



REVIEW ARTICLE

ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF GRAM NEGATIVE AND POSITIVE BACTERIA FROM RESPIRATORY TRACT INFECTIONS IN RURAL GOVERNMENT HOSPITAL PATIENTS, VANDAVASI, TAMIL NADU, SOUTH INDIA

T.SIVAKUMAR¹, R.SENTHILKUMARAN² AND R. THAMIZHMANI^{3*}

1. Department of Microbiology, Kanchi Shri Krishna College of Arts and Science, Kanchipuram, India.
2. Department of Microbiology, King Nandhivarman College of Arts and Science, Thellar, Tamil Nadu, India.
3. Dept. of Microbiology, Regional Medical Research Centre (Indian Council of Medical Research), Port Blair, Andaman and Nicobar Islands.

*Corresponding author e-mail: mailmethamizh@rediffmail.com

Abstract

Respiratory tract infection is one of the most important infectious diseases in worldwide. The etiologic agents causing respiratory tract infection (RTI) as follows: bacteria and virus. This present study, to investigate the etiological agents RTI of and antimicrobial susceptibility pattern in RTI. We conducted a prospective, the respiratory tract infection cases in government hospital, Vandavasi, Tamil Nadu, during the period of October 2012 to February 2012. Throat swabs were collected from respiratory tract infection patients. Tests were conducted for detection of five known different bacterial pathogens by standard methods. An etiological diagnosis was established in 98 (89.09%) of the 110 patients who participated in the study. The distribution of the etiological agents was as follows: *Staphylococcus aureus* in 47 (47.9%) patients followed by *P. aeruginosa* 39 (39.7%), *P. mirabilis* 6 (6.1%) and *K. pneumoniae* 7 (7.14%). The antimicrobial resistance pattern were observed among the isolates showed *Pseudomonas aeruginosa* CTX, CTR, CEP, CoT, ERN, GEN, OFX, TET (100%), *S. aureus* showed for CTX, OFX (100%), *P. mirabilis* for AMP, CTX and *K. pneumoniae* for AMP, CTX. It is concluded that RTI is caused by a broad spectrum of etiological agents, a considerable number of patients having evidence of infection with more than one pathogen. The therapeutic significance of these findings should be elucidated in further studies.

Keywords: Respiratory tract infection, *Staphylococcus aureus*, Antimicrobial agents, Resistance

Introduction

Respiratory tract infection is one of the most important infectious diseases in worldwide. Globally more than 1.5 million death annually from respiratory infections is attributable to the environment, including at least 42% of lower respiratory infections and 24% of upper respiratory infections in developing countries (Boschet *et al.*, 2013). The upper respiratory tract infections 24% were reported was attributable to environmental risk factors, such as outdoor and indoor air pollution, environmental tobacco smoke in developing countries (Stenstrom *et al.*, 1993). The lower respiratory

infections, the rate for upper respiratory infections and otitis were estimated to be lower in developed countries at 12%. *S. pneumoniae*, *H. influenzae*, *Klebsiella pneumoniae*, *M. catarrhalis*, and *S. aureus* are commonly recognized etiological agents in respiratory tract infections (Bogaert *et al.*, 2004). All these major reports indicate that, the need for obtaining data on prevalent strains with the antimicrobial susceptibility pattern, to help in revising antibiotic strategy and guiding clinicians for the better administration of patients. Prevalent flora and antimicrobial resistance pattern may vary from

region to region depending upon the antibiotic pressure in that locality. Some of the studies reported in literature regarding the aetiology and antimicrobial susceptibility patterns of the Lower respiratory tract infections. The present study is an attempt to understand the distribution of various gram positive and gram negative pathogens causing Respiratory tract infection and their antibiotic resistance pattern in Vandavasi, Tamil Nadu.

Materials and Methods

Patients and Samples

The Patients included in the study were the respiratory tract infection admitted to Government Hospital, Vandavasi, Tamil Nadu during from October 2012 to February 2012. Throat samples were collected after obtaining signed consent from the patients/guardians prior to the antibiotic administration.

Microbiological examination for bacteriology

The throat swab samples were processed and the pathogenic bacteria isolates were identified and confirmed following standard techniques. The primary media used for gram positive bacteria isolation was Baird parker agar (BPA), Mannitol salt agar (MSA), Blood agar (BA) and the gram negative bacteria isolation was MacConkey agar (MaC). Conventional biochemical characterizations were performed on the isolates to identify them. Include as (Indole, Methyl red, Voges-proskauer, Citrate utilization, Catalase production, Oxidase, Urease, Gelatin hydrolysis and Oxidation fermentation, respectively), sugar fermentation (Monosaccharides, Disaccharides, Polysaccharides, Trisaccharides, respectively), alcohols, glycosides and non-carbohydrate substances such as inositol.

Antimicrobial susceptibility tests

The antimicrobial susceptibility tests were performed by Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2012) using commercially disks (Himedia Laboratories, Mumbai) of ampicillin (AMP), amoxicillin (), cefotaxime (CTX), ceftriaxone (CTR), cephalexin (CN), ciprofloxacin (CIP), cloxacillin, co-trimoxazole (CoT), erythromycin (ERN), gentamicin (GEN), penicillin, norfloxacin (NOR), ofloxacin (OFX), methicillin,

tetracycline (TET) in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2012). Control strains of *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923 were included in each test.

Statistical analysis

The proportions of respiratory pathogens isolated strains resistant to each of the antibacterial drugs were calculated for each of the bacterial pathogens separately and were compared for statistical significance by the χ^2 test using Epi Info 7 software (<http://www.cdc.gov/epiinfo/>).

Results

Patients and Isolates

During the study period from October 2012 to February 2012, a total of 110 samples (69 (62.9%) were male and 41 (37.2%) were female) were received from patients suffering with respiratory tract infections belonging to all age groups. Ninety eight (89.09%, 95% CI 83.26-94.92%) pathogenic isolates were found, *Staphylococcus aureus* accounted for majority of the isolates 47(47.9%) followed by *Pseudomonas aeruginosa* 39 (39.7%), *Proteus mirabilis* 6 (6.1%) and *K. pneumoniae* 7 (7.14%).

Antibiotic resistance

A wide spectrum of antibiotic resistance was observed among the isolates obtained during this study. Most of the respiratory bacterial pathogens showed a wide spectrum of resistance involving 3–21 drugs (Table 1). Resistance was observed among the isolates showed *Pseudomonas aeruginosa* CTX, CTR, CEP, CoT, ERN, GEN, OFX, TET (100%), *Staphylococcus aureus* showed for CTX, OFX (100%), *Proteus mirabilis* for AMP, CTX and *Klebsiella pneumoniae* for AMP, CTX (Table-1). The two isolates *P. mirabilis* and *K. pneumoniae* showed similar resistance profile of this study.

Fluoroquinolone resistance

Out of these 98 isolates, 85 (86.7%, 95% CI 79.98-93.42%) isolates were fluoroquinolone resistant, which include 47(47.9%) *S.aureus*, 39 (39.7%) *P.aeruginosa*, 1 (1.02%) *P.mirabilis* and 1 (1.02%) *K.pneumoniae*.

Table.1 Details of the antimicrobial resistance patterns of the isolates among the respiratory pathogens isolated in this study

| Antimicrobial agents | Isolates | | | |
|----------------------|---------------------------|---------------------------|------------------------------|-------------------------------|
| | <i>S. aureus</i> n=(%) | <i>P. aeruginosa</i> =(%) | <i>P. mirabilis</i> n=(%) | <i>K. pneumoniae</i> n=(%) |
| Ampicillin | 0 | 0 | 6(100) | 7(100) |
| Amoxicillin | 0 | 0 | 1(16.6) | 1(14.2) |
| Cefotaxime | 47(100) | 39(100) | 6(100) | 7(100) |
| Ceftriaxone | 0 | 39(100) | 0 | 0 |
| Cephalexin | 0 | 39(100) | 1(16.6) | 0 |
| Ciprofloxacin | 0 | 0 | 1(16.6) | 1(14.2) |
| Cloxacillin | 0 | 0 | 0 | 0 |
| Co-trimoxazole | 0 | 39(100) | 0 | 1(14.2) |
| Erythromycin | 1(2.1) | 39(100) | 1(16.6) | 1(14.2) |
| Gentamicin | 7(14.8) | 39(100) | 1(16.6) | 1(14.2) |
| Penicillin | 14() | 0 | 0 | 0 |
| Norfloxacin | 0 | 0 | 1(16.6) | 0 |
| Ofloxacin | 47(100) | 39(100) | 0 | 1(14.2) |
| Methicillin | 7(14.8) | 0 | 0 | 0 |
| Tetracycline | 0 | 39(100) | 1(16.6) | 1(14.2) |

Third generation cephalosporins resistance

Out of these isolates, 39 (39.7%, 95% CI 30.01-49.39%) isolates *P.aeruginosa* were resistance to third generation cephalosporins, which include as ceftriaxone, cefotaxime.

Discussion

Our study demonstrated the emergence of multidrug resistance among the respiratory pathogens causing Respiratory tract infection in Government Hospital, Vandavasi, Tamil Nadu. The present study is first of its kind conducted in this island evaluating the drug resistance pattern among the respiratory tract pathogens. It is frequently poly-microbial with predominantly multi drug resistant gram negative bacteria, such as *A. baumannii*, *P. aeruginosa*, *K. pneumoniae*, *E. coli* (Prashanth and Badrinath, 2004; Goel et al., 2009). In our study showed that, 13.2% isolates were gram negative bacteria (*P. mirabilis* and *K. pneumoniae*). *S. aureus* (47.9%) being the most common isolate followed by *P. aeruginosa* (39.7%). High level of resistance (79-98%) was reported

against all gram negative bacteria. Increasing trend in resistance to cephalosporins and decreasing trend in resistance to aminoglycosides against most gram negative bacteria were also reported (Gagneja et al., 2011).

The present study shows that the respiratory tract pathogens are rapidly acquiring resistance to the commonly used drugs, which will pose a great challenge for the effective treatment of gram positive and gram negative bacteria in this location. The emergence of newer mechanisms of resistance in resource-poor facilities particularly in developing countries is troublesome. Early, cost-effective and adequate detection of new mechanisms of resistance is crucial for infection control and prevention. The emergence of multidrug resistant isolates strengthens the need for a continuous surveillance system in these remote Islands. Information gathered as part of this investigation will be instrumental in identifying emerging antimicrobial resistance, for developing treatment guidelines appropriate for that community, and to provide baseline data, which will help the clinicians in better formulation of treatment strategy.

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