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Original Research

Assessment of staphylococcus aureus in the neonatal ICU

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ABSTRACT:

Background: Staphylococcus aureus infections represent a significant clinical burden for infants worldwide and were recently found to be the second most common cause of late-onset sepsis in very-low birth weight infants admitted to neonatal intensive care units. The present study was conducted to assess prevalence of staphylococcus aureus in the neonatal ICU. **Materials & Methods:** 60 neonates who developed sepsis in NICU of both genders were studied. The neonatal septicaemia was divided as early -onset sepsis and late-onset sepsis. All the blood cultures were collected from the peripheral veins. Staphylococcus aureus ATCC 27853 was included as the control strain. **Results:** Out of 60 neonates, males were 34 and females were 26. Organism isolated were staphylococcus aureus 20 in early onset sepsis and 11 in late onset sepsis, Escherichia coli 1 each in early and late onset sepsis, Pseudomonas aeruginosa 1 each in early and late onset sepsis, Klebsiella pneumoniae 6 in early onset sepsis and 2 in late onset sepsis, coagulase negative staphylococcus 8 in early onset sepsis, Citrobacter diversus 1 each in early and late onset sepsis and enterobacter cloacae 1 in early onset sepsis. The difference was significant (P< 0.05). **Conclusion:** In NICU neonates, most commonly organism isolated were staphylococcus aureus followed by Klebsiella pneumoniae, coagulase negative staphylococcus, acinetobacter cloacae.

Key words: staphylococcus aureus, Klebsiella pneumoniae, neonates

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INTRODUCTION

Staphylococcus aureus infections represent a significant clinical burden for infants worldwide and were recently found to be the second most common cause of late-onset sepsis in very-low birth weight (VLBW) infants admitted to neonatal intensive care units (NICUs) in the United States and United Kingdom.¹ Preterm infants are also at high risk for S. aureus colonization, a potential risk factor for subsequent infection.² In a recent meta-analysis involving patients admitted to NICUs and intensive care units (ICUs), methicillin-resistant S. aureus (MRSA) colonization was associated with a 24.2 times increased MRSA infection risk. Endemic transmission and outbreaks due to MRSA and methicillinsusceptible S. aureus (MSSA) occur frequently in NICUs.³

Staphylococcus aureus infections represent a significant clinical burden for infants worldwide and

were recently found to be the second most common cause of late-onset sepsis in very-low birth weight (VLBW) infants admitted to neonatal intensive care units (NICUs).⁴ The molecular characteristics of and risk factors for S. aureus colonization and infection have been described for NICU populations across the globe and have increased our knowledge of the global burden.⁵ The present study was conducted to assess prevalence of staphylococcus aureus in the neonatal ICU.

MATERIALS & METHODS

The present study consisted of 60 neonates who developed sepsis of both genders. Parents gave their written consent to participate in the study.

Data such as name, age, gender etc. was recorded. The neonatal septicaemia was divided as early -onset sepsis and late-onset sepsis. All the blood cultures were collected from the peripheral veins. 2- 3 ml of

blood was inoculated into brain-heart infusion broth and were incubated at 37°C. Subcultures were done on blood and MacConkey's agar plates on days 1,2,3,5,7 and 10. The colonies which were isolated were identified on the basis of their colony morphology,

their gram staining patterns, and their standard biochemical tests. Staphylococcus aureus ATCC 27853 was included as the control strain. Data thus obtained were subjected to statistical analysis. P value < 0.05 was considered significant.

RESULTS Table I Distribution of patients

Total- 60				
Gender	Male	Female		
Number	34	26		

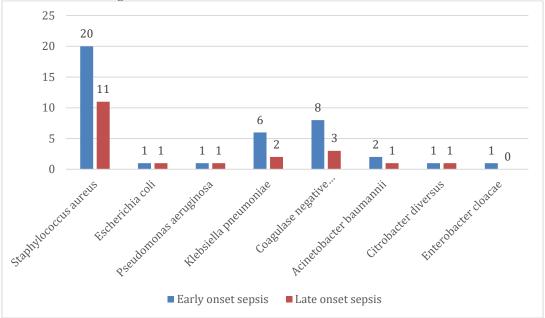
Table I shows that out of 60 neonates, males were 34 and females were 26.

Table II	Assessment of	organisms	isolated

Organism	Early onset sepsis	Late onset sepsis	P value
Staphylococcus aureus	20	11	0.05
Escherichia coli	1	1	
Pseudomonas aeruginosa	1	1	
Klebsiella pneumoniae	6	2	
Coagulase negative staphylococcus	8	3	
Acinetobacter baumannii	2	1	
Citrobacter diversus	1	1	
Enterobacter cloacae	1	0	
Total	40	20	

Table II, graph I shows that organism isolated were staphylococcus aureus 20 in early onset sepsis and 11 in late onset sepsis, Escherichia coli 1 each in early and late onset sepsis, Pseudomonas aeruginosa 1 each in early and late onset sepsis, Klebsiella pneumoniae 6 in early onset sepsis and 2 in late onset sepsis, coagulase negative staphylococcus 8 in early onset sepsis and 3 in late onset sepsis, acinetobacter baumannii 2 in early onset sepsis and 1 in late onset sepsis, Citrobacter diversus 1 each in early and late onset sepsis and enterobacter cloacae 1 in early onset sepsis. The difference was significant (P < 0.05).

Graph I Assessment of organisms isolated



DISCUSSION

The molecular characteristics of and risk factors for S. aureus colonization and infection have been described for NICU populations across the globe and have increased our knowledge of the global burden.⁶ However, the molecular characteristics of MSSA and

MRSA strains isolated from neonates in NICUs in Mainland China have been incompletely described and important gaps in knowledge remain.^{7,8} Existing studies have focused mainly on MRSA in infants or neonates, whereas little is known about MSSA colonization and infection risks.⁹ The present study was conducted to assess prevalence of staphylococcus aureus in the neonatal ICU.

We found that out of 60 neonates, males were 34 and females were 26. Huang YC et al¹⁰ reported that more than 40% of hospitalized infants were colonized with MRSA during their stay in NICUs and 93% of the colonized neonates were infected with an indistinguishable MRSA isolate.

We found that organism isolated were staphylococcus aureus 20 in early onset sepsis and 11 in late onset sepsis, Escherichia coli 1 each in early and late onset sepsis, Pseudomonas aeruginosa 1 each in early and late onset sepsis, Klebsiella pneumoniae 6 in early onset sepsis and 2 in late onset sepsis, coagulase negative staphylococcus 8 in early onset sepsis and 3 in late onset sepsis, acinetobacter baumannii 2 in early onset sepsis and 1 in late onset sepsis, Citrobacter diversus 1 each in early and late onset sepsis and enterobacter cloacae 1 in early onset sepsis. Karthikeyan et al¹¹ included 96 consecutive inborn neonates with blood culture proven bacterial sepsis. Lethargy with refusal of feeds (28%), fever (28%) and respiratory distress (31.3%) were the major presenting features. Half of them (n=48) were of early onset (<48 hours) and the remaining half were of late onset (> 48 hours). Staphylococcus aureus (n=59, 61.5%) was the predominant pathogen and 66% of them were methicillin resistant followed by Klebsiella pnemoniae (n=24, 21.9), Escherichia coli (n=13, 13.5%) and streptococci (n=3, 3.1%). Antibiotic resistance was common, with the sensitivity to various antibiotics being ampicillin 19%, gentamicin 21.6%, cefotaxime 32.8%, amikacin 50%, chloromycetin 59.6% and ciprofloxacin 90.3%.

Sharma et al¹² studied 311 newborns admitted in an NICU with sepsis. The isolates were identified by doing standard biochemical tests. A total of 131 organisms were isolated from the 311 blood cultures. These included Staphylococcus aureus (n=68), Coagulase Negative Staphylococcus (CoNS) (n=30), Klebsiella pneumoniae (n=10), Acinetobacter baumannii (n=9), Escherichia coli (n=05), Enterobacter cloacae (n=04), Citrobacter diversus (n=02), Pseudomonas aeruginosa (n=02) and Candida (n=01). Staphylococcus aureus was the main pathogen in both early and late-onset sepsis. On antibiotic sensitivity testing, 57.35% of the Staphylococcus aureus isolates were found to be methicillin resistant. More than 90% gram negative rods were resistant to amikacin.

The limitation the study is small sample size.

CONCLUSION

Authors found that in NICU neonates, most commonly organism isolated were staphylococcus aureus followed by Klebsiella pneumoniae, coagulase negative staphylococcus, acinetobacter baumannii, Escherichia coli, Pseudomonas aeruginosa, Citrobacter diversus and enterobacter cloacae.

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