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Incidence rate of multidrug-resistant organisms in a tertiary care hospital, North Delhi



Manoj Kumar^{*}, Sanjay Jain, Neetu Shree, Mukesh Sharma

Department of Microbiology, Hindu Rao and NDMC Medical College, Delhi 110007, India

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ABSTRACT

Background/Objectives: Antimicrobial resistance to microorganisms is a growing public health concern globally, especially in developing countries. This study was conducted to study the incidence rate of multidrug-resistant organisms with their antibiotic sensitivity pattern. Methods: An observational retrospective study was conducted for a period of 1 year from Jan 2013 to Dec 2013 in a tertiary care hospital in North Delhi. Sample processing and identification of organisms up to species level were done as per standard protocol, and antibiotic sensitivity was done as per CLSI guidelines.

Results: A total of 12,250 samples were received from OPDs (7000), wards (3025), and ICUs (2225) of various departments. Of these, 3080 showed significant growth of organisms. Among the 3080 isolates, 1838 were gram-negative bacilli, 1086 were gram-positive cocci and 156 were Candida spp. Escherichia coli (1080) was the most commonly isolated organism followed by Klebsiella spp. (446), MSSA (372), and Enterococcus (295).

Amongst GNB, maximum resistance was seen with ceftazidime followed by ceftriaxone, ofloxacin, norfloxacin, and cotrimoxazole. Least resistance was observed with amikacin, nitrofurantoin, netilmicin, and carbapenems. Among the GPC, maximum resistance was seen with cefepime followed by cotrimoxazole, ciprofloxacin and gentamicin. Least resistance was seen with nitrofurantoin, linezolid, and chloramphenicol.

Multidrug resistance was observed more from ward isolates, with E. coli (64.35%) topping the list followed by Acinetobacter (63.53%), Enterococcus (59.66%), Klebsiella (52.47%), MRSA (43.13%), Streptococcus (42.86%), and Pseudomonas (37.96%).

Conclusion: There is an urgent need to employ strategies that will slow the development of resistance to the current armamentarium.

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1. Introduction

Antimicrobial resistance (AMR) in microorganisms is a growing public health concern globally, especially in developing countries. Number of organisms developing resistance to commonly used antibiotics is increasing ever since the discovery of first antibiotic Penicillin in 1928. Extended spectrum β -lactamase (ESBL) was first reported in 1987.¹ Similarly, vancomycin resistance in Enterococci and Methicillin

Corresponding author. Tel.: +91 9873832875.

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E-mail address: drmanu_05@rediffmail.com (M. Kumar).

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resistance in Staphylococcus aureus (MRSA) were identified in 1980 and 1990, respectively. Vancomycin-resistant Staphylococcus aureus (VRSA) was first reported from the US in 2002, Brazil in 2005, and Jordan and India in 2006.²

According to a 2011 report from Center for Disease Control and Prevention, an estimated 722,000 health-care-associated infections occurred in American hospitals and were associated with 75,000 deaths.³ Repeated courses of antimicrobial therapy are common in acutely ill, febrile patients, who frequently have endotracheal tubes, urinary catheters, and central venous catheters.⁴ In combination with host factors, indwelling devices are routes for transmission and colonization of resistant infections.⁵ Lengthy or inappropriate antimicrobial therapy allows microbes to mutate into new forms that help them survive antibiotics and quickly become new dominant strains.⁶

Social factors such as demographic changes, deficient hygienic practices, and overcrowding have also been enumerated for the emergence of AMR. The multidrug-resistant (MDR) *Escherichia coli* has been isolated in carriers and in water samples in rural Tamil Nadu.^{2,7} Self medication, poor compliance, and inappropriate and irrational uses of antibiotics in humans and animals for therapeutic and nontherapeutic use are the other factors for hospital and community-acquired resistant infections, as documented by World Health Organization (WHO). A study conducted in Odisha⁸ has witnessed the presence of MDR E. coli in cow dung and drinking water.

A study conducted by Gruson et al. in France⁹ has documented an increased susceptibility to antibiotics by previously resistant gram-negative organisms by following antibiotic policy and antibiotic rotation in ventilator-associated pneumonia among intensive care units (ICU) patients.

The knowledge of national scenario of AMR is limited in India due to the absence of central monitoring agency. This study was undertaken in a tertiary care hospital in North Delhi to identify the multidrug-resistant organisms, their resistance pattern, and to develop antibiotic policy for the proper and effective use of antibiotics.

2. Material and methods

2.1. Type of study

An observational retrospective study was conducted for a period of 1 year from Jan 2013 to Dec 2013 in a tertiary care hospital in North Delhi.

2.2. Study population

Hospital-based population: Different clinical samples of patients such as blood, body fluids, CSF, female genital tract specimens, pus discharge, respiratory secretions, semen, stool, and urine were received in the Department of Microbiology from various OPDs and wards of Hindu Rao Hospital, a North Delhi tertiary care hospital. Relevant patient data, such as collection date, OPD/Ward, sex, culture results, and antimicrobial sensitivity results were collected and analyzed. A total of 12,250 nonrepetitive samples were included during the study period.

2.3. Culture

The various samples were cultured on different media using Blood Agar, MacConkey's Agar, Hichrome Media (for urine culture). Sample processing and identification of organisms to the species level were done as per standard microbiological protocol.

2.4. Bacterial identification and antimicrobial sensitivity test

Appropriate biochemical tests were done on culture isolates to identify the organisms based on colony morphology and results of Gram staining. Antimicrobial sensitivity test was performed using Kirby Bauer disk diffusion method (HiMedia, Mumbai) and carried out as per the Clinical and Laboratory Standards Institute (CLSI) guidelines.¹⁰ A 0.5 McFarland's physiological saline suspension prepared by picking up a single colony from pure culture was used. AST was done by placing standard antimicrobial impregnated disk (HiMedia, India) on lawn cultured Mueller-Hinton agar followed by incubation for 18-24 h at 37 °C. Results were determined as sensitive and resistant based on diameter of zone of inhibition. The control strains used were E. coli (ATCC 25922), S. aureus (ATCC 25923), and Pseudomonas aeruginosa (ATCC 27853) and they were included in the study. Organisms resistant to at least one agent in three or more antimicrobial classes were considered as MDR.11

Antibiotics tested for the sensitivity against gram-negative bacteria (GNB) were amikacin (30 µg), amoxicillin-clavulanic acid (20/10 µg), carbenicillin (100 µg), cefepime (30 µg), ceftazidime (30 µg), ceftriaxone (30 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), co-trimoxazole (23.75/1.25 µg), furazolidone (100 μ g) (only for stool specimens), gentamicin (10 μ g), imipenem (10 μ g), meropenem (10 μ g), netilmicin (30 μ g), nitrofurantoin (300 µg) (only for urine specimens), norfloxacin (10 μ g), ofloxacin (5 μ g), piperacillin-tazobactam (100/10 μ g) and tigecycline (15 µg). For gram-positive bacteria (GPC), amikacin (30 µg), amoxicillin-clavulanic acid (20/10 µg), cefepime (30 µg), cefoxitin (30 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), co-trimoxazole (23.75/1.25 µg), gentamicin (10 μ g), levofloxacin (5 μ g), linezolid (30 μ g), nitrofurantoin (300 µg) (only for urine specimens), oxacillin (30 µg), tetracycline (30 μ g), and vancomycin (30 μ g) were used.

All data were tabulated and analyzed. After collection of data, it was verified twice in Microsoft Excel sheet.

3. Results

During the study period, a total number of 12,250 samples were analyzed; of which, 7000 (57.14%), 3025 (24.69%), and 2225 (18.17%) samples were from OPDs, wards, and ICUs, respectively.

Out of 12,250 samples, 3080 (25.14%) showed significant growth on culture. Of these 3080 samples, 1260 (40.91%) samples were from male patients and 1820 (59.09%) from female patients (Fig. 1a), and 995 (32.31%), 1705 (55.36%), and 380 (12.34%) were from OPD, ward, and ICU patients, respectively (Fig. 1b). Remaining samples either had no growth

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