Review Article Bacterial Infections and Their Antibiotic Resistance Pattern in Ethiopia: A Systematic Review

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Background. Antibiotic resistance is a global challenge in the public health sector and also a major challenge in Ethiopia. It is truly difficult to report bacterial antibiotic resistance pattern in Ethiopia due to the absence of a review which is done comprehensively. The aim of this systematic review was to provide an overview of the works of literature on the antibiotic resistance pattern of the specific bacterial isolates that can be obtained from different clinical samples in the context of Ethiopia. Materials and Methods. A web-based search using PubMed, Google Scholar, Hinari, Sci Hub, Scopus and the Directory of Open Access Journals was conducted from April to May 2018 for published studies without restriction in the year of publication. Works of literature potentially relevant to the study were identified by Boolean search technique using various keywords: Bacterial infection, antimicrobial resistance, antibiotic resistance, drug resistance, drug susceptibility, anti-bacterial resistance, Ethiopia. Study that perform susceptibility test from animal or healthy source using <10 isolates and methods other than prospective cross-sectional were excluded. Results. The database search delivered a total of 3459 studies. After amendment for duplicates and inclusion and exclusion criteria, 39 articles were found suitable for the systematic review. All studies were prospective cross-sectional in nature. The review encompasses 12 gram-positive and 15 gram-negative bacteria with their resistance pattern for around 12 antibiotics. It covers most of the regions which are found in Ethiopia. The resistance pattern of the isolates ranged from 0% up to 100%. The overall resistance of M. tuberculosis for antituberculosis drugs ranges from 0% up to 32.6%. The percentage of resistance increases among previously treated tuberculosis cases. Neisseria gonorrhea, S. typhimurium, S. Virchow, Group A Streptococci (GAS), and Group B Streptococci (GBS) were highly susceptible for most of the tested antibiotics. Methicillin-Resistant Staphylococcus aureus was highly resistant to most of the antibiotics with a slightly increased susceptibility to gentamycin. Conclusions. Total bacterial isolates obtained from a different source of sample and geographic areas were 28, including M. tuberculosis. Majority of the bacterial isolates were resistant to commonly used antibiotics. A continuous monitoring and studies on the multidrug-resistant bacterial isolates are important measures.

1. Introduction

Human beings have been living unfriendly with a lot of microorganisms that can be a potential cause of infections and diseases. In the case of bacterial infections, due to the introduction of Penicillin for treatment in the early 1940s, there was an improvement [1]. Majority of naturally derived antibiotics are produced from Actinomycetes [2, 3]. In this day, even though the struggle to defeat bacterial pathogens continues, bacteria are evolving ever more clever by manifesting different forms of resistance [4].

The current antimicrobial profile studies have been proved that, bacteria that can cause nosocomial as well as

community acquired infections become pan resistant for different groups of antibiotics. Hence, this situation becomes a clinical threat to the human beings [5–13]. Most of the bacterial antibiotic resistance mechanisms are acquired by altering of target genes or acquisition of plasmid encoding resistance genes. These encoded genes may lead to the production of lytic enzymes, change of membrane permeability, efflux action, and hiding from the action of antibiotics [14].

Centers for Disease Control and Prevention (CDC) stated that antibiotic resistance is responsible for around 2 million infections, more than twenty thousand deaths and, costs \$55 billion each year in the United States [15]. The national pharmaceutical sales data on global antibiotic consumption

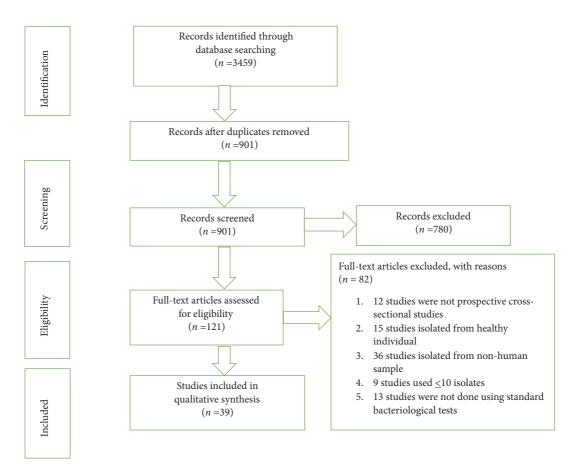


FIGURE 1: A flow diagram of the selection of eligible studies. The flow diagram shows the procedure of selecting an eligible study to undergo the systematic review. To perform this we start by identifying 3459 studies using a web-based search and goes to a screening of 901 studies after removing duplicates. Using eligibility criteria only 121 studies went to eligibility testing. Finally, 39 studies were included.

(2000-2010) reveals that total antibiotic consumption grew by more than 30%. The greatest increase in antibiotics use was recorded in Low and Middle Income Countries (LMIC) [16].

As long as Ethiopia is one of the LMICs, antibiotic resistance is a major challenge. Yet, there is no antibiotic stewardship that helps to establish surveillance system for tracking current antibiotic use and its resistance in Ethiopia. Therefore, it is truly difficult to report bacterial antibiotic resistance pattern in Ethiopia. So, the aim of this systematic review emphasizes on the antibiotic resistance pattern of the specific bacterial isolates that can be obtained from different clinical samples in the context of Ethiopia.

2. Materials and Methods

2.1. Eligibility Criteria. All available studies and data were incorporated based on the following predefined eligibility criteria:

- (1) should be published and written in English,
- (2) had to describe the microbial isolation, identification, and antimicrobial sensitivity test methods according to the criteria of the Clinical Laboratory Standards

Institute (CLSI) and defined antimicrobial resistance range according to CLSI manual,

- (3) studies which used human infection sample (isolated from a diseased individual),
- (4) had to report the number of tested isolates (>10) and the number of isolates resistant or sensitive,
- (5) should be a prospective cross-sectional study.

2.2. Study Selection Procedure and Search. The search and selection of eligible studies were shown in Figure 1. To make it more elaborative; a web-based search using PubMed, Google Scholar, Hinari, Sci Hub, Scopus, and the Directory of Open Access Journals (DOAJ) was conducted from April to May 2018 and pieces of literature potentially relevant to the study were identified. The search was performed using various keywords: Bacterial infection, antimicrobial resistance, antibiotic resistance, drug resistance, drug susceptibility, anti-bacterial resistance, Ethiopia. These key terms were used in various combinations using Boolean search technique. The search was not limited to the year of publication.

Relevant search results from the above site were individually downloaded and the reference lists of the identified studies were used to scrutinize to identify extra articles. 2.3. Data Extraction. Essential data were extracted from eligible studies using Excel spreadsheet format prepared for this purpose and any discrepancies were resolved by the author. The data extracted from eligible studies include the name of regions, study area/city, the name of the author(s), year of the study, study design, types of specimens, numbers of patients/study participants, number of resistant isolates, resistance pattern of the isolates, and references.

3. Results

3.1. Literature Search Results. The search from PubMed, Google Scholar, Hinari, Sci Hub, Scopus, and DOAJ delivered a total of 3459 studies. After amendment for duplicates, 901 endured. Of these, 780 studies were castoff, since, after a review of their titles and abstracts, they did not meet the criteria. The full texts of the remaining 121 studies were reviewed in detail. Of these, 85 studies were discarded after the full text had been reviewed for appropriate study method, sample source, number of isolates, and standard bacteriological test. Finally, 39 studies were included in the review (Figure 1).

3.2. Antibiotic Resistance for Gram-Positive Bacteria. The review tries to encompass 12 gram-positive bacteria and their resistance pattern for around 12 antibiotics. It covers most of the regions which are found in Ethiopia. The resistance pattern of the isolates ranged from 0% up to 100%. GAS and GBS were highly susceptible for most of the tested antibiotics, but they have a relatively increased resistance to tetracycline. In contrast with these, MRSA was highly resistant for most of the antibiotics with a slightly increased susceptibility to gentamycin. The rest bacterial isolates have a different resistance pattern for different antibiotics and also a variable pattern from sample to sample (Table 1). The average resistance pattern of gram-positive bacteria shows a cumulative antibiotic resistance pattern of bacterial isolates from different clinical cases, geographic location, and source of sample for a similar antibiotic. Still, the average resistance range of the gram-positive bacteria is similar with the detailed resistance pattern (Figure 2).

3.3. Antibiotic Resistance for Gram-Negative Bacteria. Fifteen gram-negative bacteria were recovered from various specimens. Like the gram-positive bacteria, the resistance pattern ranges from 0% up to 100%. Almost all bacterial isolates were highly resistant for ampicillin. Relatively, isolates obtained from conjunctival swab were highly susceptible to different antibiotics. Neisseria gonorrhea, S. typhimurium, and S. Virchow were susceptible for many antibiotics. Moraxella spp. and S. Virchow had a similar resistance pattern for different antibiotics, even if the number of isolates varies between the two (Table 2). The average resistance pattern of gram-negative bacteria shows a cumulative antibiotic resistance pattern of bacterial isolates from different clinical cases, geographic location, and source of sample for a similar antibiotic. Still, the average resistance range of the gram-negative bacteria is similar with the detailed resistance pattern (Figure 3).

3.4. Drug Resistance of M. tuberculosis. The overall resistance of M. tuberculosis for antituberculosis drugs ranges from 0% up to 32.6%. The percentage of resistance increases among previously treated tuberculosis cases. New pulmonary and extra-pulmonary cases relatively had decreased resistance for antituberculosis drugs (Table 3).

4. Discussion

Our results indicate that the antibiotic resistance pattern of both gram-negative and gram-positive bacteria varied across the studies reviewed, ranging from 0% to 100%. This variation was found depending on the type of isolate, the source of the sample, type of infection, type of antibiotics, and geographical difference used in each study.

Even though it is difficult to discuss average resistance pattern of gram positive and gram negative bacteria with a single study for various antibiotics, a study done in Nigeria revealed that gram-negative and gram-positive bacteria had a resistance pattern of 19.8%-92.3% and 10%-87%, respectively [17]. And also a study in Gondar, Northwest Ethiopia, showed 20%-100% and 23.5%-58.8% for gram-negative and grampositive bacteria, respectively [18]. If we look at the overall resistance pattern of the above studies, it ranges from 10% to 100%. This was relatively comparable to the current review result.

A systematic review done on antimicrobial resistance in Sub-Saharan Africa (1990–2013) has been reported that Gram-positive pathogens show high prevalence of resistance to chloramphenicol, trimethoprim/sulfamethoxazole, and tetracycline and gram negative bacteria specifically the enterobacteriaceae groups show resistance to chloramphenicol, isolated from patients with a febrile illness, ranged between 31.0% and 94.2%, whereas resistance to third-generation cephalosporins ranged between 0.0% and 46.5% [13].

The current review revealed that majority of the bacterial isolates are resistant to commonly used antibiotics in Ethiopia [19–54]. The possible reason might be related to scientific justifications like the following: numerous antibacterial agents, effective previously, are no longer used today because of the rise of resistance genes in the bacterial genome [55]. The emergence of resistance genes can be through natural selection in the environment over a long period of time or by a spontaneous mutation in the bacterial DNA. The resistant pattern has been reported by almost all antibiotics that have been developed [19].

5. Limitations of the Study

Most of the studies done in Ethiopia do not document the antibiogram; due to this we were unable to review and extract data related to multidrug resistance.

6. Conclusions

The main result of this study is to obtain an internationally valid reference to know the antibiotic resistance pattern in Ethiopia. The review encompasses 12 gram-positive bacteria

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TABLE 2: Antibiotic resistance for gram-negative bacteria.

Type of tuberculosis case	e Type of sample	Study area	No of isolates	Ant	ibioti	cs and	l resis	tance (%)	Reference
Type of tuberculosis case	rype of sample	Study area	130 01 1301ates	Н	R	S	Е	Р	Reference
New case	Sputum	BLUH	103	8.7	1.9	7.8	0.9	-	[51]
Previously treated	Sputum	BLUH	18	5.6	5.6	5.6	5.6	-	[51]
New case	Sputum	JUSH	136	13.2	2.2	8.1	5.2	-	[52]
New case	Sputum	Amhara region	93	3.2	0	20.4	0	-	[53]
New case	Sputum	Amhara region	214	9.8	3.7	6.5	5.6	3.7	[54]
Previously treated	Sputum	Amhara region	46	32.6	15.2	26.1	15.2	8.7	[54]
EPTB	pleural, peritoneal and synovial fluids	Addis Ababa	58	8	21.6	5.4	2.7	-	[56]

TABLE 3: Resistance pattern of *M. tuberculosis* for anti-tuberculosis drugs.

H: isoniazid; R: rifampin; S: streptomycin; E: ethambutol; P: pyrazinamide; EPTB: Extra Pulmonary Tuberculosis; JUSH: Jimma University Specialized Hospital; BLUH: Black Lion University Hospital

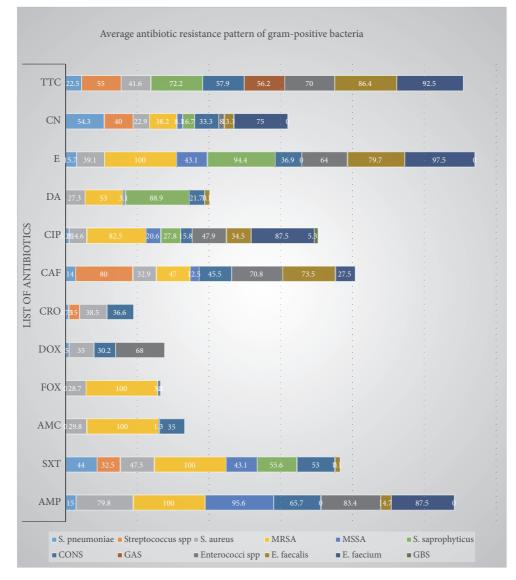
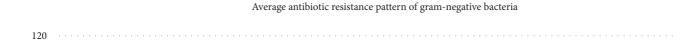


FIGURE 2: Average resistance pattern of gram-positive bacteria for different antibiotics.



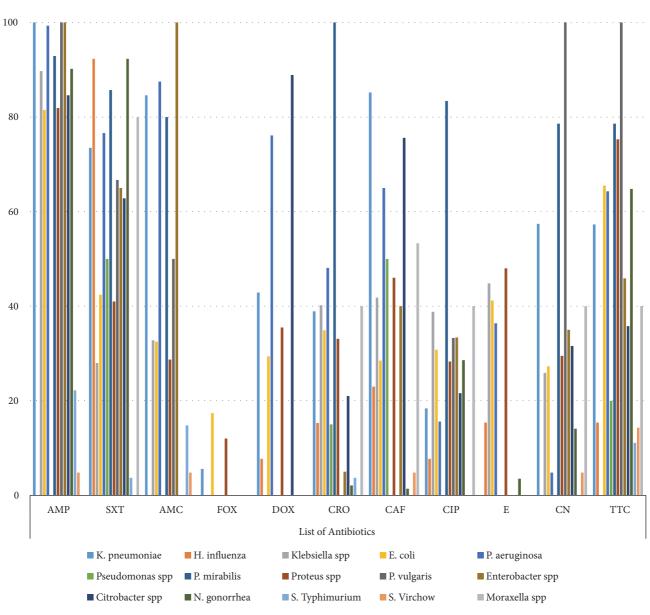


FIGURE 3: Average resistance pattern of gram-negative bacteria for different antibiotics.

and their resistance pattern for around 12 antibiotics. It covers most of the regions which are found in Ethiopia. The resistance pattern of the isolates ranged from 0% up to 100%. Fifteen gram-negative bacteria were recovered from various specimens. Like the gram-positive bacteria, the resistance pattern ranges from 0% up to 100%. Almost all bacterial isolates were highly resistant for ampicillin. Relatively, isolates obtained from conjunctival swab were highly susceptible to different antibiotics. *Neisseria gonorrhea*, *S. typhimurium*, and S. Virchow were susceptible for many antibiotics. The overall resistance of *M. tuberculosis* for antituberculosis drugs ranges from 0% up to 32.6%. Given the limitations of the current study, these findings should be interpreted carefully but warrant further evaluation in consequent studies.

Our study provides evidence that majority of the bacterial isolates were resistant to commonly used antibiotics. Antibiotic resistance should be a substantial concern for Ethiopia as well as for all countries around the globe. So to alleviate such problems and to advance the effectiveness of antibiotics in Ethiopia, the government of Ethiopia as well as the international community should do the following:

- (i) Prepare the guidelines for proper use of antibiotics in the health institutions.
- (ii) Establish antimicrobial resistance stewardship.
- (iii) Increase proper immunization coverage that may reduce the use of antibiotics.
- (iv) Implement one health policy (reduce antimicrobial use for agricultural practice and animals).
- (v) Create community awareness on rational use of drugs.
- (vi) Make strong policy for antibiotic dispensing by drug venders.
- (vii) Control Hospital and community acquired infections.
- (viii) Ensure political commitment to meet the threat of antibiotic resistance.

Conflicts of Interest

The authors declare that they have no competing interests.

Authors' Contributions

Alemayehu Reta carried out interpretation of data, drafted the manuscript, revised it critically for important intellectual content, and gave final approval of the version to be published. Abebaw Bitew Kifilie revised it critically and searched literatures. Abeba Mengist revised it critically and searched literatures. All authors have read and approved the final manuscript.

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