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Sepsis prevention in neonates in Zambia study: Impact of an infection prevention bundle on neonatal sepsis and mortality

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Background: Sepsis is a major cause of mortality in neonates in sub-Saharan Africa. Bloodstream infections (BSIs), the most common hospital-associated infections in neonates, occur more frequently in resource-limited countries than in industrialized countries and contribute to many in-hospital neonatal deaths. We assessed the efficacy of a novel bundle of low-cost infection prevention and control (IPC) measures targeted to known and suspected risk factors for neonatal hospital-associated BSI. We studied the impact of this intervention bundle on BSI and mortality in a neonatal intensive care unit (NICU) at the University Teaching Hospital (UTH) in Lusaka, Zambia.

Methods & Materials: This prospective observational cohort study of neonates who survived > 3 days after NICU admission consisted of a six-month baseline period ("baseline"), two months during which interventions were introduced ("implementation"), and 10 months of intervention assessment ("intervention"). The intervention bundle consisted of IPC training, introduction of alcohol-based hand wash, weekly bathing of neonates > 1.5 kg with 2% chlorhexidine, targeted environmental cleaning, and SMS reminders of IPC messages. The outcomes were all-cause neonatal mortality (primary) and suspected sepsis and laboratory-confirmed BSIs (secondary).

Results: From September 2015 through March 2017, we enrolled 2669 eligible neonates. Median maternal age, maternal HIV status, and newborn characteristics were similar in the baseline, implementation, and intervention periods (with the exception of birth weight). Half of neonates had one or more episodes of sepsis, including 549 (41%) who had a positive blood culture. *Klebsiella pneumoniae*, predominantly ESBL-producing, was most common (n = 289, 70%); possible contaminants were isolated in most other positive cultures (n = 140, 25.5%). All-cause neonatal mortality was lower during the intervention (18.0%) than the baseline period (23.6%), and similar reductions in mortality were seen in all birth-weight categories. The incidence density rates for suspected sepsis and BSI with a pathogen were significantly lower in the intervention relative to baseline periods for all birth weight categories, except babies weighing < 1 kg.



Conclusion: This bundle of infection prevention measures resulted in reductions in all-cause neonatal mortality, suspected sepsis, and BSI with pathogens. This combination of low-cost measures has potential to be applied in other contexts where hospital-associated sepsis is a major contributor to neonatal mortality.

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Genotyping and Sero-Virological characterization of Hepatitis B Virus in blood donors, Southern Ethiopia

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Background: Hepatitis B virus (HBV) prevalence is highest in Sub-Saharan Africa including Ethiopia. HBV genotypes have distinct geographic distributions, also play a role in course of infection and treatment management. However, in Ethiopia there is paucity of information about distribution of HBV genotypes. This study was done to determine genotype, mutation and sero-virological profiles of HBV isolates in Southern Ethiopia.

Methods & Materials: Cross-sectional study was conducted on a total of 103 HBsAg sero-positive samples collected from blood donors visiting Hawassa Blood Bank in May to September 2016. HBV serological markers and biochemical assays were done. Serum viral load was measured using quantitative real-time PCR. Partial HBV S-gene was amplified with nested PCR and sequenced. Bioinformatics tools were utilized to determine genotypes, serotypes and presence of mutations.

Results: Of 103 HBsAg reactive serum samples, HBeAg (14.6%) and HBeAb (70.9%) were detected. The median serum ALT was 21(17–29) IU/L. Ninety-eight samples gave detectable viral load with a median of 3.46 (2.62–4.82) log IU/ml. Eighty five isolates were successfully amplified, sequenced and genotyped into 58 (68.2%) genotype A (HBV/A) and 27 (31.8%) genotype D (HBV/D). HBV serotypes found were *adw2* (74.1%), *ayw2* (24.7%), and *ayw3* (1.2%). In twenty-four (28.2%) samples mutations in the major hydrophilic region (MHR) were observed. Donors infected with HBV/A had higher viral load and more frequent MHR mutation than those infected with HBV/D.

Conclusion: This study illustrated distribution of HBV genotype A and D among blood donors in southern Ethiopia. It also demonstrated occurrence HBV variants that may influence clinical aspects of HBV infection. The study contributes in narrowing the existing gap of HBV molecular study in Ethiopia.

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