PREVALENCE AND SURVEILLANCE OF ANTIMICROBIAL RESISTANCE IN SOCIETY OF BASRA- IRAQ

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ABSTRACT

Antibiotic-resistant bacteria have become more wide spread due to overuse and misuse of antibiotics, as well as social and economic issues. The WHO produced a list of pathogens that posed the greatest threat to humans, the most important are Enterobacter species, Acinetobacter baumannii, Pseudomonas aeruginosa, Klebsiella pneumoniae, and Staphylococcus aureus. These pathogens were assigned the highest "priority list." The lack of health information systems, inadequate management of medical facilities, minimal laboratory capability, and scarce resources make life difficult in countries with low or middle incomes. It has been shown that resistant bacteria can spread to people in a variety of situations, including public areas in metropolitan built environments with high densities of human activity, such as schools, and public transportation. This article describes many months' worth of surveillance operations that were carried out in Basra-Iraq. These efforts are not only significant on a national level, but they also contribute to the worldwide effort to combat the threat that antibiotic resistance poses.

KEYWORDS: Surveillance, Antimicrobial resistance, resistant organisms, multidrug resistance.

INTRODUCTION

Antimicrobial resistance (AMR) is a global health crisis. Antimicrobial resistance currently causes at least 700,000 deaths globally annually. The World Health Organization (WHO) estimates that this number might increase to 10 million by 2050 in the absence of new and improved therapies.[1]

However, data of AMR surveillance from low and middle−income countries (LMICs) are scarce[1,2], and data of mortality associated with AMR infections are rarely available. The studies also proposed that hospitals in LMICs should utilize routinely available microbiological and hospital admission databases to generate reports on AMR surveillance systematically.[3]

Reports on AMR surveillance can have a wide range of benefits (2); including:
1. Characterization of the frequency of resistance and organisms in different facilities and regions.
2. Prospective and retrospective information on emerging public health threats.

3. Evaluation and optimization of local and national standard treatment guidelines.

4. Evaluation of the impact of interventions beyond antimicrobial guidelines that aim to reduce AMR.

5. Data sharing with national and international organizations to support decisions on resource allocation for interventions against AMR and to inform the implementation of action plans at national and global levels.

Gram-positive and gram-negative bacteria with multidrug resistance patterns have caused illnesses that are challenging to cure or even untreatable with standard antimicrobials.

Broad spectrum antibiotics are frequently and typically unnecessary utilized in healthcare settings because early identification of pathogenic bacteria and their antimicrobial susceptibility patterns in patients with bacteremia and other serious illnesses is missing.

Important bacterial infections are becoming more resistant to standard antibiotic treatments, and multidrug-resistant bacteria are emerging at an alarming rate.[3]

With the aim of restricting the spread of resistant bacteria and preventing their selection during antibiotic treatment, the fight against the development of antibiotic resistance has traditionally focused mostly on medical facilities, and more lately, in agriculture as well.

Both bacterial uptake of foreign DNA and changes in a bacterium's pre-existing genome can result in antibiotic resistance.[4]

The WHO's list classifies bacteria into three priority categories: critical, high, and medium priority, depending on how quickly new antibiotics must be developed to tackle these infections.[5]

The pathogens in the most dangerous category are multidrug resistant bacteria, which are a hazard to people requiring medical devices like ventilators and blood catheters as well as to people who are residents of nursing homes and hospitals.[6,7]

Acinetobacter, Pseudomonas, and a few Enterobacteriaceae species like K. pneumoniae, E. coli, and Enterobacter spp. are among the bacteria with a critical priority.[8]

These organisms can cause serious and frequently fatal infectious disorders such bloodstream infections and pneumonia, and they are resistant to a variety of antibiotics.[7]

Bacteria that are resistant to a variety of medicines, including vancomycin and fluoroquinolones, fall under the high priority category. These bacteria include Enterococcus faecium and Staphylococcus aureus.

The medium priority group contains germs like Shigella and Streptococcus pneumoniae that, despite having some resistance, are still treatable with powerful antibiotics.[7,9]

Antimicrobial resistance (AMR) was listed as one of the top ten dangers to world health by the World Health Organization (WHO) in 2019 due to its effects on human health.[10]

Since it is well recognized that AMR develops naturally over time through diverse processes, in other words, overuse of antibiotics accelerates this natural process in both humans and animals, resulting in the spread of AMR.[11,12]
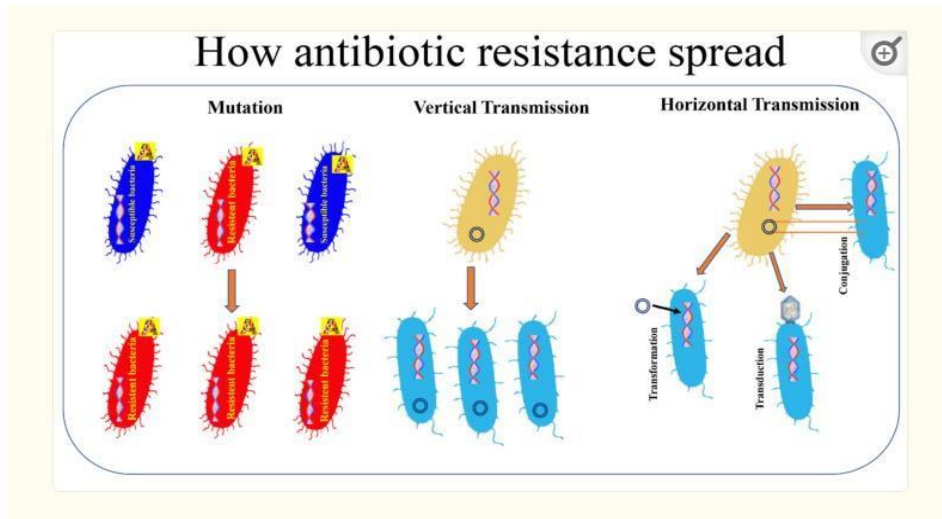
Figure 1: How antibiotic resistance spread.

Bacterial resistance towards antibiotics can be natural, or acquired by vertical or horizontal transmission.[13]

METHODOLOGY

Every year, countries and areas report routine antimicrobial susceptibility testing (AST) results collected from one or more medical microbiology laboratories. Countries and areas can report data from sentinel laboratories if it is not possible to include data from all their relevant laboratories. AMR surveillance focuses on invasive isolates of bacterial species (Escherichia coli (E. coli), Klebsiella pneumoniae (K. pneumoniae), Pseudomonas aeruginosa (P. aeruginosa), Acinetobacter species (spp.), Staphylococcus aureus (S. aureus).[14]

RESULT AND DISCUSSION

Due to the simple accessibility of antimicrobial medications that may be acquired without a prescription from a doctor or other qualified healthcare provider, excessive use is common in developing countries. In both cases, there is a misconception that antibiotics are "wonder drugs" that can effectively treat any illness.

The establishment and spread of highly antibiotic-resistant nosocomial infections in the hospital setting are likely primarily caused by the extensive and protracted use of antimicrobial medicines; The presence of highly immunosuppressed patients (such as AIDS patients, cancer patients, or transplant recipients) and frail elderly patients, invasive surgical procedures, the intensity of clinical therapy, a prolonged hospital stay, and the failure to control the spread of infections from patient to patient are all factors that may be significant.[15]

More pathogenic organisms are developing resistance to one or more antimicrobial medications. As a result, it is now very difficult and in some cases practically impossible to treat some common infections.

S. aureus is a Gram-positive bacteria that is normally found and one of the most widely distributed sources of nosocomial and community-acquired pneumonia, skin and soft tissue infections (SSTIs), and bloodstream infections. Strains of S. aureus resistant to antistaphylococcal penicillins are termed Methicillin Resistant S. aureus (MRSA).

MRSA can cause life-threatening infections in hospitals, including pneumonia, sepsis, bloodstream infections, and surgical site infections.

Haemodialysis, the insertion of medical devices like central venous catheters, or surgical procedures like joint replacement are all linked to hospital-acquired MRSA (HA-MRSA) infections. MRSA has recently emerged as a frequent source of infections in the general population that afflict children and young people who are healthy otherwise.

K. pneumoniae is a major cause of infections (bloodstream infections, urinary tract infections, and respiratory tract infections) in hospitals, especially in patients with weak immune systems, the elderly, and preterm infants.

K. pneumoniae can easily spread among patients in intensive care units and newborn care centers, which can result in nosocomial outbreaks. Multidrug-resistant K. pneumoniae has become more prevalent recently. All penicillins, cephalosporins (including third-generation cephalosporins), and aztreonam are resistant to extended-spectrum beta-lactamases (ESBLs).

carbapenem-resistant K. pneumoniae quickly become a global source of illnesses with multiple medication resistance.[15]

Acinetobacter baumannii: is a gram-negative, aerobic bacillus. It is an opportunistic pathogen that causes hospital-acquired infections all over the world. It has the ability to develop antibiotic resistance through a variety of methods, including the creation of enzymes that break down beta- lactam medicines also by the expression of efflux pumps and other mechanisms.

P. aeruginosa is a common pathogen that causes a number of acute and chronic nosocomial infections, including severe respiratory infections in patients with weakened host defenses. It is an aerobic gram-negative bacterium that can be found in the environment.

P. aeruginosa has demonstrated intrinsic resistance to a variety of antibiotics, which is caused by many resistance mechanisms that are both inherent and acquired from other microbes. The three primary mechanisms of resistance are increased efflux pumps, decreased permeability of the outer membrane, and the acquisition or mutation of resistance genes that produce proteins that regulate the passive diffusion of antibiotics through the outer membrane.[13]

Gram-negative, aerobic, motile bacteria of the Enterobacteriaceae family are known as Enterobacter species. Numerous strains of Enterobacter produce ESBLs and carbapenemases.

These MDR strains are resistant to almost all available antimicrobial drugs, except tigecycline and colistin.

Antibiotic	Pseudomonas aeruginosa/ isolate (36)	Staphylococcus aureus (19)	Klebsiella pneumoniae (17)	Escherichia coli (59)	Acinetobacter baumannii (6)
Ceftazidime	53.8		100	84.6	100.0
Ceftriaxone	100.0		0	81.5	100.0
Cefotaxime	100.0		77.8	71.4	90.0
Imipenem	80.0		100	80.0	100.0
Meropenem	20.0		50	13.0	100.0
Gentamicin	37.4	24.0	30.8	14.6	100.0

Ciprofloxacin	54.3	0	27.3	57.9	0.0
Colistin	22.2		0	0.0	0.0
Penicillin G		100			
Oxacillin		100			
Cefoxitin		100			
Trimethoprim/Sulfamethoxazole		20	0	83.3	100
Clindamycin		50			
Erythromycin		41.7			
Nitrofurantoin		0			
Vancomycin		13.3		0.0	
Ampicillin			100.0	95.2	
Amoxicillin/Clavulanic acid			50.0		
Ticarcillin/Clavulanic acid			100.0	85.7	
Piperacillin/Tazobactam			100.0	30.8	
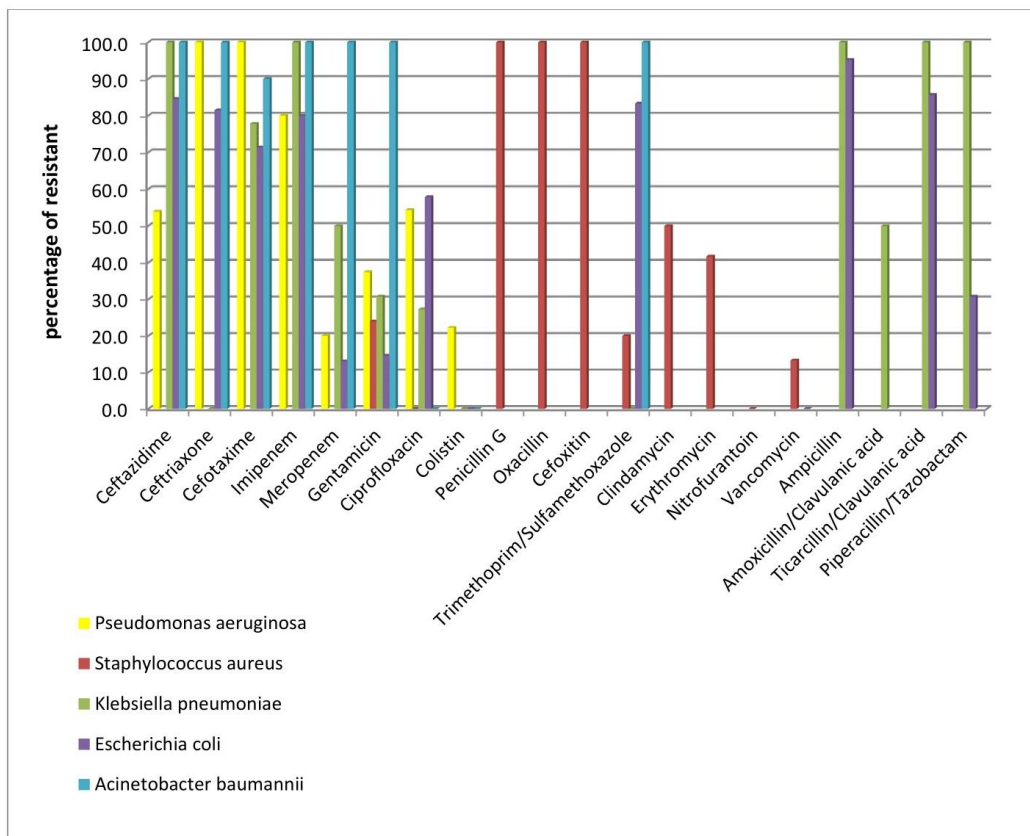
CONCLUSION

Although there is a lack of research, it seems that a significant proportion of AMR isolates that exhibit resistance to therapeutically significant antibiotics could potentially spread from hospitals via high-touch surfaces. For a better understanding of the current state of issues, short-term studies will be needed to establish baselines, and long-term longitudinal studies will be needed to identify trends, areas of risk, and intervention priorities. Teamwork between social scientists will play a significant role in identifying movements and behaviors that may either cause or exacerbate the spread of the problem. Dissemination of surveillance data in a timely and focused manner will remain a crucial element in countering the potential of resistance.

REFERENCES

1. O'Neill J. (2014) Antimicrobial resistance: tackling a crisis for the health and wealth of nations. Review on antimicrobial resistance. http://amr−review.org. (accessed on 3 Dec 2018).

2. World Health Organization (2018) Global Antimicrobial Resistance Surveillance System (GLASS) Report. Early implantation 2016−2017.
   http://apps.who.int/iris/bitstream/handle/10665/259744/9789241513449−eng.pdf. (accessed on 3 Dec 2018)

3. Antibiotic resistance. Marianne Frieri, Krishan Kumarb, Anthony Boutinc, Journal of Infection and Public Health, 2017; 10: 369—378

4. D. G. Joakim Larsson 1,2 and Carl-Fredrik Flach 1,2. Antibiotic resistance in the environment. NaTuRe RevIewS | MiCrobiology. volume 20 | May 2022

5. De Oliveira D.M.P., Forde B.M., Kidd T.J., Harris P.N.A., Schembri M.A., Beatson S.A., Paterson D.L., Walker M.J. Antimicrobial Resistance in ESKAPE Pathogens. Clin. Microbiol. Rev. 2020; 33: 181. doi: 10.1128/CMR.00181-19. [PMC free article] [PubMed] [CrossRef] [Google Scholar].

6. Santajit S., Indrawattana N. Mechanisms of Antimicrobial Resistance in ESKAPE Pathogens. BioMed Res. Int, 2016; 2016: 2475067. doi: 10.1155/2016/2475067. [PMC free article] [PubMed] [CrossRef] [Google Scholar].

7. Breijyeh Z., Jubeh B., Karaman R. Resistance of Gram-Negative Bacteria to Current Antibacterial Agents and Approaches to Resolve It. Molecules, 2020; 25: 1340. doi: 10.3390/molecules25061340. [PMC free article] [PubMed] [CrossRef] [Google Scholar]

8. WHO W.H.O. 10 Threats to Global Health in 2018. [(accessed on 18 December 2020)]. Available online: https://medium.com/@who/10-threats-to-global-health-in-2018- 232daf0bbef32018

9. Abdelaziz S., Aboshanab K., Yahia I., Yassien M., Hassouna N. Correlation between the Antibiotic Resistance Genes and Susceptibility to Antibiotics among the Carbapenem-Resistant Gram-Negative Pathogens. Antibiotics, 2021; 10: 255. doi: 10.3390/antibiotics10030255. [PMC free article] [PubMed] [CrossRef] [Google Scholar]

10. World Health Organization Ten Threats to Global Health in 2019. [(accessed on 18 December 2020)]. Available online: https://www.who.int/emergencies/ten-threats-to-global- health-in-2019

11. Iramiot J.S., Kajumbula H., Bazira J., Kansiime C., Asiimwe B.B. Antimicrobial resistance at the human–animal interface in the Pastoralist Communities of Kasese District, South Western Uganda. Sci. Rep, 2020; 10: 14737. doi: 10.1038/s41598-020-70517-w. [PMC free article] [PubMed] [CrossRef] [Google Scholar]

12. Malik B., Bhattacharyya S. Antibiotic drug-resistance as a complex system driven by socio- economic growth and antibiotic misuse. Sci. Rep., 2019; 9: 9788. doi: 10.1038/s41598-019-46078-y. [PMC free article] [PubMed] [CrossRef] [Google Scholar]

13. Giuseppe Mancuso, Angelina Midiri, Elisabetta Gerace and Carmelo Biondo. Bacterial Antibiotic Resistance: The Most Critical Pathogens. Pathogens 2021, 10, 1310. https://doi.org/10.3390/pathogens10101310

14. Antimicrobial resistance surveillance in Europe 2020 data 2022.

15. Francesca Prestinaci, Patrizio Pezzotti, Annalisa Pantosti. Antimicrobial resistance: a global multifaceted phenomenon.