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Literature Review: Isolation and Identification of Bacteria in Children with Respiratory Infections

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Abstract

Background: Acute Respiratory Tract Infection (ARI) is one of the most common diseases and a leading cause of death in toddlers in Indonesia. This disease can be caused by bacteria, viruses, fungi, or aspiration. Objective: This study aims to determine the types of bacteria present in children with ARI and the most common bacteria found in children with ARI. Method: The study used a literature review with a narrative review design, where the research process started from searching in database search engines: Pubmed, NCBI, Google Scholar, then sorted related to the title of Isolation and Identification of ISPA bacteria in children in 2017-2025, The search results yielded 904 journals. The journals were re-selected based on the standard isolation method and PCR (Polymerase Chain Reaction) with keywords acute respiratory tract infection, ISPA children, ISPA bacteria children, yielding 60 journals. The next selection looked at the entire text containing tables and graphs, yielding 32 journals. Then, they were re-selected by looking at their suitability in the field of microbiology, yielding 8 journals. Results: The results of the study showed that various types of bacteria were successfully identified as the cause of ARI in children, including Streptococcus pneumoniae, Staphylococcus aureus, Haemophilus influenzae, Klebsiella pneumoniae, Pseudomonas aeruginosa, Corynebacterium diphtheriae, Moraxella catarrhalis, Bacillus sp., and Sphingomonas paucimobilis. Most studies reported that Gram-positive bacteria were more dominant, with Streptococcus pneumoniae and Staphylococcus aureus as the most common species, although Gram-negative bacteria such as Klebsiella pneumoniae and Pseudomonas aeruginosa were also found, especially in cases of severe ARI. Conclusion: This study shows that acute respiratory infections (ARI) in children are caused by various bacteria, predominantly Gram-positive. Streptococcus pneumoniae and Staphylococcus aureus are the most frequently found bacteria, while Klebsiella pneumoniae and Pseudomonas aeruginosa play a significant role in more severe cases.

***Keywords**: Acute Respiratory Infection, Acute Respiratory Infections (ARI) In Children, Acute Respiratory Infections (ARI) Bacteria In Children.*

INTRODUCTION

Acute Respiratory Tract Infection (ARTI) is a disease that infects the upper respiratory tract and even the entire lower respiratory tract (alveoli), such as sinus tissue, pleura, and the middle ear cavity. This disease lasts up to 14 days, so it can be said that this disease is an acute infection. ARI has symptoms such as fever, coughing for less than two weeks, runny nose/stuffy nose, and sore throat. ARI affects the structures of the respiratory tract above the larynx, but most cases affect both the upper and lower respiratory tracts simultaneously or sequentially. ARI is an acute infection of the upper or lower respiratory tract caused by microorganisms or bacteria, viruses, or rickettsia, with or without inflammation of the lung parenchyma. Acute respiratory tract infection (ARI) is a very common disease and is the leading cause of death in children under five years of age. **(**1)

According to *the World Health Organization* (WHO) in 2019, the number of ARI sufferers was 59,417 children, and it is estimated that in developing countries this number is 40-80 times higher than in developed countries. The WHO states that tobacco kills more than 5 million people per year, and it is projected to kill 10 million by 2020. Of that number, 70% of victims come from developing countries. Acute respiratory infections (ARI) are still a major health problem because they are the leading cause of death and illness in the world. Upper respiratory tract infections are the leading cause of death and illness among toddlers and children in Indonesia. Until now ( ), ARI is still a very important health issue for the people of Indonesia. (2)

A common problem encountered in ARI patients is the inability to expel secretions from the airways, which can result in ineffective airway clearance. Acute respiratory infections (ARI) are one of the causes of death in children in developing countries. ARI is an upper or lower respiratory tract disease, usually contagious, which can cause a spectrum of illnesses ranging from asymptomatic or mild infections to severe and fatal diseases, depending on environmental and host factors. However, ARI is often defined as an acute respiratory tract disease caused by infectious agents transmitted from person to person. Symptoms usually appear quickly, within a few hours to a few days. Symptoms include fever, cough, and often sore throat, coryza (runny nose), shortness of breath, wheezing, or difficulty breathing.

Acute respiratory infections (ARI) are infections of the respiratory tract that affect the upper and lower respiratory tracts. These are acute infectious diseases that attack one or more parts of the respiratory tract, from the nose (upper tract) to the tissues inside the lungs (lower tract). ARIs are caused by bacteria, viruses, fungi, and aspiration. Microorganisms that commonly cause ARIs include *Diplococcus pneumonia, Pneumococcus, Streptococcus, Staphylococcus aureus, and Haemophilus influenzae. Viruses: Influenza, Adenovirus, Silomegavirus, Aspergillus sp, Candida albicans, Histoplasma,* and others. (4)

According to the Indonesian Ministry of Health, infectious diseases are one of the leading causes of death in the country. Indonesia, as a developing country, has a high incidence of acute respiratory infections (ARI). ARI is also often included in the list of the ten most common diseases recorded in hospitals and community health centers. Based on the 2021 Indonesian Health Profile, there were 4,432,177 cases of ARI in children. In South Sulawesi, ARI is the most common disease in children, with a prevalence of 7.3% of the total number of ARI cases in Indonesia, which is equivalent to 323,549 cases of ARI in children in 2021.

Gram staining is a method used to classify bacteria into two main groups, namely gram-positive and gram-negative, based on the chemical and physical characteristics of their cell walls. Gram-positive bacteria have cell walls with a thick layer of peptidoglycan, which will appear purple after Gram staining. Examples of gram-positive bacteria include *Neisseria gonorrhoea, Treponema pallidum, Vibrio choleraes,* and *Bacillus subtilis.* In contrast, gram-negative bacteria have a thinner peptidoglycan layer in their cell walls, causing these bacteria to appear pink or red after Gram staining. Examples of gram-negative bacteria include *Streptococcus mutans, Staphylococcus aureus,* and *Escherichia coli.*

RESEARCH METHODS

Literature Search Strategy Design

Literature search using accredited/indexed electronic databases such as PubMed, NCBI, Google Scholar, and other database sources with keywords Isolation, Identification, bacteria, ISPA, and ISPA. Articles or journals that meet the inclusion and exclusion criteria were selected for further analysis. This literature review uses references published between 2017 and 2025.

Reference Criteria

Inclusion Criteria

1. References that match the search keywords (Isolation, Identification, Bacteria, ISPA, Pediatric ISPA).
2. References that comply with Dean's Decree No. 613/h.23/FK-UMI/V1/2020, namely literature containing at least 20 references published within the last 3 years counting backwards from the year the KTI was conducted. If none are found, then it is permissible to go back up to a maximum of 10 years.

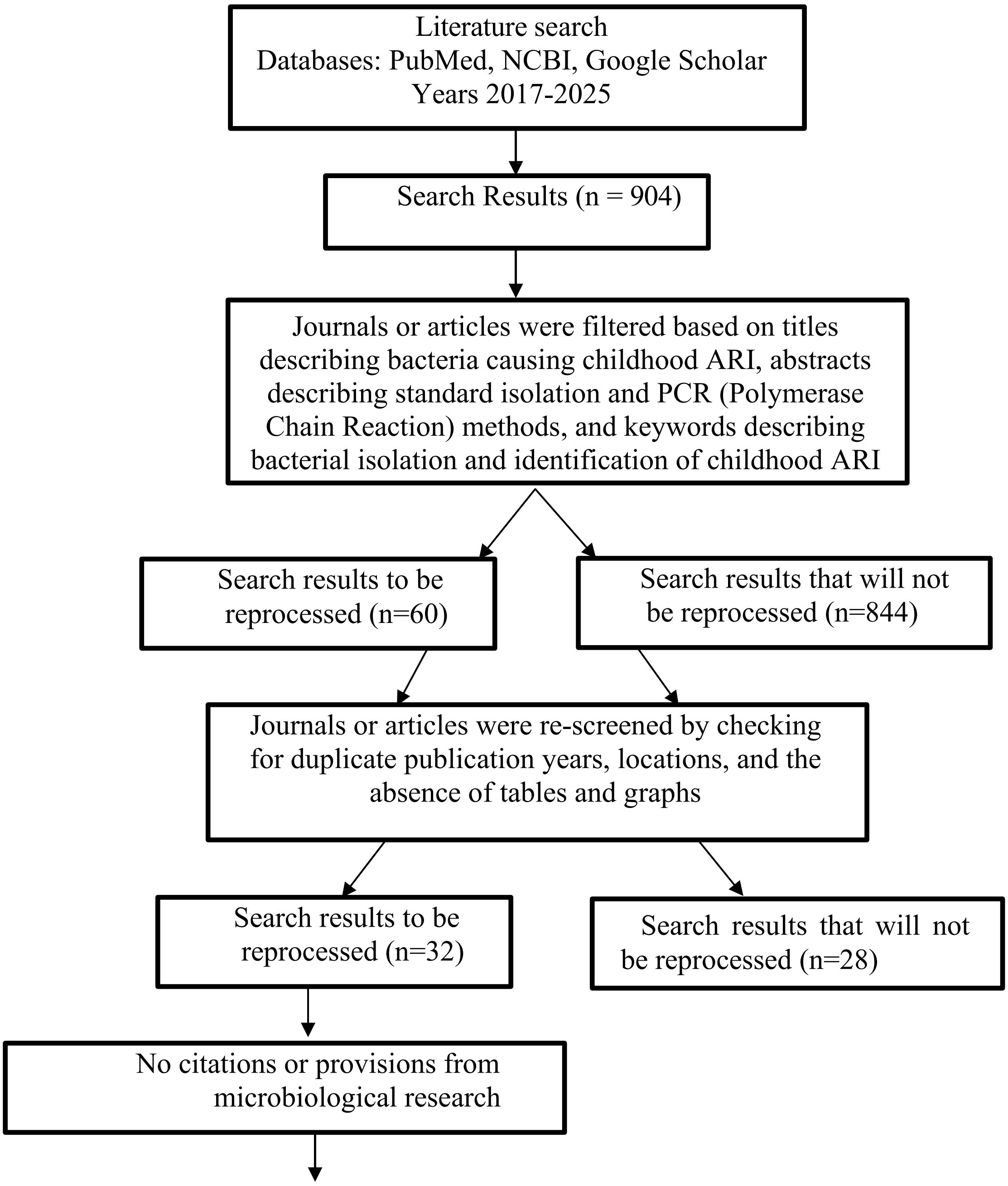
Reference Criteria

1. References not related to the research.
2. References that are not fully accessible.

Table 1. Electronic-Based

Electronic-Based	Findings	Literature
Elsevier / Clinical Key	0	0
PubMed	0	0
Google Scholar	904	10
TOTAL	**904**	**10**

Literature Search Flow



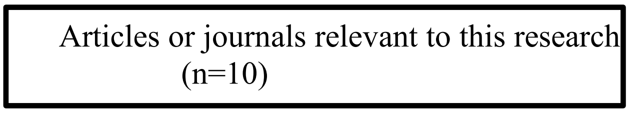


Figure 1. Literature Search Flowchart

RESULTS AND DISCUSSION

Results

This study used a literature review method by collecting data from various sources discussing the process of isolating and identifying bacteria in children with ARI. The collected literature was then analyzed and linked to the research topic to gain a deeper understanding. Some of the most relevant references are presented in the following table:

Table 2. Literature Review

Year	Title	Author	Method	Media	Type of Bacteria	Results
2023	Bacterial Culture Profile in Throat Swabs of Patients with Acute Respiratory Tract Infections at the Kalumpang Community Health Center in Ternate City	Erpu Nurdin, Mukhtasya m Zuchrullah, Fifi B Umagapi	Descriptive	Nutrient Agar (NA), Mannitol Salt Agar (MSA)	*Staphylococcus aureus* (50%), *Streptococcus pyogenes* (33%), *Pseudomonas aeruginosa* (7%), *Corynebacterium diphtheriae* (10%)	The majority of bacteria found were Gram-positive (93%), with *S. aureus* as the dominant bacterium in patients ISPA.
2022	Bacterial Identification Using Gram Staining in Patients with Acute Respiratory Tract Infections in Elementary School Children at the Tamalanrea Community Health Center in Makassar	Nomarihi Goraahe, Nadyah Haruna, Najamuddin, Andi Irhamnia Sakinah, Arifuddin Ahmad	Descriptive cut latitude	Direct Gram Stain	*Streptococcus pneumonia, Haemophilus influenza, Staphylococcus aureus, Neisseria sp., Pseudomonas sp.*	62.1% of bacteria were found Gram-positive positive, with *Staphylococcus aureus* as the the dominant species. A polymicrobial in 14% of samples.
2021	The Association Between Bacteria Colonizing the Upper Respiratory Tract and Lower Respiratory Tract Infection in Young Children: A Systematic Review and Meta-Analysis	Shantelle Claassen Weitz, Katherine Y.L. Lim, Christopher Mullally, Heather J. Zar, Mark P. Nicol	Systematic review meta-analysis	Nasopharyng al yngeal Swab, PCR, 16S rRNA Sequencing ng	*Haemophilus influenza, Klebsiella spp., Streptococcus pneumoniae, Moraxella catarrhalis, Staphylococcus aureus*	*H. influenzae* and *Klebsiella spp.* associated with infections respiratory tract . Evidence for *S. pneumoniae* remains variable.

2017	Burden of Bacterial Upper Respiratory Tract Pathogens in School Children in Nepal	Sangita Thapa, Shishir Gokhale, Annavarap U Laxminara Simha Sharma, Lokendra Bahadur Sapkota, Shamshul Ansari, Rajendra Gautam, Sony Shrestha, Puja Neopane	Observasional	Blood Agar, Chocolate Agar, Potassiumm Tellurite Agar	*Streptococcus pneumoniae (16.6%), Staphylococcus aureus (14.7%), Streptococcus pyogenes (5.3%), Corynebacteriumm diphtheriae (3.4%), Haemophilus influenzae (3.4%), Neisseria meningitidis (1.4%)*	*Colonization of S. pneumoniae is high among school children in Nepal, indicates the need for pneumococcal vaccine in the immunization program. High high resistance to certain .*
2024	Isolation and Antimicrobial Susceptibility Patterns of Bacterial Pathogens Causing Respiratory Tract Infections in Children	Zainab Mohsin Mohammed Hasan, Hassan Ali Hussein Al-Saadi	Cross-sectional	Blood Agar, MacConkyey Agar, Chocolate Agar, Mannitol Salt Agar	*Pseudomonas aeruginosa (21.6%), Klebsiella pneumoniae (20%), Streptococcus pneumoniae (15%), Haemophilus influenzae (16.6%), Staphylococcus aureus (13.3%), Streptococcus pyogenes (8.3%), Moraxella catarrhalis (5%)*	*Respiratory tract lower lower common (71.7%) compared to upper upper (28.3%). P. aeruginosa and K. pneumoniae most commonly found in severe cases, while S. pyogenes is dominant in mild cases. Antibiotic resistance is high in some bacterial isolates.*
2025	Aerobic Bacteria in Sputum Samples and Antibiotic Sensitivity Testing of Inpatients at Gmim Pancaran Kasih General Hospital, Manado	Vanessa Caitlin Euginia Kho, Heriyannis Homenta, Olivia Amelia Waworuntu	Observational, descriptive, cross-sectional	Nutrient Agar, MacConkey	*Staphylococcus sp. (62.5%), Sphingomonas paucimobilis (18.75%), Bacillus sp. (12.5%), Streptococcus sp. (6.25%)*	*The aerobic bacterial patterns identified in sputum are Staphylococcus sp., Streptococcus sp., Bacillus sp., and Sphingomonas paucimobilis, with Staphylococcus sp. as the most*

						dominant bacterial . most dominant.
2025	Aerobic Bacterial Patterns in Sputum Samples and Antibiotic Sensitivity Tests of Inpatients at Dr. J.H Awaloei Hospital	Ribka Milkallah Sepang, Heriyannis Homenta, Fredine E. S. Rares	Observational, descriptive, cross-sectional	Nutrient Agar, MacConkey	*Staphylococcus sp. (86.67%), Staphylococcus aureus (6.67%), Streptococcus sp. (6.67%)*	*The most common bacteria found was Staphylococcus sp., which was most sensitive to Amikacin and Meropenem and most resistant to Ampicillin, Aztreonam, Clindamycin, Erythromycin.*
2025	Aerobic Bacterial Patterns in Sputum Samples and Inpatient Antibiotic Sensitivity Tests Antibiotic Sensitivity Tests in Inpatients at S Sitti Maryam Islamic Hospital Manado	Aiko Budiman, Heriyannis Homenta, Fredine Rares	Descriptive, cross-sectional	Nutrient Agar (NA), Mac Conkey	*Sphingomonas paucimobilis (27.27%), Staphylococcus sp. (27.27%), Bacillus sp. (27.27%), Staphylococcus aureus (9.09%), Streptococcus sp. (9.09%)*	*The majority of bacteria found were Gram-positive (72.7%), with Staphylococcus sp., Bacillus sp., and Sphingomonas paucimobilis being the most abundant.*
2021	Identification of Gram-Negative Bacteria from Sputum of Patients with Acute Respiratory Tract Infections at Dustira Hospital, Cimahi City	Murleni Dorawati, Iis Herawati, Prima Nanda Fauziah	Descriptive	MacConkey Agar (MCA), IMVIC biochemical test	*Pseudomonas aeruginosa, Klebsiella pneumoniae, Enterobacter aerogenes, Proteus mirabilis*	*Four species of Gram-negative bacteria were identified from sputum samples of patients with acute respiratory tract infections, with Pseudomonas aeruginosa being the most dominant (26.6%). The study highlights the importance of sputum testing for accurate diagnosis and*

						appropriate antibiotic therapy.
2025	Bacterial Profile of Throat Swabs from Elementary School-Aged Patients with Respiratory Tract Infections at the Tamalanrea Community Health Center in Makassar	Nomarihi Goraahe, Nadyah Haruna, Najamuddin, Andi Irhamnia Sakinah, Arifuddin Ahmad	Descriptive cross-sectional study with laboratory testing using throat swab samples	Gram staining and microscopic identification	*Staphylococcus aureus (most common), Streptococcus sp., and several Gram-negative bacteria (e.g., Klebsiella pneumoniae, Pseudomonas sp.)*	*Out of 57 samples from school-aged children, 50.8% were Gram-positive bacteria and 49.2% were Gram-negative; Staphylococcus aureus was the most dominant cause.*

Discussion

Acute Respiratory Tract Infection (ARTI) is an infection that occurs suddenly and attacks one or more parts of the respiratory system, from the nose to the alveoli, including related structures such as the sinuses, middle ear cavity, and pleura. In Indonesia, ARI is still the leading cause of death in infants and toddlers, with a prevalence rate of 25% and a morbidity rate due to malnutrition of 14.9% ([22].

ARI is an acute respiratory disease caused by infectious agents and can cause symptoms within hours to several days[22]. One type of infectious agent that plays a role in the development of ARI is bacteria, which is the main focus of this study. In the first study by Erpi Nurdin et al. (2023), bacteria were identified from ARI patients' throat swabs using a culture method on selective media. The samples were cultured on blood agar to detect Gram-positive and Gram-negative bacteria, and tested with Gram staining and biochemical tests with a bacterial culture profile on throat swabs from patients with acute respiratory tract infections at health centers using a descriptive method with *Nutrient Agar (*NA) media. *Mannitol Salt Agar (*MSA). The types of bacteria produced were *Staphylococcus aureus, Streptococcus pyogenes, Pseudomonas aeruginosa, Corynebacterium diphtheriae*, and the results obtained showed that the majority of bacteria found were Gram-positive, with S. aureus being the dominant species. The results indicated that Gram-positive bacteria dominated (98%), with *Staphylococcus aureus (*50%) and *Streptococcus pyogenes (*33%) as the main bacteria, while only 2% were Gram-negative bacteria such as *Pseudomonas aeruginosa.* What distinguishes this study from others is the use of bacterial culture as the main method, allowing for more specific identification of the bacteria causing ARI. The conclusion of this study is that ARIs in patients are more often caused by Gram-positive bacteria, with a predominance of *Staphylococcus aureus (*[23].

Meanwhile, in a study by Bhuyan et al. (2017), bacterial pathogens were identified from nasal swab specimens of toddlers with ARI using conventional microbiological culture methods and biochemical tests. Samples were taken from 200 toddlers with symptoms, of which 43 specimens (21.5%) showed positive results for bacterial growth through culture. Bacterial identification was performed using selective media such as *MacConkey Agar, Blood Agar, and Chocolate Agar,* as well as antibiotic sensitivity tests. The bacteria most frequently isolated from symptomatic children were *Streptococcus pneumoniae (*39%), *Klebsiella pneumoniae* (24%), *Streptococcus spp. (*22%), *Enterobacter agglomerans (*9%), and *Haemophilus influenzae (*6%). Interestingly, E. *agglomerans*, which was found in 9% of symptomatic cases, was not found in the asymptomatic group, indicating its possible role as a pathogen causing ARI in toddlers in the region. What distinguishes this study is its focus on comparing symptomatic and asymptomatic groups, as well as identifying specific pathogens based on culture and biochemistry. The conclusion of this study is that ARI in toddlers in Bangladesh can be caused by various pathogenic bacteria, including less common pathogens such as *Enterobacter agglomerans (*(24).

Research by Erpi Nurdin et al. (2023) and Bhuyan et al. (2017) shows significant differences, both in the dominant group and in species diversity. In the study by Erpi Nurdin et al., Gram-positive bacteria dominated absolutely, accounting for 98%, with *Staphylococcus aureus (*50%) and *Streptococcus pyogenes (*33%) as the most abundant species. Only 2% of isolates were Gram-negative bacteria, such as *Pseudomonas aeruginosa.* This indicates that in the population of patients with upper respiratory tract infections ( ) studied, URTI infections tend to be caused by Gram-positive bacteria commonly found in the upper respiratory tract. In contrast, Bhuyan et al.'s study found a more diverse bacterial composition with significant involvement of Gram-negative bacteria. The most commonly found bacteria were *Streptococcus pneumoniae (*39%), followed by *Klebsiella pneumoniae (*24%), which are Gram-negative bacteria that can cause infection when the body's resistance is weak and are potentially resistant to antibiotics. Other types of bacteria also found were *Streptococcus spp. (*22%), *Enterobacter agglomerans (*9%), and *Haemophilus influenzae (*6%). A striking difference was seen in the presence of *Enterobacter agglomerans,* which was not found in the asymptomatic group and indicated its potential as a pathogen causing ARI in children. Thus, while Erpi Nurdin's study highlights the dominance of Gram-positive bacteria, Bhuyan et al. show that ARI, especially in toddlers, may involve a more diverse range of Gram-negative bacteria, including rare species that show antibiotic resistance. (23,24)

In the second study by Nomarihi Goraahe et al. (2023), entitled Identification of Bacteria Using Gram Staining in Patients with Acute Respiratory Tract Infections in Elementary School Children at the Tamalanrea Community Health Center in Makassar Using a Cross-Sectional Description Method, the media used was *direct Gram stain*, and the bacteria obtained were *Streptococcus pneumonia, Haemophilus influenza, Staphylococcus aureus, Neisseria sp., and Pseudomonas sp.* The results of this study found more Gram-positive bacteria, with *Staphylococcus aureus* as the dominant species, and polymicrobial infections were also found in the samples. Bacteria causing ARI in children were identified using the descriptive cross-sectional method and Gram staining. The samples used were throat swabs from pediatric patients diagnosed with ARI, which were then Gram-stained to distinguish between Gram-positive and Gram-negative bacteria. The results showed that the majority of bacteria found were Gram-positive (62.1%), with *Streptococcus sp.* and *Staphylococcus sp.* as the dominant bacteria. The advantage of this study compared to other studies is its focus on Gram staining as the main method of bacterial identification, without the use of selective culture. The conclusion obtained is that ARI in children is caused more by Gram-positive bacteria than Gram-negative bacteria, so that the Gram staining method can be the first step in the laboratory diagnosis of ARI in children(25) .

Meanwhile, in a study by Jia et al. (2023), bacteria were identified from sputum specimens of pediatric patients with Acute Respiratory Infections (ARI) in Wuxi, China, during the period from 2014 to 2021. The method used was bacterial culture from sputum, which was inoculated into various growth media, namely chocolate agar, blood agar, MacConkey agar (for Gram-negative bacteria selection), and Sabouraud agar (for fungus detection), all of which were produced by Zhengzhou Renfa Sai Biotechnology, Henan, China. Of the total 4,610 sputum specimens cultured, 508 samples (11.0%) showed growth of microbial colonies. The identification results showed that the majority of isolates found belonged to the Gram-negative bacteria group (59.84%), followed by Gram-positive bacteria (33.86%), and the rest were fungi (6.30%). The dominant species from the Gram-negative group included *Haemophilus influenzae (*12.20%), *Escherichia coli (*11.42%), *Klebsiella pneumoniae (*10.63%), and *Acinetobacter baumannii (*9.06%). Meanwhile, from the Gram-positive group, *Staphylococcus aureus* was the most isolated (16.73%). The uniqueness of this study lies in its long time span of eight years and the use of various selective culture media, which allowed for the detection of a wide spectrum of microorganisms. This study indicates that Gram-negative pathogens consistently dominate respiratory tract infections in children, and their increasing prevalence over the years is a significant concern in clinical practice, particularly in infection control and appropriate antibiotic selection strategies(26).

Research by Nomarihi Goraahe et al. (2023) identified bacteria causing ARI in children through Gram staining and found that the majority of isolates were Gram-positive (62.1%), dominated by *Streptococcus* and *Staphylococcus sp*. This research is simple but effective as an initial detection without culture. In contrast, Jia et al. (2023) performed sputum culture on various selective media and found that

59.84% of isolates were Gram-negative, such as H. *influenzae, E. coli,* and K. *pneumoniae.* This difference in bacterial dominance is due to differences in methods and sample sources, where the culture approach provides more detailed and specific results. ([25,26])

In the third study by Shantelle Claassen-Weitz et al. (2021), entitled *The Association Between Bacteria Colonizing the Upper Respiratory Tract and Lower Respiratory Tract Infection in Young Children: A Systematic Review and Meta-analysis,* using the *systematic review meta-analysis* method, the types of bacteria found were *Haemophilus influenza,Klebsiella spp., Streptococcus pneumoniae, Moraxella catarrhalisis,* and *Staphylococcus aureus*. The results of this study showed that *H. influenzae* and *Klebsiella spp*. were most commonly associated with lower respiratory tract infections, while the other bacteria varied. A systematic review and meta-analysis was conductedanalysis aimed at identifying the relationship between bacterial colonization in the upper respiratory tract and lower respiratory tract infections (LRTI) in children. Data were collected from various studies that used culture and PCR methods to identify bacteria from nasopharyngeal swabs. The results showed that the presence *of Haemophilus influenzae* and *Klebsiella sp.* in the upper respiratory tract was significantly correlated with an increased risk of lower respiratory tract infection. What distinguishes this study from others is its meta-analysis-based approach, which allows data from various sources to be combined to obtain stronger conclusions. This study concludes that bacteria in the upper respiratory tract can be a major predictor of lower respiratory tract infections, highlighting the importance of controlling bacterial colonization to prevent LRTI([27]) .

Meanwhile, in a study by Takeyama et al. (2021), bacterial identification was performed on nasopharyngeal swab samples from 1,056 preschool children treated for lower respiratory tract infections in Japan during the period 2016–2018. Bacterial culture was performed using blood agar, mannitol salt agar, and chocolate agar media in a 5–6% CO_2 atmosphere. The results showed that 1,046 (99%) of the total patients had positive culture results, with a total of 1,676 bacterial isolates. The three main species found were *Moraxella catarrhalis (*31%), *Haemophilus influenzae (*27%), and *Streptococcus pneumoniae (*25%). The proportion of bacterial isolates resistant to antibiotics such as PRSP (penicillin resistant), BLNAR/BLPAR (ampicillin resistant), and MRSA was also recorded, but the study concluded that the presence of resistant bacteria did not significantly affect clinical severity (duration of fever or length of hospital stay). The uniqueness of this study lies in the large number of patients and the approach of using nasopharyngeal microbiota as a proxy for lower respiratory tract microbiota. In conclusion, although Gram-positive and Gram-negative bacteria were commonly found in patients with lower respiratory tract infections, the presence of resistant strains did not necessarily worsen the course of the disease, and the use of narrow-spectrum antibiotics is still recommended([28]) .

Both the study by Shantelle Claassen-Weitz et al. (2021) and Takeyama et al. (2021) focused on the role of bacterial colonization in the upper respiratory tract as an important factor in the occurrence of lower respiratory tract infections (LRTI) in children. Both highlight the presence of bacteria such as *Haemophilus influenzae,* which consistently emerges as one of the dominant pathogens. Additionally, both studies used nasopharyngeal samples as the starting point for examination, with the aim of evaluating their association with lower respiratory tract infections. Both studies also make important contributions to understanding the microbiome profile and emphasize the need for controlling bacterial colonization in efforts to prevent LRTI. ([27,28])

In the fourth study by Sangita Thapa et al. (2017), titled *Burden of Bacterial Upper Respiratory Tract Pathogens in School Children of Nepal*, using observational methods, while the media used in this study were *Blood Agar, Chocolate Agar, and Potassium Tellurite Agar.* The types of bacteria obtained in this study were quite numerous because, as we can see, the media used were also quite adequate, such as *Streptococcus pneumoniae, Staphylococcus aureus, Streptococcus pyogenes, Corynebacterium diphtheriae, Haemophilus influenzae, and Neisseria meningitidis*. In this study, S. *pneumoniae* was found to be the most prevalent bacterium among school children in Nepal, highlighting the need for pneumococcal vaccination. Antibiotic resistance was also identified. A study was conducted on the prevalence of upper respiratory tract pathogens in school children using bacterial culture and antibiotic resistance testing. Samples were taken from the posterior pharyngeal wall and tonsils, then cultured on *blood agar* and *chocolate agar* to identify the main pathogens. The results showed that *Streptococcus pneumoniae (*16.6%) was the most common bacterium, followed by *Staphylococcus aureus (*14.7%) and *Haemophilus influenzae (*3.4%).

The uniqueness of this study lies in the analysis of antibiotic resistance, which found that *Streptococcus pneumoniae* had a very high level of resistance to penicillin (91.17%), which was not found in other studies. The conclusion drawn was that *Streptococcus pneumoniae* was the dominant pathogen in school children and its resistance to antibiotics was a major concern in the treatment of ARI[29].

Meanwhile, research conducted by Angriani Fusvita and Ani Umar (2016) aimed to identify the bacteria causing ARI in children under five years of age. The study lasted three months and involved 25 toddlers as respondents. Nasal mucus samples were taken using sterile swabs, then planted on BHIB media and isolated using BAP, MCA, and MSA media. Identification was carried out through colony morphology, hemolysis, and Gram staining. The results showed that of the 50 samples analyzed, three types of bacteria causing ARI were found, namely *Haemophilus influenzae* (60%), *Staphylococcus aureus* (30%), and *Streptococcus sp.* (10%). This study confirmed that *Haemophilus influenzae* is the bacterium that most commonly infects the upper respiratory tract in toddlers, and emphasized that age, sampling technique, and environment also influence the variation of bacteria found. Both studies identified bacteria that cause upper respiratory tract infections in children, but with differences in age groups and dominant bacteria types. In a study by Sangita Thapa et al. (2017), *Streptococcus pneumoniae* was the most dominant bacterium (16.6%), followed by *Staphylococcus aureus (*14.7%) and *Haemophilus influenzae (*3.4%). This study was conducted on school-aged children and emphasized the importance of antibiotic resistance, especially to penicillin (29).In contrast, a study by Angriani Fusvita and Ani Umar (2016) conducted on toddlers found *Haemophilus influenzae* to be the most common bacterium (60%), followed by *Staphylococcus aureus (*30%) and *Streptococcus sp. (*10%)(30) .This difference indicates that *Haemophilus influenzae* is more commonly found in toddlers, while *Streptococcus pneumoniae* tends to be more dominant in school-aged children.(29,30)

In the fifth study by Zainab Mohsin Mohammed Hasan et al. (2024), entitled *Isolation and Antimicrobial Susceptibility Patterns of Bacterial Pathogens Causing Respiratory Tract Infections in Children*, using a *cross-sectional* method with *Blood Agar, Mac Conkey Agar, Chocolate Agar, and Mannitol Salt Agar*, the bacteria obtained in this study were *Klebsiella pneumoniae, Streptococcus pneumoniae, Haemophilus influenzae, Staphylococcus aureus, Streptococcus pyogenes, and Moraxella catarrhalis.* From the bacterial results adapted in this study, upper respiratory tract infections were mostly found in P. *aeruginosa* and K. *pneumoniae* bacteria, which were most commonly found in severe cases, while S. *pyogenes* was dominant in mild cases and high antibiotic resistance in several bacterial isolates. Bacteria causing respiratory tract infections in children were isolated and analyzed for their resistance patterns to antibiotics. The method used was bacterial culture from throat swab and sputum samples, which were grown on *blood agar*, *MacConkey agar,* and *chocolate agar.* The results showed that lower respiratory tract infections were more dominant (71.7%) than upper respiratory tract infections (28.3%), with *Pseudomonas aeruginosa (*21.6%) and *Klebsiella pneumoniae (*20%) as the main pathogens. What distinguishes this study from others is its focus on lower respiratory tract infections and analysis of disease severity differences based on the types of bacteria found. The conclusion drawn is that Gram-negative bacteria such as *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* more often cause more severe respiratory tract infections compared to Gram-positive bacteria.

Meanwhile, in a study by Dorawati et al. (2021), bacteria were identified from the sputum of ARI patients using the bacterial culture method on MacConkey Agar (MCA) selective media. The identification process was continued with Gram staining and IMViC biochemical tests to identify Gram-negative bacterial species. Of the total 15 samples, 13 samples (86.6%) showed bacterial colony growth, with the final results indicating that all colonies analyzed belonged to the Gram-negative bacteria group. The species found included *Pseudomonas aeruginosa (*26.6%), *Klebsiella pneumoniae (*13.3%), *Enterobacter aerogenes (* 13.3%), *and Proteus mirabilis (* 13.3%). What distinguishes this study from others is its exclusive focus on the identification of Gram-negative bacteria and the use of advanced biochemical tests for specific species. The conclusion of this study is that ARI can also be caused by the dominance of Gram-negative bacteria, especially from the Enterobacteriaceae family, and their presence needs to be watched out for, especially in patients with low immunity or nosocomial infections. A comparison of the types of bacteria found in ARI patients in both studies shows similarities and differences (32).

In a study by Zainab Mohsin Mohammed Hasan et al. (2024), the most frequently found bacteria were *Pseudomonas aeruginosa* (21.6%) and *Klebsiella pneumoniae* (20%), with a focus on more severe lower respiratory tract infections. Meanwhile, the study by Dorawati et al. (2021) also found a predominance of *Pseudomonas aeruginosa (*26.6%) and *Klebsiella pneumoniae (*13.3%), but with the addition of other species such as *Enterobacter aerogenes* and *Proteus mirabilis (*13.3% each). This indicates that although both studies identified *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* as common pathogens in ARIs, the study by Dorawati et al. (2021) noted a wider diversity of Gram-negative bacteria. ([31,32])

In the sixth study by (Caitlin et al., 2025), aerobic bacterial patterns were identified in the sputum of patients hospitalized with ARI at GMIM Pancaran Kasih Manado General Hospital, and antibiotic sensitivity tests were conducted. The study design used was descriptive observational with a cross-sectional approach, using Gram staining, biochemical tests, disc diffusion method, and Vitek test. The results showed that Gram-positive bacteria were more dominant (81.25%) than Gram-negative bacteria (18.75%). The bacteria found were *Staphylococcus sp. (62.5%), Sphingomonas paucimobilis (18.75%), Bacillus sp. (12.5%), and Streptococcus sp. (6.25%).* Sensitivity tests showed that all bacteria were sensitive to Meropenem and Gentamicin (100%), but resistant to Ampicillin and Aztreonam (100%). The conclusion of this study is that Staphylococcus sp. is the dominant bacterium in patients with ARI, and the bacterial sensitivity pattern shows the highest effectiveness of Meropenem and Gentamicin, while Ampicillin and Aztreonam are ineffective.

In the seventh study by (Sepang et al., 2025), the identification of aerobic bacterial patterns and antibiotic sensitivity tests were conducted on the sputum of inpatients at Dr. J.H. Awaloei Hospital in Manado. The study design used was descriptive with a cross-sectional approach using 15 sputum samples, cultured on Nutrient Agar and Mac Conkey media, then Gram staining, biochemical tests, and antibiotic sensitivity tests were performed. The results showed that all samples grown produced Gram-positive bacteria (100%) without any Gram-negative bacteria. The types of bacteria identified were *Staphylococcus sp. (86.67%), Staphylococcus aureus (6.67%), and Streptococcus sp. (6.67%).* Sensitivity tests showed that all bacteria were highly sensitive to Amikacin (100%) and Meropenem, while the highest resistance was found to Ampicillin, Aztreonam, Clindamycin, and Erythromycin. The conclusion of this study is that *Staphylococcus sp.* is the most dominant bacterium in patients with ARI at Dr. J.H Awaloei Hospital, and Amikacin and Meropenem are the most effective antibiotics, while Ampicillin and Clindamycin show complete resistance. ([35])

In the eighth study by (Budiman et al., 2025), aerobic bacterial patterns were identified and antibiotic sensitivity tests were conducted on the sputum of inpatients at Sitti Maryam Islamic Hospital in Manado. The study design used was descriptive with a cross-sectional approach using 12 sputum samples cultured on Nutrient Agar and Mac Conkey, then tested with Gram staining, biochemical tests, and antibiotic sensitivity tests. The results showed that out of 12 samples, 8 Gram-positive bacteria (72.73%) and 3 Gram-negative bacteria (27.27%) were found. The types of bacteria identified were: *Staphylococcus sp. (27.27%), Bacillus sp. (27.27%), Sphingomonas paucimobilis (27.27%), Staphylococcus aureus (9.09%), and Streptococcus sp. (9.09%).* Sensitivity tests showed that all bacteria were sensitive to Meropenem, Amikacin, and Ciprofloxacin (100%), but showed high resistance to Ampicillin and Aztreonam (100%). The conclusion of this study is that *Staphylococcus sp., Bacillus sp., and Sphingomonas paucimobilis* were the most commonly found bacteria, with sensitivity patterns showing Meropenem, Amikacin, and Ciprofloxacin as the most effective antibiotics, while Ampicillin and Aztreonam were ineffective. ([33])

In the ninth study by (Dorawati et al., 2021), Gram-negative bacteria were identified from the sputum of patients with acute respiratory infections (ARI) at Dustira Hospital in Cimahi City. This study used a descriptive method through sputum culture examination planted on MacConkey Agar (MCA) media, followed by microscopic Gram staining and IMVIC biochemical testing. The results showed that four species of Gram-negative bacteria were found in 15 sputum samples from ARI patients, namely Pseudomonas aeruginosa (26.6%), Klebsiella pneumoniae (13.3%), Enterobacter aerogenes (13.3%), and Proteus mirabilis (13.3%). The conclusion of this study indicates that Pseudomonas aeruginosa is the most dominant species, and sputum examination is important to confirm the diagnosis of ARI so that antibiotic therapy is more effective and targeted. ([36])

In the tenth study by (Goraahe et al., 2025), bacterial profiles were identified from throat swabs of elementary school-aged patients with ARI at the Tamalanrea Community Health Center in Makassar. This study used a descriptive cross-sectional design with laboratory tests on 57 throat swab samples, which were then subjected to Gram staining and microscopic identification tests to determine the type of bacteria causing the infection ( ). The results showed that 50.8% of the bacteria were Gram-positive and 49.2% were Gram-negative, with Staphylococcus aureus being the most dominant bacterium. The conclusion of this study confirms that ARI infections in elementary school children in the Tamalanrea Community Health Center area are more commonly caused by Gram-positive bacteria, especially Staphylococcus aureus, than Gram-negative bacteria. ([37])

CONCLUSION

Based on the results of eight *studies* related to "Isolation and Identification of Bacteria in Children with ARI," it can be concluded that various types of bacteria causing ARI in children have been identified, including *Streptococcus pneumoniae, Staphylococcus aureus, Haemophilus influenzae, Corynebacterium diphtheriae, Pseudomonas aeruginosa, Klebsiella pneumoniae, Moraxella catarrhalis, Bacillus sp., Sphingomonas paucimobilis,* and several other bacteria. Based on the results of the study, Gram-positive bacteria were more commonly found in pediatric ARI than Gram-negative bacteria. *Streptococcus pneumoniae and Staphylococcus aureus* were the dominant bacteria in several studies, while Gram-negative bacteria such as *Pseudomonas aeruginosa, Klebsiella pneumoniae, and Haemophilus influenzae were also found,* especially in more severe cases of ARI. The media used in the study to isolate the bacteria causing ARI included *Blood agar, MacConkey agar, Chocolate agar, Mannitol Salt agar, and Nutrient agar.* Several studies also used Gram staining, biochemical tests, antibiotic sensitivity tests, as well as systematic review and meta-analysis approaches to strengthen the identification results.

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