>Addis Ababa, Jimma</td>
<td>1225</td>
<td>65</td>
<td>65 (100.0)</td>
<td>46 (70.0)</td>
<td>Concord Typhi Enteritidis</td>
<td>TEM, SUL, CHL, GEN, CRO</td>
<td>9</td>
<td>Beyene et al. (2011)</td>
</tr>
<tr>
<td>2007</td>
<td>Harar</td>
<td>244</td>
<td>28</td>
<td>28 (100.0)</td>
<td>-</td>
<td>-</td>
<td>AMP, AMX</td>
<td>6</td>
<td>Ayalu et al. (2011)</td>
</tr>
<tr>
<td>2009/2010</td>
<td>Jimma</td>
<td>260</td>
<td>1</td>
<td>1 (100.0)</td>
<td>1 (100.0)</td>
<td>-</td>
<td>AMX, AMP, CHL, CEP, TET, SXT</td>
<td>6</td>
<td>Tizazu et al. (2011)</td>
</tr>
<tr>
<td>2013</td>
<td>Gonder</td>
<td>300</td>
<td>4</td>
<td>4 (100.0)</td>
<td>3 (75.0)</td>
<td>Typhi</td>
<td>CHL, AMP, TET</td>
<td>5</td>
<td>Dagnew et al. (2013)</td>
</tr>
<tr>
<td>2013</td>
<td>Addis Ababa</td>
<td>382</td>
<td>40</td>
<td>39 (97.5)</td>
<td>(27.5)</td>
<td>Serogroup A (6) Serogroup B (5)</td>
<td>TET, COT, AMP,</td>
<td>-</td>
<td>Mengistu et al. (2014)</td>
</tr>
<tr>
<td>2014</td>
<td>Harar</td>
<td>384</td>
<td>56</td>
<td>56 (100.0)</td>
<td>-</td>
<td>-</td>
<td>CIP, NAL, AMP, TET, TMP, SMX, CHL</td>
<td>7</td>
<td>Dinkineh et al. (2014)</td>
</tr>
</tbody>
</table>

CAR: Carboncillin; COT: co-trimoxazole; CRO: ceftriaxone; SUL: sulfasoxazole; AMP: Ampicillin; AMX: amoxicillin acid; CHL: chloramphenicol; CEP: cephalothin; CIP: ciprofloxacin; GEN: gentamycin; KAN: kanamycin; SMX: sulphamethoxazole; STR: streptomycin; SXT: trimethoprim-sulfamethoxazole; TET: tetracycline; TMP: trimethoprim; MDR: multiple drug resistance.

opportunity of infection by resistant bacteria. Therefore, developing strategies in order to minimize the expansion of antimicrobial resistance is critically important for protecting both public and animal health. Collaboration involving the public, the public health, animal health, and animal agriculture communities on the development and implementation of such strategies is needed to assure that the public health is protected while also assuring that such strategies are feasible.

Conflict of interests
The author(s) did not declare any conflict of interest.

ACKNOWLEDGEMENTS
The authors would like to acknowledge Dr Dagmar Nolkes for her valuable materials provision and advice. They are also intensely grateful to all sources of materials used for this review article.

REFERENCES


Pui CF, Wong WC, Chai LC, Tunung R, Jeyaletchumi P, Noor Hidayah


