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Review

Antibiotic resistance in Bangladesh: A systematic review

Iftekhar Ahmed*, Md. Bodiuzzaman Rabbi, Sakina Sultana

Department of Pharmacy, Jahangirnagar University, Savar, Dhaka 1342, Bangladesh

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ABSTRACT

Background: Antibiotic resistance (ABR) is a worldwide problem and Bangladesh is a major contributor to this owing to its poor healthcare standards, along with the misuse and overuse of antibiotics. This systematic review was conducted to summarize the present scenario of ABR in Bangladesh, to identify gaps in surveillance, and to provide recommendations based on the findings.

Methods: Google Scholar, PubMed, and Bangladesh Journals Online were searched using relevant keywords to identify articles related to ABR in Bangladesh published between 2004 and 2018. Inclusion or exclusion was based on a predefined set of criteria. The resistance of a bacterium to a given drug was presented as the median resistance (MR) and interquartile range (IQR).

Results: Forty-six articles were included in this systematic review. Antimicrobial susceptibility testing was performed by disk diffusion method in 82.6% of studies, while the Clinical and Laboratory Standards Institute (CLSI) guidelines were followed in 78.3%. Data regarding the susceptibility testing method, guidelines for interpretation, and source of infection (hospital/community) were absent in 10.9%, 19.6%, and 73.9% of the studies, respectively. A high prevalence of resistance was detected in most tested pathogens, and many of the common first-line drugs were mostly ineffective. Resistance to carbapenems was low in most cases. The presence of extended-spectrum beta-lactamase (ESBL)-producing organisms was indicated by the high resistance to beta-lactams. Methicillin-resistant *Staphylococcus aureus* (MRSA) was identified in four studies. Three studies reported vancomycin susceptibility of enterococci, and the median susceptibility was 100%. *Streptococcus pneumoniae* exhibited high susceptibility to penicillin (MR 4%). Resistance data were available from only six out of the 64 districts of Bangladesh.

Conclusions: A high prevalence of resistance to most antibiotics was detected, along with major gaps in surveillance and information gaps in the methodological data of the studies (susceptibility testing method, guidelines for susceptibility interpretation, source of infection). Based on the findings, we recommend appropriate initiatives to monitor and control the use of antibiotics, as well as nationwide surveillance following standardized methodologies.

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Contents

* Corresponding author.
E-mail address: iftekhar2727@gmail.com (I. Ahmed).

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Introduction

In recent years, there has been both a surge in antibiotic resistance (ABR) (European Centre for Disease Prevention and Control (ECDC), 2017; Okeke et al., 2005; World Health Organization (WHO), 2014) and a decline in the rate of new antibiotic development (Luepke and Mohr, 2017; Spellberg et al., 2004). ABR poses a significant risk in terms of mortality and economic burden worldwide. However, the developing countries are more affected because of the widespread misuse of antibiotics, non-human antibiotic use, poor quality of drugs, inadequate surveillance, and factors associated with individual and national poverty (poor healthcare standards, malnutrition, chronic and repeated infections, unaffordability of more effective and costly drugs) (Ayukekbong et al., 2017; Sosa et al., 2010). Furthermore, the scarcity of newer drugs means resistance must be contained before we run out of options to battle it.

According to the 2014 WHO report on global surveillance of antimicrobial resistance, significant gaps in surveillance prevail, along with a lack of standards for methodology, data sharing, and coordination. However, the Southeast Asia, African, and Eastern Mediterranean regions have been identified as having major gaps (WHO, 2014).

Bangladesh, a developing country of Southeast Asia with a high degree of ABR, poses a regional and global threat. In a study performed in Chittagong in 2003, typhoid patients were found to be unresponsive to second-line therapy (ciprofloxacin). First-line therapy was not even attempted because of existing resistance (Asna et al., 2003). Therapeutic failures like this are not rare at all. Furthermore, in relation to this, multiple studies have demonstrated irrational antibiotic prescribing by physicians, a habit of self-medication among patients, and the indiscriminate use of antibiotics in agriculture and farming in different parts of the country (Biswas et al., 2014a,b; Mostafa Shamsuzzaman and Kumar Biswas, 2012; Sutradhar et al., 2014).

Despite the fact that many studies have been performed on the prevalence of ABR in Bangladesh, no attempts have yet been made to systematically unify them. This systematic review was conducted to depict the present rate of resistance shown by the clinically significant pathogens. It was further sought to discuss the gaps in surveillance and provide recommendations based on the key findings. The goal was to provide a reference for future works and to guide policymakers and prescribers towards adopting the best strategy to lower the extent of ABR, as well as to mitigate the problems resulting from increasing resistance.

Methods

Literature search

Searches were conducted to identify articles related to ABR in Bangladesh published between 2004 and August 30, 2018. Multiple searches were conducted in Google Scholar, PubMed, and Bangladesh Journals Online using different relevant keywords (Antibiotic (also Antimicrobial) AND Resistance (also Susceptibility) AND Bangladesh; Antibiotic (also Antimicrobial) AND Bangladesh; and searches specifying pathogens).

Study selection

Articles reporting the ABR of various pathogens were included in the review if they met the predefined inclusion criteria, as follows: (1) reported ABR in humans from Bangladesh; (2) studied ABR of the pathogens listed in the WHO global priority list of antibiotic-resistant bacteria (WHO, 2017); (3) were published after 2004; (4) had a sample size $\geq$10; and (5) the total number of samples and the number/percentage of resistant/susceptible strains was clearly reported.

Data extraction and analysis

All selected papers were assessed to accumulate data on publication year, study period, study location, clinical syndrome and pathogen, method of susceptibility testing, susceptibility testing standard, source of infection, etc. Quantitative data on ABR were also collected. It is important to note that intermediate-resistant samples were recorded as resistant in this study. Data extraction was performed independently by two researchers to negate any possibility of error.

The resistance of each bacterium to different antibiotics is presented as the median resistance (MR) along with the interquartile range (IQR), combining all of the studies. Since the majority of the studies did not provide any information on the source of infection (hospital-acquired or community-acquired), no attempt was made to differentiate between the two groups and ABR data from all of them were combined. The data analysis was conducted in Microsoft Excel 2013.

Results

Study characteristics

From an initial pool of 140 articles, 46 were included in the review. All of the studies were published between 2004 and 2018, and the data collection period extended to 2001. The majority of the studies (82.6%, 38/46) were conducted in the capital district, Dhaka. Among the three different susceptibility testing methods used, disk diffusion was used in 82.6% (38/46) of the studies. Data interpretation was mostly based on Clinical and Laboratory Standards Institute (CLSI) guidelines for antimicrobial susceptibility testing (CLSI, 2017) (78.3%, 36/46). Ten of the 46 studies (21.7%) collected samples from urinary tract infection (UTI), while cultures from gastroenteritis and bloodstream infection were analyzed in 17.4% (8/46) and 15.2% (7/46) of the studies, respectively. Most of the isolates were from multiple sample types (30.4%, 14/46). A summary of the characteristics of the studies included in this review is given in Table 1.

The MR was calculated for nine of the 14 selected pathogens (Table 2). *Helicobacter pylori*,*Enterobacter* spp., *Proteus* spp., *Serratia* spp., and *Campylobacter* spp. were excluded from the statistical analysis because of a very small number of studies (at least three studies are required for calculation of the IQR). The following references report their resistance patterns: Aftab et al. (2016), Ahmed et al. (2011), Dutta et al. (2013), Jobayer et al. (2017), Khan et al. (2013), Monjur et al. (2010), Nahar et al. (2004).

Table 1
Characteristics of the studies included in the review ($N = 46$).

Characteristics	Frequency (%)	Reference
Publication year		
2004–2010	11 (23.9)	(Arifeen et al., 2009; Brooks et al., 2005; Haque and Salam, 2010; Khan et al., 2004; Mahbubur et al., 2007; Monjur et al., 2010; Nahar et al., 2004; Rahman et al., 2005; Saha et al., 2009; Shahriar et al., 2010; Shill et al., 2010)
2011–2014	14 (30.4)	(Afroz et al., 2014; Ahmed et al., 2011, 2014; Akram et al., 2014; Akter et al., 2014; Begum et al., 2013; Chiou et al., 2014; Dutta et al., 2013; Haque et al., 2011; Hossain et al., 2014; Islam et al., 2014; Khan et al., 2013; Rahman et al., 2014; Ud-Din et al., 2013)
2015–2018	21 (45.7)	(Aftab et al., 2016; Ahmed et al., 2017, 2018; Ahsan et al., 2016; Akter et al., 2016, 2017; Begum et al., 2016; Chakraborty et al., 2016; Chowdhury and Parial, 2015; Haque et al., 2015; Hasan et al., 2016; Islam and Shamsuzzaman, 2015; Jobayer et al., 2017; Khanam et al., 2015; Nazme et al., 2017; Roy et al., 2017; Saha et al., 2015; Suchi et al., 2017; Uddin et al., 2017; Ullah et al., 2016; Yasmeen et al., 2015)
End of data collection		
2001–2008	10 (21.7)	
2009–2012	13 (28.3)	
2013–2016	18 (39.1)	
Did not mention	5 (10.9)	
Location[a]		
Dhaka	38 (82.6)	
Rajshahi	4 (8.7)	(Begum et al., 2013; Haque et al., 2015; Haque and Salam, 2010; Rahman et al., 2005)
Chittagong	3 (6.5)	(Chowdhury and Parial, 2015; Saha et al., 2009; Uddin et al., 2017)
Tangail (Mirzapur)	2 (4.3)	(Arifeen et al., 2009; Saha et al., 2009)
Others (Sylhet, Jessore)	2 (4.3)	(Chakraborty et al., 2016; Saha et al., 2015)
Source of infection		
Community-acquired	5 (10.9)	(Akter et al., 2014; Arifeen et al., 2009; Brooks et al., 2005; Mahbubur et al., 2007; Rahman et al., 2014)
Hospital-acquired	4 (8.7)	(Haque and Salam, 2010; Hasan et al., 2016; Islam et al., 2014; Islam and Shamsuzzaman, 2015)
Both	3 (6.5)	(Akram et al., 2014; Hossain et al., 2014; Jobayer et al., 2017)
Unknown	34 (73.9)	
Patient type		
Inpatient	15 (32.6)	
Outpatient	3 (6.5)	
Inpatient and outpatient	9 (19.6)	
Did not mention	19 (41.3)	
Susceptibility testing method[b]		
Disk diffusion	38 (82.6)	
Dilution	7 (15.2)	(Aftab et al., 2016; Chiou et al., 2014; Hasan et al., 2016; Islam and Shamsuzzaman, 2015; Nahar et al., 2004; Rahman et al., 2014; Suchi et al., 2017)
E-test	5 (10.9)	(Arifeen et al., 2009; Begum et al., 2016; Khan et al., 2013; Mahbubur et al., 2007; Saha et al., 2009)
Did not mention	5 (10.9)	(Ahmed et al., 2018; Akram et al., 2014; Islam et al., 2014; Nazme et al., 2017; Shill et al., 2010)
Susceptibility testing standard		
CLSI	36 (78.3)	
EUCAST	1 (2.2)	(Aftab et al., 2016)
Did not mention	9 (19.6)	(Ahmed et al., 2014, 2018; Akram et al., 2014; Islam et al., 2014; Monjur et al., 2010; Nazme et al., 2017; Rahman et al., 2005; Shill et al., 2010; Yasmeen et al., 2015)
Pathogen		
Escherichia coli	21	
Klebsiella spp.	13	
Pseudomonas spp.	10	
Staphylococcus aureus	9	
Salmonella spp.	8	
Acinetobacter spp.	7	
Enterococcus spp.	5	
Streptococcus pneumoniae	5	
Shigella spp.	4	
Enterobacter spp.	2	
Helicobacter pylori	2	
Proteus spp.	2	
Serratia spp.	1	
Campylobacter spp.	1	
Clinical syndrome		
Urinary tract infection	10 (21.7)	(Akter et al., 2016; Chowdhury and Parial, 2015; Haque et al., 2015; Khan et al., 2013; Nazme et al., 2017; Rahman et al., 2014; Saha et al., 2015; Shill et al., 2010; Suchi et al., 2017; Yasmeen et al., 2015)
Bloodstream infection	7 (15.2)	(Afroz et al., 2014; Ahmed et al., 2017, 2018; Ahsan et al., 2016; Brooks et al., 2005; Khanam et al., 2015; Monjur et al., 2010)
Gastroenteritis	8 (17.4)	(Ahmed et al., 2011, 2014; Akter et al., 2017; Begum et al., 2016; Khan et al., 2004; Mahbubur et al., 2007; Ud-Din et al., 2013; Uddin et al., 2017)
Hospital-acquired infection	4 (8.7)	
Wound infection	1 (2.2)	(Roy et al., 2017)
Respiratory tract infection	1 (2.2)	(Ullah et al., 2016)
Multiple syndromes	14 (30.4)	
Unavailable	1 (2.2)	(Chiou et al., 2014)

CLSI, Clinical and Laboratory Standards Institute; EUCAST, The European Committee on Antimicrobial Susceptibility Testing.
[a] Studies involving multiple locations were counted more than once.
[b] Some studies adopted more than one method.

Table 2
Antibiotic resistance (percentage) of the selected pathogens.

Drug	*Acinetobacter* spp. MR (IQR) Total sample	*Enterococcus* spp. MR (IQR) Total sample	*Escherichia coli* MR (IQR) Total sample	*Klebsiella* spp. MR (IQR) Total sample	*Pseudomonas* spp. MR (IQR) Total sample	*Salmonella* spp. MR (IQR) Total sample	*Shigella* spp. MR (IQR) Total sample	*Staphylococcus aureus* MR (IQR) Total sample	*Streptococcus pneumoniae* MR (IQR) Total sample
Amikacin	67.5 (25–85.8) 418	67.3 (63.2–78.4) 161	12 (7–26.7) 1953	37.4 (10.3–60.3) 289	50 (32.7–70.6) 1272	–	–	–	–
Amoxicillin	–	45.5 (31.6–60.9) 55	91.1 (28.2–95.3) 857	94.8 (90.2–99.7) 216	–	–	–	64.3 (44.7–84.9) 142	–
Amoxiclav	–	–	67.1 (52–85.5) 750	58 (14.3–84.6) 147	86.4 (85.7–97) 146	–	–	–	–
Ampicillin	–	–	94.6 (85.9–100) 1464	100 (100–100) 176	–	34.8 (29.2–58.4) 9680	47.1 (17.9–56.3) 3540	83.8 (74–93.1) 374	0 (0–15) 322
Azithromycin	–	–	58.9 (28.6–83.4) 1318	–	–	–	–	38.1 (20.6–68.5) 179	43.7 (31–65) 160
Aztreonam	–	–	79 (35.5–95.8) 150	–	–	–	–	–	–
Cefalexin	–	–	62 (50.1–76.6) 673	–	–	–	–	17.4 (7–51) 154	–
Cefepime	–	–	46.3 (28.2–94.4) 142	–	–	–	–	–	–
Cefixime	–	–	69.3 (28.7–76.3) 804	78.6 (50–89) 248	–	0 (0–8.5) 6843	–	–	43.7 (7–50) 160
Cefotaxime	82.9 (60.9–96.4) 63	–	55.4 (16.1–96.4) 129	97.8 (81.2–100) 73	59 (55.6–77.5) 148	–	–	–	–
Ceftazidime	80 (55– 92) 427	–	65.3 (34.5–83.4) 1650	82.5 (58.8–98.2) 315	56 (19.6–73.4) 1276	–	–	–	–
Ceftriaxone	82.6 (42.5–92.5) 823	74.3 (51.8–90.9) 139	59 (41.7–81.8) 2731	78 (54.1–84.6) 718	63.3 (52.5–73.2) 197	3 (0–7.2) 9970	–	44.4 (16.8–49.1) 328	10 (0–33.1) 338
Cefuroxime	84 (62–87.5) 51	100 (60.9–100) 55	78.8 (39.9–90.9) 691	74.7 (54.9–96.4) 156	–	–	–	–	–
Cephradine	–	–	62.6 (55.8–74) 623	–	–	–	–	22 (17.4–40.7) 105	–
Chloramphenicol	–	–	33.7 (0–77.5) 510	43.8 (33.8–64.3) 105	–	20.8 (13–57.1) 3580	–	17.4 (4–45) 271	–
Ciprofloxacin	82.2 (43.6–90.7) 815	66 (64.3–87.7) 184	65.2 (52.4–80.5) 3272	67.4 (43.6–80.9) 835	59.3 (22–87.3) 2090	32.6 (4–84.5) 10023	8.9 (1.4–15.8) 3540	51.7 (41.4–68.3) 548	8.3 (4–31.3) 457
Cloxacillin	–	–	–	–	–	–	–	45.6 (23.7–49.7) 142	–
Colistin	–	–	–	18.8 (0–21.4) 44	–	–	–	–	–
Co-trimoxazole	75.5 (48.8–94) 71	87.5 (74.2–100) 100	72 (56.6–82.2) 3170	72.7 (48–78.9) 402	86.6 (34.1–97.8) 171	29.4 (20.8–46.7) 9985	74.5 (71–85.9) 3540	43.2 (31–65) 493	77 (73.2–80.2) 457
Doxycycline	–	–	61.1 (44.6–93.8) 1212	–	–	–	–	–	–
Erythromycin	–	–	–	–	–	–	–	65 (52.2–69.5) 271	–
Gentamicin	83.3 (53.5–92) 836	57.1 (32.3–85) 184	34.5 (25.8–50) 2230	63.6 (26.2–73.8) 849	72.6 (48.5–91.2) 2095	–	–	27.8 (19.7–40.1) 548	–
Imipenem	27.3 (5–65.1) 375	–	2.3 (0–8.9) 1718	0 (0–23.9) 666	13.5 (5.4–29.5) 1274	–	–	7 (5.5–9.6) 144	–
Levofloxacin	–	–	62 (48.7–69.2) 863	54.9 (40–69.9) 124	–	–	–	–	–
Mecillinam	–	–	–	–	–	–	6 (0–10.5) 693	–	–
Meropenem	–	–	13.3 (0.3–37.2) 884	7.7 (0–41.9) 361	33.9 (14.6–51.7) 134	–	–	–	–
Nalidixic acid	–	100 (95.7–100) 55	85.9 (80.3–90.8) 1831	61.8 (52.5–90.9) 216	–	77.6 (46.5–89.4) 3516	66.9 (37–83.8) 3540	–	–

Table 2 (*Continued*)

Drug	*Acinetobacter* spp. MR (IQR) Total sample	*Enterococcus* spp. MR (IQR) Total sample	*Escherichia coli* MR (IQR) Total sample	*Klebsiella* spp. MR (IQR) Total sample	*Pseudomonas* spp. MR (IQR) Total sample	*Salmonella* spp. MR (IQR) Total sample	*Shigella* spp. MR (IQR) Total sample	*Staphylococcus aureus* MR (IQR) Total sample	*Streptococcus pneumoniae* MR (IQR) Total sample
Netilmicin	58.3 (34.5–80.3) 374	–	18.2 (4–59.8) 913	60 (13.4–80.8) 133	50.5 (42.3–68.9) 1125	–	–	–	–
Nitrofurantoin	–	21.7 (20–90.9) 55	16.1 (10–36.1) 1560	39.9 (20.2–60.2) 216	–	–	–	–	–
Oxacillin	–	–	–	–	–	–	–	46.7 (44.1–68.1) 214	–
Penicillin	–	–	–	–	–	–	–	89.7 (58.2–96.5) 237	4 (3.5–15) 441
Piperacillin–tazobactam	–	–	12.1 (0–36.4) 181	57.1 (0–76.5) 44	–	–	–	–	–
Tetracycline	–	–	65 (40.6–72) 1510	–	–	–	–	43.5 (25.9–59.5) 237	–
Vancomycin	–	0 (0–27.3) 140	–	–	–	–	–	6.8 (0–29.7) 436	–

MR, median resistance; IQR, interquartile range.

Antibiotic resistance pattern

Escherichia coli, the most common causative organism of UTI, was studied in 21 articles and showed high resistance to commonly used drugs such as ampicillin (MR 94.6%, IQR 85.9–100%), amoxiclav (MR 67.1%, IQR 52–85.5%), ciprofloxacin (MR 65.2%, IQR 52.4–80.5%), and co-trimoxazole (MR 72%, IQR 56.6–82.2%). Similar patterns were observed for other organisms causing UTI. Resistance to ampicillin, amoxiclav, ciprofloxacin, and co-trimoxazole was 100% (IQR 100–100%), 58% (IQR 14.3–84.6%), 67.4% (IQR 43.6–80.9%), and 72.7% (IQR 48–78.9%), respectively, in *Klebsiella* spp. Co-trimoxazole was ineffective against 86.6% (IQR 34.1–97.8%) of tested *Pseudomonas* spp. isolates, and 87.5% (IQR 74.2–100%) of *Enterococcus* spp. isolates were non-susceptible. Ciprofloxacin resistance was displayed by 66% (IQR 64.3–87.7%) of *Enterococcus* spp. isolates and 59.3% (IQR 22–87.3%) of *Pseudomonas* spp. isolates. There was an indication of extended-spectrum beta-lactamase (ESBL) production from a significantly high resistance to beta-lactams. Resistance of *E. coli* to cefotaxime, ceftazidime, and ceftriaxone was 55.4%, 65.3%, and 59%, respectively, while *Klebsiella* spp. showed 97.8%, 82.5%, and 78% resistance to these antibiotics. In contrast, most of the aforementioned bacteria were highly sensitive to carbapenems. Only 2.3% (IQR 0–8.9%) of *E. coli*, 0% (IQR 0–23.9%) of *Klebsiella* spp., and 13.5% (IQR 5.4–29.5%) of *Pseudomonas* spp. strains were resistant to imipenem, and resistance to meropenem was recorded in 13.3% (IQR 0.3–37.2%), 7.7% (IQR 0–41.9%), and 33.9% (IQR 14.6–51.7%) of the strains, respectively.

High susceptibility to penicillin (MR 4%, IQR 3.5–15%) and ampicillin (MR 0%, IQR 0–15%) was recorded for *Streptococcus pneumoniae* isolates from pneumonia patients. *Staphylococcus aureus* exhibited high resistance to penicillin (MR 89.7%, IQR 58.2–96.5%), ampicillin (MR 83.8%, IQR 74–93.1%), co-trimoxazole (MR 43.2%, IQR 31–65%), and amoxicillin (MR 64.3%, IQR 44.7–84.9%). Again, of 436 isolates of *Sta. aureus*, 6.8% (IQR 0–29.7%) were resistant to vancomycin, while 7.0% (IQR 5.5–9.6%) of 144 *Sta. aureus* isolates were resistant to imipenem. Methicillin-resistant *Sta. aureus* (MRSA) was detected in four studies by testing susceptibility to oxacillin, with 93 of 199 isolates found to be MRSA. Eight studies reported the ABR of *Salmonella* spp., which were highly susceptible to cefixime (MR 0%, IQR 0–8.5%) and ceftriaxone (MR 3%, IQR 0–7.2%). Only 8.9% (IQR 1.4–15.8%) of *Shigella* spp. isolates were resistant to ciprofloxacin and 6% (IQR 0–10.5%) to mecillinam. *Acinetobacter* spp. showed significant resistance (>55%) to all of the tested antibiotics except imipenem.

Discussion

The effectiveness of common first-line antibiotics against UTI was unsatisfactory. A similar situation has been observed in Africa; however, in the present study, resistance of *E. coli* to amoxicillin, amoxiclav, ampicillin, and ciprofloxacin was higher (Tadesse et al., 2017). Given this scenario, clinicians may resort to alternative drugs such as fosfomycin, nitrofurantoin, tigecycline, carbapenems, etc., if required (Garau, 2008; Shaikh et al., 2015). Of the staphylococcal groups, MRSA is associated with a greater risk of mortality, longer duration of hospitalization, and higher hospital costs compared with methicillin-susceptible *Sta. aureus* (Cosgrove et al., 2003, 2005; Engemann et al., 2003). Vancomycin was found to be an effective drug against MRSA in this study. Penicillin resistance of *Str. pneumoniae* was negligible, hence it remains a choice of treatment for pneumococcal disease. However, different results were observed in studies conducted in Asia and Africa (Song et al., 2004; Tadesse et al., 2017). Again, a common organism of nosocomial infections is vancomycin-resistant Enterococci. In spite of its prevalence in many countries (Cetinkaya et al., 2000; Orsi and

Ciorba, 2013; Wisplinghoff et al., 2004), finding in this study was different, with only three out of 140 isolates of *Enterococcus* spp. found to be vancomycin resistant (MR 0%). However, only three studies tested vancomycin susceptibility, and more extensive research needs to be done to obtain a definitive insight. For the treatment of shigellosis, clinicians may resort to both ciprofloxacin and mecillinam, since both of these appeared to be highly efficacious in this study.

Significant gaps in surveillance were noted in this study. ABR data were unavailable from 58 out of the 64 districts of Bangladesh. Furthermore, among the six districts with data, all five other than Dhaka were poorly represented. Gaps in the methodological data were also identified. Some of the studies lacked important data such as the susceptibility testing method (10.9%), standard for susceptibility interpretation (19.6%), and source of infection (hospital/community) (73.9%). This raises questions regarding the quality of their data and makes it difficult to make comparisons among the different studies. Future works on ABR must address these issues. Moreover, more research needs to be conducted on the pathogens that were left out because of an inadequate number of studies, as mentioned in the Results section.

Although the coverage of this study was limited to Bangladesh, the implications of the findings are global. It is known that resistant strains are rarely confined to a specific place; any region with a high prevalence of resistance can serve as a reservoir from which resistant strains can migrate to other parts of the world via humans, animals, agricultural products, water, etc. (Okeke and Edelman, 2001; Sjölund et al., 2008). Bangladesh, along with some of its neighbors, is serving as an excellent reservoir of drug-resistant pathogens.

As there is a shortage of new antibiotics, it is of utmost importance that the existing ones are used cautiously. There is evidence that controlled and lowered use of antibiotics can abate resistance (Barbosa and Levy, 2000). This can be achieved by implementing stricter regulations on antibiotic use, as well as by educating healthcare professionals and the public, as irrational antibiotic use is common in Bangladesh through prescription and self-medication (Biswas et al., 2014a,b; Sutradhar et al., 2014). Antibiotic stewardship programs should also be implemented to optimize the use of antibiotics in healthcare settings. Moreover, in order to obtain more comparable and quality data, standardization of the surveillance methodology is essential. At the same time, regular surveillance needs to be conducted throughout the country to keep track of the resistance patterns of the pathogens.

Limitations

Since most of the studies included in this review were clustered in Dhaka, there is a risk of selection bias, and this review might not be a proper representation of the whole country. Also, it would have been preferable to include studies reporting at least 30 isolates to ensure a high degree of precision of the data (WHO, 2014); however, due to the small number of available studies, the minimum requirement for inclusion had to be set at 10. There is also a possibility of bias from the lack of data regarding the source of infection in many studies, since hospital-acquired infections tend to be more resistant to antibiotics than community-acquired infections. Furthermore, data from different patient groups and obtained through different methodologies were combined in this study. Nevertheless, since most of the studies used the disk diffusion method and followed the CLSI guidelines, the extent of variation should be minimal.

Conclusions

There are three key findings of this review. First, the prevalence of ABR is very high in Bangladesh. Second, significant gaps in surveillance exist; resistance data were not available for most parts of the country and the number of studies for some pathogens was too few to assess their resistance patterns. Finally, many studies had gaps in their methodological data (susceptibility testing method, guidelines for the interpretation of susceptibility, source of infection), casting doubt on their quality and making comparisons among them difficult. Therefore, there is a need for standardization of surveillance methodology and continuous nationwide surveillance, along with proper actions to abate the prevailing rate of resistance.

Availability of data and material

All data generated or analyzed during this review were from studies available in the public domain.

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None.

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