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Heterogenecity of Micro-Organism and Antibiotic Sensitivity in Congenital Heart Disease Patients with Unresolving Fever

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Abstract
Background*: Congenital heart disease (CHD) patients with unresolving fever are at a heightened risk of severe infections due to their underlying condition and frequent hospitalizations. Understanding the microbial heterogeneity and antibiotic sensitivity patterns in this population is crucial for effective management, particularly in resource-limited settings like Bangladesh.*
Methods*: This cross-sectional study was conducted at the National Institute of Cardiovascular Disease, Bangladesh, from August 2022 to August 2023, involving 54 CHD patients with unresolving fever unresponsive to conventional antibiotics. Blood cultures were performed to identify microbial profiles and their antibiotic sensitivity patterns, and data were analyzed using SPSS software.*
Results*: The most commonly isolated pathogens were Acinetobacter (22.22%) and Pseudomonas (18.52%), with significant sensitivity to meropenem (88%) and TZ+P (94%), respectively. Staphylococcus was prevalent in 12.96% of cases, predominantly in cyanotic CHD patients (20.00%), and exhibited high sensitivity to vancomycin (96%). Other organisms, including Klebsiella (9.26%), E. coli (5.56%), and Streptococcus (5.56%), were also identified, highlighting microbial diversity in this population.*
Conclusion*: This study provides valuable insights into the microbial landscape and antibiotic resistance in CHD patients with unresolving fever, emphasizing the need for early microbiological diagnosis and targeted antibiotic therapy. The findings underscore the importance of antimicrobial stewardship and tailored treatment strategies to mitigate the burden of resistant pathogens in resource-constrained settings.*
Keywords*: Congenital Heart Disease, Unresolving Fever, Microbial Heterogeneity, Antibiotic Sensitivity, Multidrug Resistance*

I. INTRODUCTION

Congenital heart disease (CHD) is a structural abnormality of the heart and/or great vessels present at birth, making it one of the most common and potentially fatal congenital disorders. Globally, CHD affects approximately 0.8% to 1.2% of live births, underscoring its significant health burden (1). Beyond its direct impact on cardiac function, CHD often predisposes affected individuals to a range of complications, including an increased susceptibility to severe infections. Pediatric sepsis is one such critical complication, characterized by life-threatening systemic infections. It has a global incidence of 1.2 million cases annually, with reported mortality rates ranging from 1% to 5% for sepsis and from 9% to 20% for severe sepsis (2). Alarmingly, nearly half of all pediatric sepsis cases occur in children with underlying conditions such as chronic lung disease, CHD, malignancies, or neuromuscular disorders (3). The coexistence of CHD and sepsis presents a unique and significant challenge in pediatric care. Children with CHD are at heightened risk for severe infections due to a combination of physiological and immunological factors. Impaired nutrition and pulmonary congestion often associated with CHD increase vulnerability to pneumonia and other lower respiratory tract infections.

Additionally, certain genetic abnormalities or syndromes linked to CHD can lead to immunosuppression, further exacerbating the risk of infections (4). This complex interplay of factors positions children with CHD as a particularly high-risk group for infection-related complications. The microbiological landscape of pediatric sepsis further complicates the management of these cases. Blood culture positivity among pediatric sepsis suspects varies significantly across studies, with rates ranging from 22% to 35.7% (5-7). Gram-negative bacteremia is commonly observed, with pathogens such as Staphylococcus aureus, Pseudomonas, Enterobacter species, Escherichia coli, and Klebsiella frequently implicated (8). Notably, children with CHD exhibit higher rates of culture-positive sepsis, with Staphylococcus aureus emerging as the most prevalent causative organism (9). Given the unique vulnerabilities of CHD patients and the alarming trends in sepsis-related morbidity and mortality, understanding the heterogeneity of microorganisms and their antibiotic sensitivity profiles in this population is critical. This knowledge can guide the development of tailored therapeutic strategies and improve outcomes for these high-risk children.

II. METHODS

This cross-sectional study was conducted at the National Institute of Cardiovascular Disease, Bangladesh, from August 2022 to August 2023. A total of 54 patients were included in the study. The inclusion criteria encompassed all patients with congenital heart disease (CHD) admitted with fever unresponsive to conventional antibiotics, including ampicillin, gentamicin, and ceftriaxone. Patients in a post-surgical state or those who had undergone palliative procedures were excluded from the study. Eligible patients were enrolled after obtaining written informed consent from their legal guardians. Comprehensive physical examinations were performed on all participants, and blood samples were collected following standard aseptic protocols for culture and sensitivity testing. The cultures were analyzed to identify the causative microorganisms and determine their antibiotic sensitivity profiles. Data were compiled and analyzed using SPSS software to identify patterns and draw meaningful conclusions.

III. RESULTS

Table 1: Baseline data of Study Population(n=54)

Variable	Mean ± SD
Age (month)	35.32±50.67
Weight(kg)	10.68±7.24
Height (cm)	84.1±27.3
BSA(m2)	0.48±0.24
Urban area(%)	52.3%%

Data was expressed as Mean ± SD
BSA=Body surface area

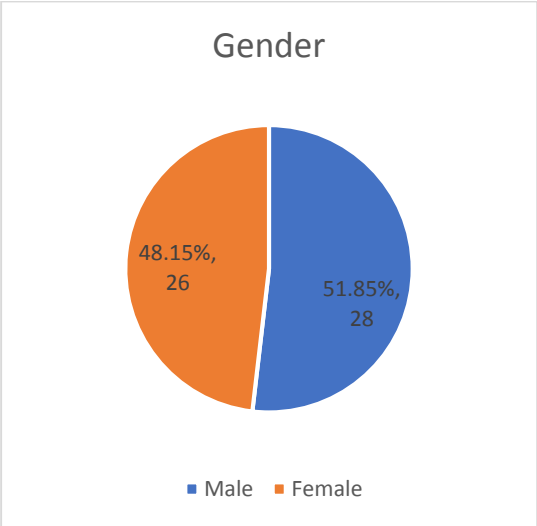

Figure 1: Gender distribution of the participants (n=54)

The gender distribution of the study participants is illustrated in Figure 1. Among the 54 participants, males constituted 51.85% (n=28), while females accounted for 48.15% (n=26). This demonstrates a nearly equal representation of genders in the study population.

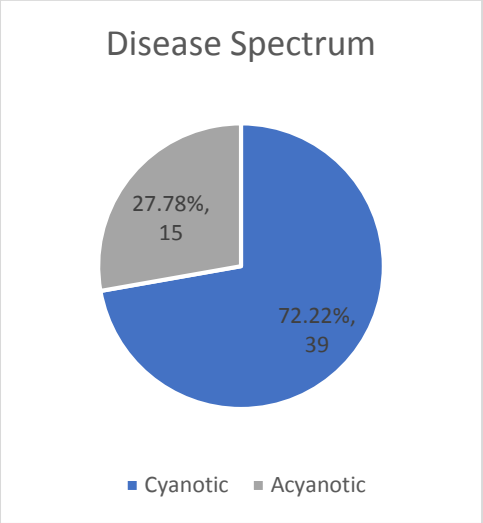

Figure 2: Spectrum of disease in study population (n=54)

The disease spectrum of the study population is depicted in Figure 2. Among the 54 participants, 72.22% (n=39) were diagnosed with cyanotic congenital heart disease, while 27.78% (n=15) had acyanotic congenital heart disease.

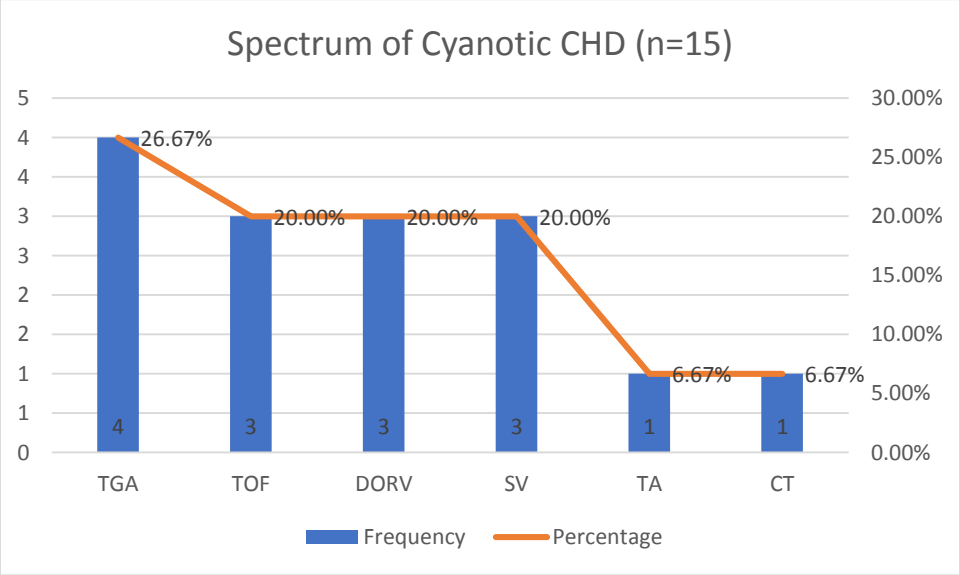

Figure 3: Spectrum of cyanotic CHD in study population (n=15)

The spectrum of cyanotic congenital heart disease (CHD) in the study population (n=15) is shown in Figure 3. The most common cyanotic CHD was transposition of the great arteries (TGA), accounting for 26.67% (n=4) of cases. Tetralogy of Fallot (TOF), double outlet right ventricle (DORV), and single ventricle (SV) were equally prevalent, each contributing 20.00% (n=3) of cases. Tricuspid atresia (TA) and common truncus (CT) were the least common, each representing 6.67% (n=1) of the cyanotic CHD spectrum.

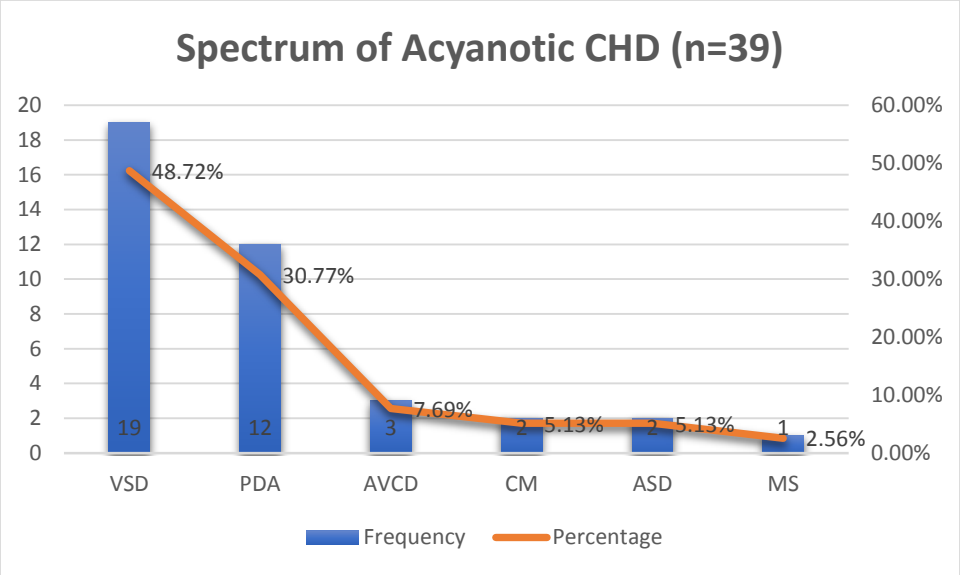

Figure 4: Spectrum of acyanotic CHD among the participants (n=39)

The spectrum of acyanotic congenital heart disease (CHD) in the study population (n=39) is illustrated in Figure 4. Ventricular septal defect (VSD) was the most prevalent acyanotic CHD, accounting for 48.72% (n=19) of cases. Patent ductus arteriosus (PDA) was the second most common, observed in 30.77% (n=12) of the participants. Atrioventricular canal defect (AVCD) accounted for 7.69% (n=3) of cases, while cardiomyopathy (CM) and atrial septal defect (ASD) were each present in 5.13% (n=2) of the participants. Mitral stenosis (MS) was the least frequent acyanotic CHD, observed in only 2.56% (n=1) of cases.

Table 2: Spectrum of blood culture organisms among participants (N=54)

Blood Culture Organisms	Cyanotic CHD (n=15)		Acyanotic CHD (n=39)		Total (N=54)	
	n	%	n	%	n	%
Acinetobacter	3	20.00%	9	23.08%	12	22.22%
Pseudomonas	2	13.33%	8	20.51%	10	18.52%
Burkholderia	3	20.00%	6	15.38%	9	16.67%
Staphylococcus	3	20.00%	4	10.26%	7	12.96%
Streptococcus	0	0.00%	3	7.69%	3	5.56%
Klebsiella	3	20.00%	2	5.13%	5	9.26%
E. Coli	1	6.67%	2	5.13%	3	5.56%
Proteus	0	0.00%	2	5.13%	2	3.70%
Enterococcus	0	0.00%	1	2.56%	1	1.85%
Candida	0	0.00%	1	2.56%	1	1.85%

The spectrum of blood culture organisms identified among participants is presented in Table 2. A total of 54 cases were analyzed, with 15 participants from the cyanotic CHD group and 39 from the acyanotic CHD group. Across both groups, Acinetobacter was the most commonly isolated organism, accounting for 22.22% (n=12) of the total cases, with a slightly higher prevalence in the acyanotic group (23.08%, n=9) compared to the cyanotic group (20.00%, n=3). Pseudomonas was the second most common organism, isolated in 18.52% (n=10) of cases, also more frequently observed in the acyanotic group (20.51%, n=8) than the cyanotic group (13.33%, n=2). Burkholderia was identified in 16.67% (n=9) of cases, with a higher prevalence in the cyanotic group (20.00%, n=3) compared to the acyanotic group (15.38%, n=6). Staphylococcus accounted for 12.96% (n=7) of the total cases, with equal prevalence (20.00%, n=3) in the cyanotic group but lower rates (10.26%, n=4) in the acyanotic group. Klebsiella was present in 9.26% (n=5) of cases, more frequently in the cyanotic group (20.00%, n=3) than the acyanotic group (5.13%, n=2). Less commonly isolated organisms included Streptococcus (5.56%, n=3), E. coli (5.56%, n=3), Proteus (3.70%, n=2), Enterococcus (1.85%, n=1), and Candida (1.85%, n=1), with most of these observed exclusively or predominantly in the acyanotic group.

Table 3: Antibiotic Sensitivity for different organisms

Name of Organism	Most Sensitive Antibiotics
Acinetobacter	Meropenem (88%), Imipenem (76%)
Streptococcus	Amoxiclav (90%), Vancomycin (80%), Linezolid (72%)
Burkholderia spp.	TZ+P (78%), Ceftazidime (56%)
Pseudomonas	TZ+P (94%), Meropenem (64%), Imipenem (60%)
Staphylococcus	Vancomycin (96%), Linezolid (80%)
Klebsiella	Amikacin (76%), Ceftazidime (58%)
E. coli	Meropenem (66%), Imipenem (66%)
Proteus	TZ+P (90%), Linezolid (90%)

TZ+P=Tazobactam + Piperacillin

The antibiotic sensitivity patterns of the isolated organisms are summarized in Table 3. Acinetobacter showed the highest sensitivity to meropenem (88%) and imipenem (76%). Streptococcus demonstrated high sensitivity to amoxiclav (90%), vancomycin (80%), and linezolid (72%). For Burkholderia spp., the most effective antibiotics were TZ+P (78%) and ceftazidime (56%). Pseudomonas exhibited the highest sensitivity to TZ+P (94%), followed by meropenem (64%) and imipenem (60%). Staphylococcus was highly sensitive to vancomycin (96%) and linezolid (80%). Klebsiella showed the greatest sensitivity to amikacin (76%) and ceftazidime (58%). Similarly, E. coli was most sensitive to meropenem and imipenem, both at 66%. Proteus exhibited the highest sensitivity to TZ+P (90%) and linezolid (90%).

IV. DISCUSSION

The present study aimed to evaluate the heterogeneity of microorganisms and their antibiotic sensitivity profiles in congenital heart disease (CHD) patients with unresolving fever, focusing on a Bangladeshi population. The findings reveal critical insights into the microbial landscape and antibiotic resistance patterns, aligning with global and regional trends observed in similar populations. The predominance of Acinetobacter (22.22%) and Pseudomonas (18.52%) as the leading pathogens underscores the significant role of Gram-negative bacteria in CHD-related infections. This observation is consistent with previous studies highlighting Acinetobacter baumannii and Pseudomonas aeruginosa as major contributors to nosocomial infections, particularly in patients with underlying comorbidities or invasive medical histories (10,11). The similarity in pathogen profiles between cyanotic and acyanotic CHD patients further emphasizes the ubiquitous nature of these microorganisms in high-risk populations. In terms of antibiotic sensitivity, the study demonstrates Acinetobacter's high susceptibility to meropenem (88%) and imipenem (76%), corroborating findings from multiple studies that identify carbapenems as highly effective against Acinetobacter baumannii (12). However, increasing resistance trends to carbapenems globally, as noted by Ahmed et al. (2015), raise concerns about the sustainability of these treatment options (11). Similarly, Pseudomonas exhibited the highest sensitivity to TZ+P (94%), followed by meropenem (64%) and imipenem (60%). These findings align with research by Sharma et al. (2024), which supports the use of TZ+P as a first-line therapy for Pseudomonas infections, especially in multidrug-resistant strains (12). The significant presence of Staphylococcus (12.96%) in this study, with a higher prevalence in cyanotic CHD cases (20.00%), underscores the clinical relevance of Gram-positive pathogens in this subgroup. The high sensitivity of Staphylococcus to vancomycin (96%) and linezolid (80%) is consistent with global data on the efficacy of these antibiotics against methicillin-resistant Staphylococcus aureus (MRSA) and other Gram-positive pathogens (13). Additionally, Streptococcus demonstrated notable sensitivity to amoxiclav (90%), vancomycin (80%), and linezolid (72%), reaffirming their role as reliable treatment options for Gram-positive infections (14). The comparative analysis of bacterial distribution and antibiotic sensitivities in CHD patients reveals similarities and disparities with studies from other regions. For example, in contrast to the predominance of Acinetobacter and Pseudomonas in this study, research conducted in tertiary care settings in India and Saudi Arabia reported higher prevalence rates of Klebsiella pneumoniae and Escherichia coli (11,13). Despite these regional variations, the common theme across studies is the emergence of multidrug-resistant organisms and the declining efficacy of older-generation antibiotics. This trend necessitates the adoption of robust antimicrobial stewardship programs and continuous monitoring of resistance patterns to guide empirical therapy. The findings of this study also highlight important public health considerations. The emergence of resistant pathogens in CHD patients with unresolving fever underscores the need for targeted interventions to mitigate nosocomial infections. Early identification of causative organisms through routine blood culture and sensitivity testing, combined with judicious use of antibiotics, is critical to optimizing patient outcomes. The integration of regional data into national antibiotic guidelines is particularly relevant in resource-limited settings like Bangladesh, where access to advanced diagnostic tools and newer antibiotics remains constrained.

Limitations of The Study

The study was conducted in a single hospital with a small sample size. So, the results may not represent the whole community.

V. CONCLUSION

This study highlights the microbial heterogeneity and antibiotic sensitivity profiles in congenital heart disease (CHD) patients with unresolving fever in a Bangladeshi cohort. The predominance of *Acinetobacter* and *Pseudomonas* as the leading pathogens, along with significant antibiotic sensitivities to meropenem, imipenem, and TZ+P, underscores the importance of early and accurate microbiological diagnosis to guide empirical therapy. The high prevalence of *Staphylococcus* in cyanotic cases and its sensitivity to vancomycin emphasizes the need for targeted treatment strategies. These findings contribute valuable insights into the local epidemiology of CHD-associated infections and reinforce the necessity for robust antimicrobial stewardship programs to combat the emergence of multidrug-resistant organisms. Further research focusing on longitudinal trends and resistance mechanisms is essential to optimize treatment outcomes in this vulnerable population.

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Ethical approval: The study was approved by the Institutional Ethics Committee

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