International Journal of Health and Clinical Research, 2021;4(15):1-3 e-ISSN: 2590-3241, p-ISSN: 2590-325X

Original Research Article

Study to Evaluate Various Microbial Infections among Subjects Reported to Department of Medicine at a Tertiary Care Hospital

Kotla Sravan Reddy [1],A. Samhitha Reddy [2], Penchila Prasad Kandikattu[2], Anand Kumar Boyapati[2*]

[1]Associate Professor, Department of General Medicine, Ananta Institute of Medical Sciences and Research Centre, Udaipur, Rajasthan, India

[2]Assistant Professor, Department of General Medicine, Ananta Institute of Medical Sciences and Research Centre, Udaipur, Rajasthan, India

Received: 19-05-2021 / Revised: 15-07-2021 / Accepted: 01-08-2021

Abstract

Background: Treatment of suspected bacterial infections is frequently initiated on the basis of clinical presentation, especially in acutely ill patients. Hence, the present study was conducted for evaluating spectrum of microbial infections among subjects reported to department of medicine. **Materials & Methods:** A total of 259 patients were enrolled in the present study. Only those patients were included in which confirmed diagnosis of microbial infection was enrolled. Swab samples were obtained from all the patients and were sent for culture analysis. Spectrum of microbial infections was obtained after culture analysis reports. All the results were recorded and analysed by SPSS software. **Results:** A total of 259 patients with presence of microbial infections were analysed. Among these patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pneumonia, Enterococcus spp., Pseudomonas aeruginosa, Candida spp. and Salmonella typhi infections were seen in 21.62 percent, 16.22 percent, 15.44 percent, 13.51 percent, 10.81 percent, 7.72 percent, 6.18 percent and 4.63 percent of the patients respectively. Among these 259 patients, 142 were males while the remaining 117 were females. **Conclusion:** Escherichia coli and Staphylococcus aureus were the most frequently encountered microbial infections in the present study.

Key words: Microbial, Bacterial, Infection.

Introduction

Treatment of suspected bacterial infections is frequently initiated on the basis of clinical presentation, especially in acutely ill patients. Laboratory tests are performed and therapy is subsequently modified based on microbial results and the clinical course. However, accurate initial empiric therapy depends on understanding of local disease prevalence and susceptibility patterns. Disease prevalence information can identify both similarities and differences in microbial etiologies of clinical syndromes when compared with other regions. The modifications to the initial empiric therapy depend heavily on timely and accurate microbial data. When laboratory diagnoses are not available, clinical decision making is based on knowledge or assumptions regarding prevalent pathogens[1-3].Microbial threats to health are microbes that lead to disease in humans. The challenges posed by microbial threats to health are daunting. Most developing nations have not shared fully in the public health and technological advances that have aided in the fight against infectious disease in the developing countries—a fight that some had hoped would come close to eliminating these threats in these countries[4-6]. Hence; the present study was conducted for evaluating spectrum of microbial infections among subjects reported to department of medicine.

Materials & methods

The present study was conducted for evaluating spectrum of microbial infections among subjects reported to Department of General Medicine, Ananta Institute of Medical Sciences and Research Centre, Udaipur, Rajasthan, India. A total of 259 patients were enrolled in the present study. Only those patients were included in which confirmed diagnosis of microbial infection was enrolled. Swab samples were obtained from all the patients and were sent for culture analysis. Spectrum of microbial infections was obtained after culture analysis reports. All the results were recorded and analysed by SPSS software.

Results

In the present study, a total of 259 patients with presence of microbial infections were analysed. Among these patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pneumonia, Enterococcus spp., Pseudomonas aeruginosa, Candida spp. and Salmonella typhi infections were seen in 21.62 percent, 16.22 percent, 15.44 percent, 13.51 percent, 10.81 percent, 7.72 percent, 6.18 percent and 4.63 percent of the patients respectively. Among these 259 patients, 142 were males while the remaining 117 were females.Among 142 male patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pneumonia, Enterococcus spp., Pseudomonas aeruginosa, Candida spp. and Salmonella typhi infections were seen in 21.83 percent, 15.49 percent, 14.79 percent, 13.38 percent, 10.56 percent, 9.15 percent, 5.63 percent and 4.63 percent of the patients respectively.

Among 117 female patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pneumonia, Enterococcus spp., Pseudomonas aeruginosa, Candida spp. and Salmonella typhi infections were seen in 21.37 percent, 17.09 percent, 16.24 percent, 13.68 percent, 11.11 percent, 5.98 percent, 6.84 percent and 4.27 percent of the patients respectively.

**Correspondence*

Dr. Anand Kumar Boyapati

Assistant Professor, Department of General Medicine, Ananta Institute of Medical Sciences and Research Centre, Udaipur, Rajasthan, India.

E-mail: anandboyapati@gmail.com

Table 1: Spectrum of microbial infections

Microbial infection	Number	Percentage
Escherichia coli	56	21.62
Staphylococcus aureus	42	16.22
Klebsiella pneumonia	40	15.44
Streptococcus pneumonia	35	13.51
Enterococcus spp.	28	10.81
Pseudomonas aeruginosa	20	7.72
Candida spp.	16	6.18
Salmonella typhi	12	4.63
Others	10	3.86
Total	259	100

Table 2: Gender-wise distribution and spectrum of microbial infections

Microbial infection	Males		Females		Total	
	Number	Percentage	Number	Percentage	Number	Percentage
Escherichia coli	31	21.83	25	21.37	56	21.62
Staphylococcus aureus	22	15.49	20	17.09	42	16.22
Klebsiella pneumonia	21	14.79	19	16.24	40	15.44
Streptococcus pneumonia	19	13.38	16	13.68	35	13.51
Enterococcus spp.	15	10.56	13	11.11	28	10.81
Pseudomonas aeruginosa	13	9.15	7	5.98	20	7.72
Candida spp.	8	5.63	8	6.84	16	6.18
Salmonella typhi	7	4.93	5	4.27	12	4.63
Others	6	4.23	4	3.42	10	3.86
Total	142	100	117	100	259	100

Discussion

Prevalence, a key measure in studies of disease ecology, is defined as the percentage of individuals in a population infected with a given pathogen. This measure describes the occurrence of a pathogen in a population and is an essential component of mathematical models in epidemiology. Because determining the “true” prevalence of a pathogen in a population would require exhaustive sampling from every individual in the target population, studies generally estimate pathogen prevalence by determining the infection status of a proportion of the population via necropsy or sampling of feces, urine, blood, or saliva. Because invasive procedures may be impractical or prohibited, particularly in studies of threatened populations, the analysis of noninvasive samples of material that potentially contains evidence of infection (e.g., feces or urine) is often preferred[7-10]. Hence; the present study was conducted for evaluating spectrum of microbial infections among subjects reported to department of medicine. In the present study, a total of 259 patients with presence of microbial infections were analysed. Among these patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pneumonia, Enterococcus spp., Pseudomonas aeruginosa, Candida spp. and Salmonella typhi infections were seen in 21.62 percent, 16.22 percent, 15.44 percent, 13.51 percent, 10.81 percent, 7.72 percent, 6.18 percent and 4.63 percent of the patients respectively. Among these 259 patients, 142 were males while the remaining 117 were females. Among 142 male patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia,Streptococcus pneumonia, Enterococcus spp., Pseudomonas aeruginosa, Candida spp. and Salmonella typhi infections were seen in 21.83 percent, 15.49 percent, 14.79 percent, 13.38 percent, 10.56 percent, 9.15 percent, 5.63 percent and 4.63 percent of the patients respectively. Maina D et al analyzed the spectrum of microbial agents and resistance patterns seen at a 300 bed tertiary private teaching hospital. For blood isolates, we used culture collection within the first three days of hospitalization as a surrogate for community onset, and within that group, Escherichia coli was the most common, followed by Staphylococcus aureus. In contrast, Candida spp. and Klebsiella pneumoniae were the most common hospital onset causes of bloodstream infection. Antimicrobial resistance rates for the most commonly isolated Gram-negative organisms were higher than many recent reports from Europe and North America. In contrast, Gram positive resistance rates were quite low, with 94% of S. aureus being susceptible to oxacillin and only rare isolates of vancomycin-resistant enterococci. Their study demonstrated high rates of antimicrobial resistance in Gram negative organisms, even in outpatients with urinary tract infections[10].In the present study, among 117 female patients, Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia,Streptococcus pneumonia,Enterococcus spp., Pseudomonas aeruginosa,Candida spp. and Salmonella typhi infections were seen in 21.37 percent, 17.09 percent, 16.24 percent, 13.68 percent, 11.11 percent, 5.98 percent, 6.84 percent and 4.27 percent of the patients respectively. Amaku M et al proposed a method to approximately estimate the full prevalence (and any other variable or parameter related to transmission intensity) of infectious diseases. The model assumes incomplete notification of incidence and allows the estimation of the non-notified number of infections and it is illustrated by the case of hepatitis C in Brazil. The method has the advantage that it can be corrected iteratively by comparing its findings with empirical results. The application of the model for the case of hepatitis C in Brazil resulted in a prevalence of notified cases that varied between 163,902 and 169,382 cases; a prevalence of non-notified cases that varied between 1,433,638 and 1,446,771; and a total prevalence of infections that varied between 1,597,540 and 1,616,153 cases. They concluded that the model proposed can be useful for estimation of the actual magnitude of endemic states of infectious diseases, particularly for those where the number of notified cases is only the tip of the iceberg[11].Rosenburg et al estimated that for every 100 persons infected with Shigella, 76 become symptomatic, 28 consulted a physician, nine submitted stool samples, seven had positive results, six were reported to the local health department and five were reported nationally to the Centers for Disease Control and Prevention. Thus they proposed a multiplication factor of 20 to estimate the number of Shigella infections based on national Shigellosis case reports[12].

Conclusion

Escherichia coli and Staphylococcus aureus were the most frequently encountered microbial infections in the present study.

References

1. Power E. Impact of Antibiotic Restrictions: The Pharmaceutical Perspective. Clin Microb Infect. 2006;12(Suppl. 5):25–34.
2. Boucher HW, Talbot GH, Benjamin DK, Jr, et al. 10 x '20 Progress–Development of New Drugs Active Against Gram-negative Bacilli: An Update from the Infectious Diseases Society of America. Clin Infect Dis. 2013;56(12):1685–94.
3. Bennett JW, Murray CK, Holmes RL, Patterson JE, Jorgensen JH. Diminished vancomycin and daptomycin susceptibility during prolonged bacteremia with methicillin-resistant Staphylococcus aureus. Diagn Microbiol Infect Dis. 2008; 60(4):437-40.
4. Shehab N, Patel PR, Srinivasan A, Budnitz DS. Emergency department visits for antibiotic-associated adverse events. Clin Infect Dis. 2008;47(6):735-43.
5. Salkind AR, Cuddy PG, Foxworth JW. Is this patient allergic to penicillin? an evidence-based analysis of the likelihood of penicillin allergy. JAMA. 2001;285(19):2498-505.
6. del Real GA, Rose ME, Ramirez-Atamoros MT, et al. Penicillin skin testing in patients with a history of beta-lactam allergy. Ann Allergy Asthma Immunol. 2007;98(4):355-9.
7. Dellit TH, Owens RC, McGowan JE, Jr, et al. Infectious Diseases Society of America and the Society for Healthcare Epidemiology of America guidelines for developing an institutional program to enhance antimicrobial stewardship. Clin Infect Dis. 2007;44(2):159-77.
8. Levine OS, Farley M, Harrison LH, Lefkowitz L, McGeer A, Schwartz B. Risk factors for invasive pneumococcal disease in children: a population-based case-control study in North America. Pediatrics. 1999;103(3):E28.
9. McCaig LF, Hughes JM. Trends in antimicrobial drug prescribing among office-based physicians in the United States. JAMA. 1995;273(3):214-9.
10. Maina D, Omuse G, Revathi G, Adam RD. Spectrum of Microbial Diseases and Resistance Patterns at a Private Teaching Hospital in Kenya: Implications for Clinical Practice. PLoS ONE. 2016; 11(1): e0147659.
11. Amaku M, Burattini MN, Chaib E, et al. Estimating the prevalence of infectious diseases from under-reported age-dependent compulsorily notification databases. Theor Biol Med Model. 2017;14(1):23.
12. Rosenberg ML, Gangarosa EJ, Pollard RA, Wallace M, Brolnitsky O, Marr JS. Shigella surveillance in the United States, 1975. J Infect Dis. 1977;136:458–60.

Conflict of Interest: Nil
Source of support: Nil