Journal of Biomedical Sciences | ISSN: 2960-9356
Research Article Peer-review, Open Access

Analysis of Measures to Improve the Bacteriological Characteristics of Respiratory Infections in Children

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Abstract

Globally, lower respiratory tract infections (LRTIs) are a major cause of morbidity and mortality among hospitalized patients, particularly in the elderly and children. In order to improve recovery and treatment procedures, the common bacteria and antibiotic susceptibility among LRTI patients from the respiratory ward, pediatric ward, and respiratory intensive care unit (RICU) were examined. In addition to the impacts of smoking and airborne pollution, health problems including allergies and viral illnesses can make the upper respiratory tract vulnerable to bacterial infection. The most frequent bacterial pathogens that cause upper and lower respiratory tract infections are Streptococcus pneumoniae, Haemophilus influenzae and Moraxella catarrhalis. The most common bacterial cause of tonsillitis and pharyngitis is Streptococcus pyogenes. When bacterial pathogens attach themselves to mucous membranes, colonization takes place. Edema and swelling are the outcome of the host immune system reacting to the invasive germs in an otherwise healthy person. The patient may experience recurring or chronic illness if antimicrobial therapy is unable to completely eliminate the invasive organisms and effectively stop the infection's progression. Previously susceptible to penicillin and other medicines, S. pneumoniae and other bacteria are now developing resistance. The extensive usage of antibiotics has led to the development and spread of bacterial resistance. Enzymatic inhibition, membrane impermeability, target enzyme modification, active antibiotic pumping out, and ribosomal target modification are the main mechanisms of bacterial resistance to antibiotics in upper respiratory tract infections.

Keywords: Haemophilus influenzae, Moraxella catarrhalis, Enzymatic inhibition, clinical diagnosis and treatment, respiratory pathogens.

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Introduction. Children's high rates of morbidity and mortality are caused by acute respiratory infections (ARIs), which place a heavy strain on healthcare systems around the globe. Lower respiratory tract infections (LRTIs) and upper respiratory tract infections (URTIs) are the two main categories into which ARIs fall. Viruses, common bacteria (like *Streptococcus pneumoniae*), atypical bacteria (like *Mycoplasma* and *Chlamydia species*), and fungi are among the many pathogens that cause respiratory tract infections in children. The distribution of these pathogens varies according to age, season, location, and detection techniques. According to recent studies, viruses are the main cause of respiratory infections in children, accounting for 60–70% of cases. The most common viruses include influenza, RSV, HRV, human metapneumovirus (HMPV), ADV, and parainfluenza viruses (PIV) [1-4]. The remaining substantial percentage of infections are caused by bacterial pathogens, such as *Staphylococcus aureus*, *group A Streptococcus*, MP, *Haemophilus influenzae* and *Streptococcus pneumoniae*. Traditional diagnostic techniques including culture, microscopic inspection, and immunoassay lack the sensitivity and timeliness required for early clinical diagnosis and treatment, and the symptoms of respiratory infections caused by several respiratory pathogens are frequently similar. Therefore, it is essential for prompt clinical diagnosis, disease prevention and control, and the prudent use of medications to quickly identify respiratory infections utilizing several fluorescence polymerase chain reaction (PCR) techniques. In order to evaluate the epidemiology of respiratory infections, including age and season variations, and to establish a foundation for clinical diagnosis and appropriate antibiotic use, this study retrospectively examined the nucleic acid test results of six common respiratory pathogens in 15,397 children in the urban area of Yongzhou [5-11]. Inappropriate antibiotic therapy and the illogical use of antimicrobial drugs have resulted in significant antibiotic resistance, elevated hospital mortality rates, and higher healthcare costs for LRTI patients. Of the outpatients who received antibiotic prescriptions, 74.0% received one, 23.3% received two, and 2.0% received three or more, according to Chinese researchers. As a result, choosing and using antibiotics effectively has become extremely difficult for all doctors. A comprehensive study of common bacteria and their patterns of susceptibility will enhance the treatment of LRTI patients globally. Antibiotics can also be used in surveillance programs to identify trends in microbial resistance and enhance treatment methods. However, no prior research has been done in China comparing the relative frequency and microbiological traits of the pathogens in pediatric versus adult LRTI patients hospitalized to respiratory wards and respiratory intensive care units (RICU). at order to improve recovery and treatment procedures at our hospital, the goal of this study was to look into the common bacteria and patterns of antibiotic sensitivity among LRTI patients from the pediatric ward, adult respiratory ward, and RICU [12-17].

The main purpose of this review is to analyze measures to improve the bacteriological properties of respiratory infections in children.

Co-infection epidemiology between bacteria and viruses. Children with respiratory illnesses are often found to have viral-bacterial co-infections, and there is compelling evidence that children who have co-infections experience more severe acute respiratory infections than those who just have single infections. Rates as high as 66–77% have been recorded, however the majority of research show rates between 20 and 50% for viral-bacterial co-infection. There is a lack of knowledge on the mechanisms underlying viral-bacterial co-infections and their clinical significance. Since both viruses and bacteria can coexist in the respiratory tract and their presence may indicate colonization rather than infection, it is challenging to assess the relative significance of the particular viruses and bacteria involved in co-infections. Furthermore, it is challenging to clarify the connections between bacteria and viruses in co-infections since clinical investigations cannot differentiate between primary and secondary infections [6-11]. *Streptococcus pyogenes, H. influenzae, S. pneumoniae* and *S. aureus* were the most commonly found organisms in the sputum, lung, and blood samples of infected patients. It was thought that the influenza virus worked in concert with pathogenic bacteria to increase the incidence of illness and mortality. Data from the 1957 "Asian flu" and 1968 "Hong Kong flu" pandemics, which demonstrated a correlation

between higher mortality and a higher prevalence of bacterial pneumonia, corroborated these conclusions. One of the main reasons why fewer people died during the 1957 and 1968 pandemics than during 1918 was thought to be the availability of medications that were effective against secondary bacterial infections. Bacterial co-infection was commonly documented in fatal pneumonia cases during the 2009 "swine flu" pandemic involving the H1N1 influenza virus, with S. pneumoniae being the most commonly diagnosed bacteria [12-18].

A significant contributor to both upper and lower ARI is respiratory viruses. Children are most affected by viral respiratory infections; between 6 and 10 viral infections are thought to occur in newborns and preschoolers each year. Since viruses produce 90% of URIs and bacteria only cause 10%, the involvement of viruses in URIs is well recognized. Children with LRI are also frequently found to have respiratory viruses, and while their involvement in LRI is recognized, there is ongoing discussion on the data supporting the clinical significance of respiratory viruses in LRI. Since lung aspiration is taken directly from the site of infection and would reveal etiological relevance for LRI, it is regarded as the gold standard for sample; nevertheless, its invasiveness and high rate of complications limit its use [1-4]. Because they are simple to obtain, upper respiratory tract samples—like nasopharyngeal aspirates—are employed more often in etiological investigations. It is countered, although, that viruses found in the nasopharynx simply indicate colonization and are not suggestive of LRI. However, children with LRI are more likely than asymptomatic, healthy children to have upper respiratory tract viruses. RSV, influenza, parainfluenza virus, human metapnuemovirus, and RV were shown to be causally attributed in children presenting with LRI as opposed to asymptomatic or healthy children, according to a 2015 comprehensive review and meta-analysis of case-control studies of children with and without LRI. Nevertheless, there was no discernible difference between the patients and controls in terms of adenovirus, bocavirus, or coronavirus detection. Recent developments in molecular techniques have brought attention to the importance of additional respiratory viruses, even though RSV and RV are generally accepted to be the most prevalent and significant viral causes of ARI in children [11-16].

Another frequent viral cause of ARI is adenovirus. Different serotypes of adenoviruses have been linked to various clinical syndromes, and they are divided into seven species, A through G. Although viral infections typically manifest as mild URIs, they can potentially develop LRIs such as pneumonia, bronchiolitis, and bronchitis. Additionally, gastrointestinal, ocular, genitourinary, and neurological illnesses can be brought on by adenoviruses. Up to 17% of children hospitalized with ARI have an adenovirus infection, which is most frequent in infancy and early childhood. Frequent episodes of wheezing, fever, hypoxia, and extended hospital stays are frequently linked to adenovirus [11, 14, 18].

The *Influenza Virus.* Children under the age of five and adults over 65 have the highest load of influenza virus, which is a significant contributor to ARI morbidity and mortality. Every year, seasonal flu epidemics are caused by the two primary influenza virus subtypes, A and B, which are in regular circulation. In 2008, there were an estimated 90 million new cases of influenza episodes, 20 million cases of influenza-associated ARI, and one million cases of influenza-associated severe ARI, which resulted in between 28,000 and 111,500 deaths globally, according to the first study to estimate the global incidence of influenza-associated ALRI in children under the age of five. An estimated 870,000 hospitalizations in children under the age of five were linked to influenza in a more recent comprehensive examination of the disease's burden in pediatric respiratory hospitalizations between 1982 and 2012 [7-14].

Bacteria are recognized as a significant contributor to ARI-associated morbidity and mortality, although being less commonly identified than viruses. The illness burden related to certain bacteria is not well recognized since traditional diagnostic techniques, such blood culture, which are still regarded as the gold standard in most situations, lack sensitivity. The incidence of bacteria in ARI is probably higher than is frequently stated because there is no reference standard for the identification of bacterial infections. Even though more recent studies have shown significant decreases in pneumococcal and Hib disease, most likely as a result of the widespread introduction of conjugate vaccines, *S. pneumoniae, H. influenzae, M. catarrhalis* and *S. aureus* are still recognized as the most prevalent and significant

bacterial pathogens in childhood ARI [3-10]. Additionally, culture-independent approaches have shown that just 1% of all bacteria can be cultivated using conventional diagnostic procedures, and that the human microbiome is significantly more extensive than previously thought. However, research identifying a wide variety of infections are still rare or nonexistent, and improved diagnostics are still uncommon in the majority of clinical settings. On the other hand, pathogen interactions that result in respiratory disease, the carriage of several infections, or the acquisition of novel pathogens can all be attributed to imbalances in the respiratory microbiome. The nasopharynx must first become colonized by bacterial pathogens in order to induce respiratory illness. Nasopharyngeal pathogens can cause upper and lower respiratory tract infections because the nasopharynx is situated between the nose, sinuses, ears, larynx, and lower respiratory tract. As a result, they play a significant role in the development of disease and the dissemination of pathogens. It is thought that colonization is a dynamic and intricate microbial process that includes species acquisition and eradication, interactions between bacteria and the host, and environmental influence. Since these bacteria frequently share an ecological niche, it is believed that they have highly evolved relationships with one another, and their interactions are crucial to the pathophysiology of disease. Additionally, even in healthy conditions, many species probably interact with one another. [11-19].

Clinical findings are used to diagnose acute sinusitis. Although a bacterial culture of the nasal discharge can be obtained, it is not very useful because the organisms recovered are typically contaminated by the nasal passage's existing flora. A thorough dental checkup, including sinus x-rays, may be necessary in cases of chronic sinusitis. To make a precise microbiologic diagnosis, sinusal specimens for bacterial culture must be obtained via antral puncture. Microbiologic Diagnosis: Clinical diagnosis is typically possible for common colds. Pharyngitis, epiglottitis, and laryngotracheitis are treated by bacterial and viral cultures of throat swab specimens. When epiglottitis occurs, blood cultures are also taken [1-4].

Clinical Proof of Childhood Viral-Bacterial Co-infections. The influenza virus is the most well-known and extensively researched example of a respiratory viral-bacterial co-infection. Co-infections between influenza viruses and bacteria have been extensively documented in both adults and children, and they are clearly linked to more severe illness. In contrast to other respiratory viruses like RV and RSV, influenza virus is a very uncommon viral disease, with the exception of epidemics. RSV is frequently linked to co-infections with viruses and bacteria; among children sick with RSV, co-infection rates have been observed to range from 17.5% to 44%. Using culture techniques, germs were recovered from 42% of lower airway secretions from infants with RSV in children with severe bronchiolitis that Thorburn et al. investigated. The most frequent bacteria found were *H. influenzae* and *S. aureus* and the study also found that children who had bacterial co-infection were more likely to develop bacterial pneumonia. RSV and *S. pneumoniae* were the most prevalent combination, accounting for 33% of cases, among the 39% of children with viral-bacterial co-infections found in a serological analysis of children with community-acquired pneumonia. Similar to influenza, RSV and *S. pneumoniae* infections peak in the winter, and RSV has been connected to seasonal spikes in *S. pneumoniae* infections. RSV and S. pneumoniae co-infection was more prevalent in cases than in controls in a case-control research by Benet et al., but RV and *S. pneumoniae* co-infection was the same in cases and controls[3-12].

Discussion. Worldwide, respiratory infections are a major cause of morbidity, mortality, and medical expenses for patients admitted to hospitals. Common bacterial infections known as LRTIs cause hospitalization and extensive antibiotic use, and they are responsible for 3 to 5% of adult fatalities, particularly in people over 60. According to reports, LRTIs like CAP are the main cause of death for children under the age of five and one of the most common infectious diseases in children. Clinically significant information about the identification and analysis of bacteria and their antibiotic susceptibility was provided by microbiological cultures of respiratory tract and blood specimens. Upon doing a comprehensive microbiological examination, we discovered that our hospital's pediatric ward, adult respiratory ward, and RICU showed significant differences in the distribution and drug susceptibility of LRTI bacteria. Different nations or areas have varying rates of Gram-negative infections, such as

Pseudomonas sp., Acinetobacter sp., and Klebsiella sp., with Asia having the highest rate and North America and Western Europe having the lowest. Lack of or noncompliance with antibiotic policy and infection control rules may be the cause of the high incidence of resistant species in underdeveloped nations. Different antibiotic therapies should be considered for different age groups, as Lee et al [1-7]. showed that antibiotic-resistant pathogens showed significant positive age-related trends and that a lower percentage of patients receiving appropriate antimicrobial therapy was linked to higher mortality. Nevertheless, our study has certain limitations, including the fact that it only looked at LRTI patients from one Beijing tertiary hospital, which may have resulted in enrollment bias given the location. Although many pneumonia episodes have been linked to viruses, it may be challenging to attribute pathogenicity unless the virus is consistently linked to illness. These include human metapneumovirus, adenovirus, rhinovirus influenza, respiratory syncytial virus, and parainfluenza. One of the drawbacks of this analysis is that we only looked at the drug susceptibility and bacterial dispersion of LRTI patients. The preliminary and retrospective cross-sectional design of our investigation is another limitation. Consequently, a prospective, multicenter, longitudinal study is needed to validate our results [8-14]. According to this case-control study conducted in a primary care environment in sub-Saharan Africa, the predominant causes of acute respiratory tract infections in children under five years old are influenza viruses A and B, RSV, and S pneumoniae. In this context, we advise assessing antibiotic prescribing behavior [15,16,17].

Conclusion. In conclusion, the season and the age of the child affect the rate at which dangerous germs are found in them. It is crucial to take into account the child's age as well as the season during which the respiratory pathogen is most common in order to avoid and manage infections brought on by these diseases.

There was significant variation in the microbial distribution and antibiotic susceptibility patterns of LRTI patients admitted to various hospital wards. As a result, various antibiotic treatments must to be taken into account for various age groups.

There was significant variation in the distribution of common bacteria and their antibiotic susceptibility patterns among LRTI patients hospitalized to our hospital's pediatric ward, adult respiratory ward, and intensive care unit. Therefore, it was recommended that different antibiotic treatments be used for different age groups and that excessive use of broad-spectrum antibiotics be avoided.

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